

MAD2L1 Protein, Human, Recombinant (His)

General Information

Synonyms:	MAD2 mitotic arrest deficient-like 1 (yeast);HSMAD2;MAD2
Protein Construction:	A DNA sequence encoding the human MAD2L1 (Q13257) (Met 1-Asp 205) was expressed, with a polyhistidine tag at the N-terminus. Predicted N terminal: Met
Species:	Human
Expression Host:	E. coli
Accession:	Q13257
Molecular Weight:	25.6 kDa (predicted); 28 kDa (reducing conditions)

QC Testing

Biological Activity:	Activity testing is in progress. It is theoretically active, but we cannot guarantee it. If you require protein activity, we recommend choosing the eukaryotic expression version first.
Purity:	> 96 % as determined by SDS-PAGE
Endotoxin:	Please contact us for more information.
Formulation:	Supplied as sterile PBS, 20% glycerol, pH 7.4.

Preparation and Storage

Reconstitution:

A Certificate of Analysis (CoA) containing reconstitution instructions is included with the products. Please refer to the CoA for detailed information.

Stability & Storage:

It is recommended to store the product under sterile conditions at -20°C to -80°C. Samples are stable for up to 12 months. Please avoid multiple freeze-thaw cycles and store products in aliquots.

Actual storage temperature shall be subject to the COA.

Shipping:

Proteins are shipped with blue ice.

Protein Background

Mitotic spindle assembly checkpoint protein MAD2A, also known as HsMAD2, Mitotic arrest deficient 2-like protein 1, MAD2-like protein 1, MAD2L1, and MAD2, is a nucleus and cytoplasm protein that belongs to the MAD2 family. MAD2L1 is a component of the spindle assembly checkpoint that prevents the onset of anaphase until all chromosomes are properly aligned at the metaphase plate. MAD2L1 is 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 CDC2 until all chromosomes are aligned at the metaphase plate. MAD2L1 has two highly different native conformations, an inactive open conformation that cannot bind CDC2 and that predominates in cytosolic monomers, and an active closed conformation. MAD2L1 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 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 CDC2.

Reference

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Sironi L., et al., 2002, EMBO J. 21:2496-2506.
Mapelli M., et al., 2007, Cell 131:730-743.
Ho C.-Y., et al., 2008, J. Cell. Biochem. 105:835-846.
Skinner J.J., et al., 2008, J. Cell Biol. 183:761-768.

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