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SMC1A Antibody (N-term)

Affinity Purified Rabbit Polyclonal Antibody (Pab)
Catalog # AP13544a

Product Information

Application	WB, E
Primary Accession	Q14683
Other Accession	Q9CU62, O97593, NP_006297.2
Reactivity	Human
Predicted	Bovine, Mouse, Rat, Canine, Rabbit, Chicken
Host	Rabbit
Clonality	Polyclonal
Isotype	Rabbit IgG
Clone Names	RB33672
Calculated MW	143233
Antigen Region	307-336

Additional Information

Gene ID	8243
Other Names	Structural maintenance of chromosomes protein 1A, SMC protein 1A, SMC-1-alpha, SMC-1A, Sb18, SMC1A, DXS423E, KIAA0178, SB18, SMC1, SMC1L1
Target/Specificity	This SMC1A antibody is generated from rabbits immunized with a KLH conjugated synthetic peptide between 307-336 amino acids from the N-terminal region of human SMC1A.
Dilution	WB~~1:1000 E~~Use at an assay dependent concentration.
Format	Purified polyclonal antibody supplied in PBS with 0.05% (V/V) Proclin 300. This antibody is purified through a protein A column, followed by peptide affinity purification.
Storage	Maintain refrigerated at 2-8°C for up to 2 weeks. For long term storage store at -20°C in small aliquots to prevent freeze-thaw cycles.
Precautions	SMC1A Antibody (N-term) is for research use only and not for use in diagnostic or therapeutic procedures.

Protein Information

Name	SMC1A
Synonyms	DXS423E, KIAA0178, SB1.8, SMC1, SMC1L1

Function	Involved in chromosome cohesion during cell cycle and in DNA repair. Central component of cohesin complex. The cohesin complex is required for the cohesion of sister chromatids after DNA replication. The cohesin complex apparently forms a large proteinaceous ring within which sister chromatids can be trapped. At anaphase, the complex is cleaved and dissociates from chromatin, allowing sister chromatids to segregate. The cohesin complex may also play a role in spindle pole assembly during mitosis. Involved in DNA repair via its interaction with BRCA1 and its related phosphorylation by ATM, or via its phosphorylation by ATR. Works as a downstream effector both in the ATM/NBS1 branch and in the ATR/MSH2 branch of S-phase checkpoint.
Cellular Location	Nucleus. Chromosome. Chromosome, centromere, kinetochore. Note=Associates with chromatin. Before prophase it is scattered along chromosome arms. During prophase, most of cohesin complexes dissociate from chromatin probably because of phosphorylation by PLK, except at centromeres, where cohesin complexes remain. At anaphase, the RAD21 subunit of the cohesin complex is cleaved, leading to the dissociation of the complex from chromosomes, allowing chromosome separation. In germ cells, cohesin complex dissociates from chromatin at prophase I, and may be replaced by a meiosis-specific cohesin complex. The phosphorylated form on Ser-957 and Ser-966 associates with chromatin during G1/S/G2 phases but not during M phase, suggesting that phosphorylation does not regulate cohesin function. Integral component of the functional centromere-kinetochore complex at the kinetochore region during mitosis

Background

Proper cohesion of sister chromatids is a prerequisite for the correct segregation of chromosomes during cell division. The cohesin multiprotein complex is required for sister chromatid cohesion. This complex is composed partly of two structural maintenance of chromosomes (SMC) proteins, SMC3 and either SMC1L2 or the protein encoded by this gene. Most of the cohesin complexes dissociate from the chromosomes before mitosis, although those complexes at the kinetochore remain. Therefore, the encoded protein is thought to be an important part of functional kinetochores. In addition, this protein interacts with BRCA1 and is phosphorylated by ATM, indicating a potential role for this protein in DNA repair. This gene, which belongs to the SMC gene family, is located in an area of the X-chromosome that escapes X inactivation. [provided by RefSeq].

References

Limongelli, G., et al. Am. J. Med. Genet. A 152A (8), 2127-2129 (2010) :
Homme, C., et al. Oncol. Rep. 24(1):47-56(2010)
Pie, J., et al. Am. J. Med. Genet. A 152A (4), 924-929 (2010) :
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Liu, J., et al. Hum. Mutat. 30(11):1535-1542(2009)

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