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| **Product name:** | MAD2 Rabbit Polyclonal Antibody |
| **Cat number:** | ABN13553 |
| **Conjugate:** | Unconjugated |
| **Size:** | 100µL |
| **Clone:** | Polyclonal |
| **Concentration:** | 1mg/ml |
| **Host:** | Rabbit |
| **Isotype:** | IgG |
| **Immunogen:** | The antiserum was produced against synthesized peptide derived from human MAD2L1. AA range:91-140 |
| **Reactivity:** | Human,Rat,Mouse |
| **Applications:** | WB 1:500-1:2000,ELISA 1:5000-1:10000,IP 1:200-1:500 |
| **Molecular Weight:** | 25kDa |
| **Purification:** | Affinity purification |
| **Form:** | Liquid |
| **Buffer:** | Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% New type preservative N. |
| **Storage:** | Store at 4°C short term. Aliquot and store at -20°C for 12 months. Avoid freeze/thaw cycles. |

**Background:**

MAD2L1 is a component of the mitotic spindle assembly checkpoint that prevents the onset of anaphase until all chromosomes are properly aligned at the metaphase plate. MAD2L1 is related to the MAD2L2 gene located on chromosome 1. A MAD2 pseudogene has been mapped to chromosome 14. [provided by RefSeq, Jul 2008],domain:The protein has two highly different native conformations, an inactive open conformation that cannot bind CDC20 and that predominates in cytosolic monomers, and an active closed conformation. The protein in the closed conformation preferentially dimerizes with another molecule in the open conformation, but can also form a dimer with a molecule in the closed conformation. Formation of a heterotetrameric core complex containing two molecules of MAD1L1 and of MAD2L1 in the closed conformation promotes binding of another molecule of MAD2L1 in the open conformation and the conversion of the open to the closed form, and thereby promotes interaction with CDC20.,function:Component of the spindle-assembly checkpoint that prevents the onset of anaphase until all chromosomes are properly aligned at the metaphase plate. Required for the execution of the mitotic checkpoint which monitors the process of kinetochore-spindle attachment and inhibits the activity of the anaphase promoting complex by sequestering CDC20 until all chromosomes are aligned at the metaphase plate.,PTM:Phosphorylated on multiple serine residues. The level of phosphorylation varies during the cell cycle and is highest during mitosis. Phosphorylation abolishes interaction with MAD1L1 and reduces interaction with CDC20.,similarity:Belongs to the MAD2 family.,similarity:Contains 1 HORMA domain.,subcellular location:Recruited by MAD1L1 to unattached kinetochores (Probable). Recruited to the nuclear pore complex by TPR during interphase.,subunit:Monomer and homodimer. Heterotetramer with MAD1L1. Formation of a heterotetrameric core complex containing two molecules each of MAD1L1 and of MAD2L1 promotes binding of another molecule of MAD2L1 to each MAD2L1, resulting in a heterohexamer. Interacts with CDC20, MAD2L1BP and with ADAM17/TACE. Dimeric MAD2L1 in the closed conformation interacts with CDC20. Monomeric MAD2L1 in the open conformation does not interact with CDC20. CDC20 competes with MAD1L1 for MAD2L1 binding. Interacts with TPR.,