

**SMARCA5 Rabbit mAb**  
**Catalog # AP76102****Specification**

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**SMARCA5 Rabbit mAb - Product Information**

|                   |                        |
|-------------------|------------------------|
| Application       | WB, ICC                |
| Primary Accession | <a href="#">O60264</a> |
| Reactivity        | Human, Mouse, Rat      |
| Host              | Rabbit                 |
| Clonality         | Monoclonal Antibody    |
| Calculated MW     | 121905                 |

**SMARCA5 Rabbit mAb - Additional Information****Gene ID** 8467**Other Names**  
SMARCA5**Dilution**  
WB~~1/500-1/1000  
ICC~~N/A**Format**  
Liquid**SMARCA5 Rabbit mAb - Protein Information****Name** SMARCA5 ([HGNC:11101](#))**Function**

ATPase that possesses intrinsic ATP-dependent nucleosome- remodeling activity (PubMed:<a href="http://www.uniprot.org/citations/12972596" target="\_blank">12972596</a>, PubMed:<a href="http://www.uniprot.org/citations/28801535" target="\_blank">28801535</a>). Catalytic subunit of ISWI chromatin-remodeling complexes, which form ordered nucleosome arrays on chromatin and facilitate access to DNA during DNA- templated processes such as DNA replication, transcription, and repair; this may require intact histone H4 tails (PubMed:<a href="http://www.uniprot.org/citations/10880450" target="\_blank">10880450</a>, PubMed:<a href="http://www.uniprot.org/citations/12198550" target="\_blank">12198550</a>, PubMed:<a href="http://www.uniprot.org/citations/12434153" target="\_blank">12434153</a>, PubMed:<a href="http://www.uniprot.org/citations/12972596" target="\_blank">12972596</a>, PubMed:<a href="http://www.uniprot.org/citations/23911928" target="\_blank">23911928</a>, PubMed:<a href="http://www.uniprot.org/citations/28801535" target="\_blank">28801535</a>). Within the ISWI chromatin-remodeling complexes, slides edge- and center-positioned histone octamers away from their original location on the DNA template (PubMed:<a href="http://www.uniprot.org/citations/28801535" target="\_blank">28801535</a>). Catalytic activity and histone octamer sliding propensity is regulated and determined by components of the ISWI chromatin-remodeling complexes (PubMed:<a

[28801535](http://www.uniprot.org/citations/28801535)). The BAZ1A/ACF1-, BAZ1B/WSTF-, BAZ2A/TIP5- and BAZ2B- containing ISWI chromatin-remodeling complexes regulate the spacing of nucleosomes along the chromatin and have the ability to slide mononucleosomes to the center of a DNA template in an ATP-dependent manner (PubMed:[14759371](http://www.uniprot.org/citations/14759371), PubMed:[15543136](http://www.uniprot.org/citations/15543136), PubMed:[28801535](http://www.uniprot.org/citations/28801535)). The CECR2- and RSF1-containing ISWI chromatin-remodeling complexes do not have the ability to slide mononucleosomes to the center of a DNA template (PubMed:[28801535](http://www.uniprot.org/citations/28801535)). Binds to core histones together with RSF1, and is required for the assembly of regular nucleosome arrays by the RSF-5 ISWI chromatin-remodeling complex (PubMed:[12972596](http://www.uniprot.org/citations/12972596)). Involved in DNA replication and together with BAZ1A/ACF1 is required for replication of pericentric heterochromatin in S-phase (PubMed:[12434153](http://www.uniprot.org/citations/12434153)). Probably plays a role in repression of RNA polymerase I dependent transcription of the rDNA locus, through the recruitment of the SIN3/HDAC1 corepressor complex to the rDNA promoter (By similarity). Essential component of the WICH-5 ISWI chromatin- remodeling complex (also called the WICH complex), a chromatin- remodeling complex that mobilizes nucleosomes and reconfigures irregular chromatin to a regular nucleosomal array structure (PubMed:[11980720](http://www.uniprot.org/citations/11980720), PubMed:[15543136](http://www.uniprot.org/citations/15543136)). The WICH-5 ISWI chromatin- remodeling complex regulates the transcription of various genes, has a role in RNA polymerase I transcription (By similarity). Within the B- WICH complex has a role in RNA polymerase III transcription (PubMed:[16603771](http://www.uniprot.org/citations/16603771)). Mediates the histone H2AX phosphorylation at 'Tyr- 142', and is involved in the maintenance of chromatin structures during DNA replication processes (By similarity). Essential component of NoRC- 5 ISWI chromatin-remodeling complex, a complex that mediates silencing of a fraction of rDNA by recruiting histone-modifying enzymes and DNA methyltransferases, leading to heterochromatin formation and transcriptional silencing (By similarity).

#### Cellular Location

Nucleus {ECO:0000255|PROSITE-ProRule:PRU00624, ECO:0000269|PubMed:12434153, ECO:0000269|PubMed:12972596, ECO:0000269|PubMed:15543136, ECO:0000269|PubMed:33092197}. Chromosome Note=Localizes to mitotic chromosomes (PubMed:12972596). Co-localizes with RSF1 in the nucleus (PubMed:12972596). Co-localizes with PCNA at replication foci during S phase (PubMed:15543136). Co-localizes with BAZ1B/WSTF at replication foci during late-S phase (PubMed:15543136) Recruited to DNA damage sites following interaction with SIRT6 (PubMed:23911928).

#### Tissue Location

Ubiquitously expressed.

#### SMARCA5 Rabbit mAb - Protocols

Provided below are standard protocols that you may find useful for product applications.

- [Western Blot](#)
- [Blocking Peptides](#)
- [Dot Blot](#)
- [Immunohistochemistry](#)
- [Immunofluorescence](#)
- [Immunoprecipitation](#)
- [Flow Cytometry](#)

- [Cell Culture](#)

## SMARCA5 Rabbit mAb - Images

