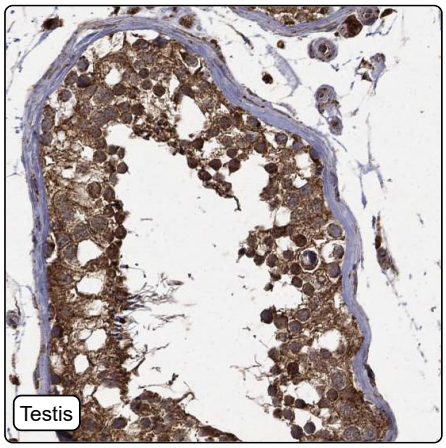
CPTC-MAP2K1-2 (CAB080093)

Uniprot ID: Q02750
Protein name: MP2K1_HUMAN
Full name: Dual specificity mitogen-activated protein kinase kinase 1
Tissue specificity: Widely expressed, with extremely low levels in brain.
Function: Dual specificity protein kinase which acts as an essential component of the MAP kinase signal transduction pathway. Binding of extracellular ligands such as growth factors, cytokines and hormones to their cell-surface receptors activates RAS and this initiates RAF1 activation. RAF1 then further activates the dual-specificity protein kinases MAP2K1/MEK1 and MAP2K2/MEK2. Both MAP2K1/MEK1 and MAP2K2/MEK2 function specifically in the MAPK/ERK cascade, and catalyze the concomitant phosphorylation of a threonine and a tyrosine residue in a Thr-Glu-Tyr sequence located in the extracellular signal-regulated kinases MAPK3/ERK1 and MAPK1/ERK2, leading to their activation and further transduction of the signal within the MAPK/ERK cascade. Activates BRAF in a KSR1 or KSR2-dependent manner; by binding to KSR1 or KSR2 releases the inhibitory intramolecular interaction between KSR1 or KSR2 protein kinase and N-terminal domains which promotes KSR1 or KSR2-BRAF dimerization and BRAF activation (PubMed:29433126). Depending on the cellular context, this pathway mediates diverse biological functions such as cell growth, adhesion, survival and differentiation, predominantly through the regulation of transcription, metabolism and cytoskeletal rearrangements. One target of the MAPK/ERK cascade is peroxisome proliferator-activated receptor gamma (PPARG), a nuclear receptor that promotes differentiation and apoptosis. MAP2K1/MEK1 has been shown to export PPARG from the nucleus. The MAPK/ERK cascade is also involved in the regulation of endosomal dynamics, including lysosome processing and endosome cycling through the perinuclear recycling compartment (PNRC), as well as in the fragmentation of the Golgi apparatus during mitosis.
Subcellular location:
Cytoplasm > Cytoskeleton > Microtubule organizing center > Centrosome (*experimental evidence*)
Cytoplasm > Cytoskeleton > Microtubule organizing center > Spindle pole body (*experimental evidence*)
Cytoplasm (*experimental evidence*)
Nucleus (*experimental evidence*)
Membrane (*experimental evidence*) (Topo: Peripheral membrane protein (*experimental evidence*))
NOTE: Localizes at centrosomes during prometaphase, midzone during anaphase and midbody during telophase/cytokinesis (PubMed:14737111). Membrane localization is probably regulated by its interaction with KSR1 (PubMed:10409742).
Protein existence: Experimental evidence at protein level

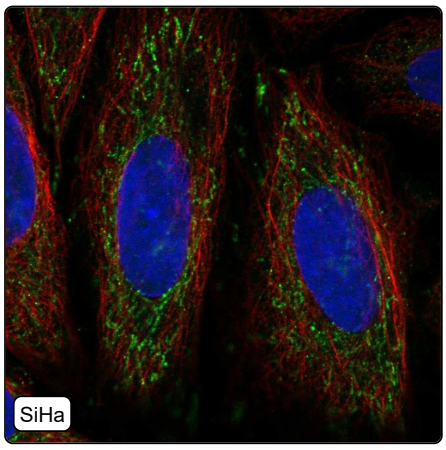
Comment:

Immunohistochemistry



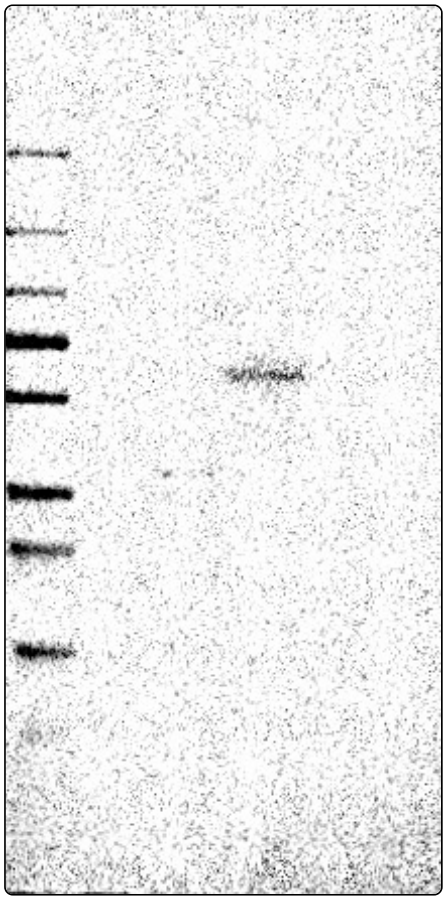
IHC protocol:	HIER pH6, Dilution 1:1100
IHC test staining:	Cytoplasmic positivity in most tissues.
Literature conformance:	Partly consistent with extensive gene/protein characterization data
Literature significance:	
RNA similarity:	Medium consistency between antibody staining and RNA expression data
RNA tissue specificity:	Low tissue specificity
RNA tissue distribution:	Detected in all
IHC Sibling similarity:	Other antibody shows similar IHC staining pattern

Immunofluorescence



IF Overlay:	antibody (green), anti-tubulin (red) and DAPI (blue)
IF main location:	Mitochondria - 5: **Approved** (auto)
IF additional location:	Cytosol - 3: **Supportive** (auto)
IF approved for publication on HPA:	No
IF in SiHa:	Mitochondria
IF in SK-MEL-30:	Mitochondria
IF in U-2 OS:	Cytosol

Western blot



WB Size markers (kDa):	250, 130, 100, 70, 55, 35, 25, 15, 10
WB Lanes:	Marker (1), RT4 (2), U-251 MG (3), Plasma (4), Liver (5), Tonsil (6)
WB Target weight (kDa):	24, 43
WB Validation:	Uncertain (Single band differing more than +/-20% from predicted size in kDa and not supported by experimental and/or bioinformatic data.)