

## MAD2 Rabbit pAb

CatalogNo: YT2618

Orthogonal Validated Comparable Abs 

### Key Features

#### Host Species

- Rabbit

#### Reactivity

- Human, Mouse

#### Applications

- WB, IP, ELISA

#### MW

- 25kD (Observed)

#### Isotype

- IgG

### Recommended Dilution Ratios

**WB 1:500-1:2000****IP 1:200-500****ELISA 1:5000****Not yet tested in other applications.**

### Storage

**Storage\*** -15°C to -25°C/1 year (Do not lower than -25°C)**Formulation** Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.

### Basic Information

**Clonality** Polyclonal

### Immunogen Information

**Immunogen** The antiserum was produced against synthesized peptide derived from human MAD2L1. AA range:91-140**Specificity** MAD2 Polyclonal Antibody detects endogenous levels of MAD2 protein.

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## | Target Information

**Gene name** MAD2L1

**Protein Name** Mitotic spindle assembly checkpoint protein MAD2A

Organism	Gene ID	UniProt ID
Human	<a href="#">4085</a> ;	<a href="#">Q13257</a> ;
Mouse		<a href="#">Q9Z1B5</a> ;

**Cellular Localization**

Nucleus . Chromosome, centromere, kinetochore. Cytoplasm . Cytoplasm, cytoskeleton, spindle pole. Recruited by MAD1L1 to unattached kinetochores (Probable). Recruited to the nuclear pore complex by TPR during interphase. Recruited to kinetochores in late prometaphase after BUB1, CENPF, BUB1B and CENPE. Kinetochore association requires the presence of NEK2. Kinetochore association is repressed by UBD. Sequestered to the cytoplasm upon interaction with isoform 3 of MAD1L1 (PubMed:19010891). .

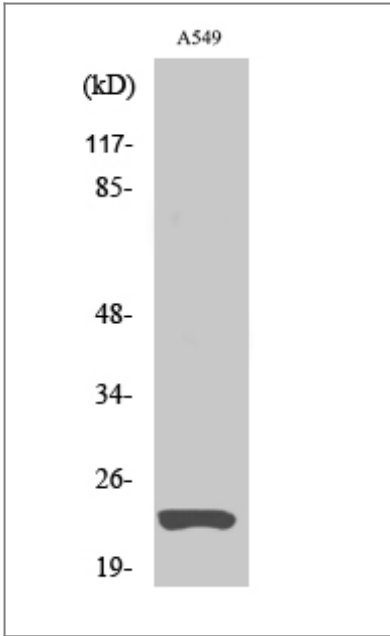
**Tissue specificity** Bone marrow,Brain,Hepatoma,Lung,Muscle,Testis,

**Function**

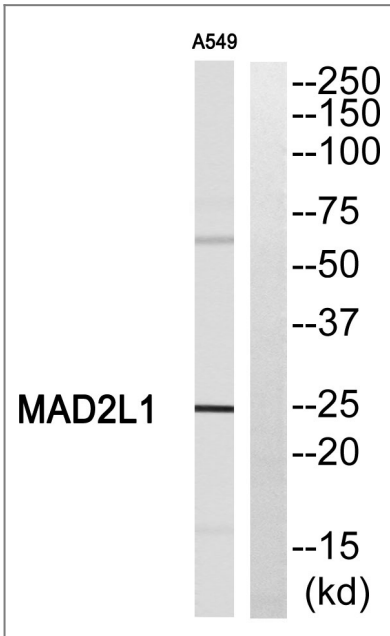
Domain:The protein has two highly different native conformations, an inactive open conformation that cannot bind CDC20 and that predominates in cytosolic monomers, and an active closed conformation. The protein in the closed conformation preferentially dimerizes with another molecule in the open conformation, 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.,

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## | Validation Data



Western Blot analysis of A549 cells using MAD2 Polyclonal Antibody diluted at 1:1000



Western blot analysis of MAD2L1 Antibody. The lane on the right is blocked with the MAD2L1 peptide.

## Contact information

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