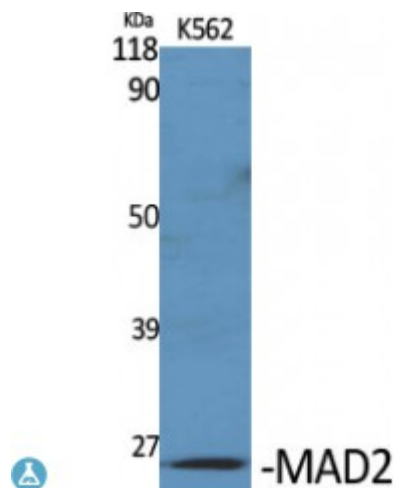


## Anti-MAD2 antibody



<b>Description</b>	Rabbit polyclonal to MAD2.
<b>Model</b>	STJ93983
<b>Host</b>	Rabbit
<b>Reactivity</b>	Human
<b>Applications</b>	ELISA, WB
<b>Immunogen</b>	Synthesized peptide derived from human MAD2
<b>Immunogen Region</b>	60-140 aa, Internal
<b>Gene ID</b>	<a href="#">4085</a>
<b>Gene Symbol</b>	<a href="#">MAD2L1</a>
<b>Dilution range</b>	WB 1:500-1:2000ELISA 1:5000
<b>Specificity</b>	MAD2 Polyclonal Antibody detects endogenous levels of MAD2 protein.
<b>Purification</b>	The antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific immunogen.
<b>Note</b>	For Research Use Only (RUO).
<b>Protein Name</b>	Mitotic spindle assembly checkpoint protein MAD2A HsMAD2 Mitotic arrest deficient 2-like protein 1 MAD2-like protein 1
<b>Molecular Weight</b>	25 kDa
<b>Clonality</b>	Polyclonal
<b>Conjugation</b>	Unconjugated

<b>Isotype</b>	IgG
<b>Formulation</b>	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.
<b>Concentration</b>	1 mg/ml
<b>Storage Instruction</b>	Store at -20°C, and avoid repeat freeze-thaw cycles.
<b>Database Links</b>	<a href="https://www.ncbi.nlm.nih.gov/condensedbook/condensedbook.cgi?acc=HGNC:6763OMIM:601467">HGNC:6763OMIM:601467</a>
<b>Alternative Names</b>	Mitotic spindle assembly checkpoint protein MAD2A HsMAD2 Mitotic arrest deficient 2-like protein 1 MAD2-like protein 1
<b>Function</b>	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.
<b>Sequence and Domain Family</b>	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.
<b>Cellular Localization</b>	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.
<b>Post-translational Modifications</b>	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. Phosphorylated by NEK2.