

# CPTC-NUMA1-1 (CAB079951)

**Uniprot ID:** Q14980

**Protein name:** NUMA1\_HUMAN

**Full name:** Nuclear mitotic apparatus protein 1

**Function:** Microtubule (MT)-binding protein that plays a role in the formation and maintenance of the spindle poles and the alignment and the segregation of chromosomes during mitotic cell division (PubMed:7769006, PubMed:17172455, PubMed:19255246, PubMed:24996901, PubMed:26195665, PubMed:27462074). Functions to tether the minus ends of MTs at the spindle poles, which is critical for the establishment and maintenance of the spindle poles (PubMed:12445386, PubMed:11956313). Plays a role in the establishment of the mitotic spindle orientation during metaphase and elongation during anaphase in a dynein-dynactin-dependent manner (PubMed:23870127, PubMed:24109598, PubMed:24996901, PubMed:26765568). In metaphase, part of a ternary complex composed of GPM2 and G(i) alpha proteins, that regulates the recruitment and anchorage of the dynein-dynactin complex in the mitotic cell cortex regions situated above the two spindle poles, and hence regulates the correct orientation of the mitotic spindle (PubMed:23027904, PubMed:22327364, PubMed:23921553). During anaphase, mediates the recruitment and accumulation of the dynein-dynactin complex at the cell membrane of the polar cortical region through direct association with phosphatidylinositol 4,5-bisphosphate (PI(4,5)P2), and hence participates in the regulation of the spindle elongation and chromosome segregation (PubMed:22327364, PubMed:23921553, PubMed:24996901, PubMed:24371089). Binds also to other polyanionic phosphoinositides, such as phosphatidylinositol 3-phosphate (PIP), lysophosphatidic acid (LPA) and phosphatidylinositol triphosphate (PIP3), in vitro (PubMed:24996901, PubMed:24371089). Also required for proper orientation of the mitotic spindle during asymmetric cell divisions (PubMed:21816348). Plays a role in mitotic MT aster assembly (PubMed:11163243, PubMed:11229403, PubMed:12445386). Involved in anastral spindle assembly (PubMed:25657325). Positively regulates TNKS protein localization to spindle poles in mitosis (PubMed:16076287). Highly abundant component of the nuclear matrix where it may serve a non-mitotic structural role, occupies the majority of the nuclear volume (PubMed:10075938). Required for epidermal differentiation and hair follicle morphogenesis (By similarity).

**Subcellular location:**

**Unnamed:**

Nucleus (*experimental evidence*)

Nucleus > Nucleoplasm (*experimental evidence*)

Nucleus matrix (*experimental evidence*)

Chromosome (*experimental evidence*)

Cytoplasm > Cytoskeleton (*experimental evidence*)

Cytoplasm > Cytoskeleton > Microtubule organizing center > Centrosome (*experimental evidence*)

Cytoplasm > Cytoskeleton > Spindle pole (*experimental evidence*)

Cytoplasm > Cell cortex (*experimental evidence*)

Cell membrane (*experimental evidence*) (Topo: Lipid-anchor (*experimental evidence*); Orientation: Cytoplasmic side (*experimental evidence*))

Lateral cell membrane (*by similarity*)

**NOTE:** Mitotic cell cycle-dependent shuttling protein that relocalizes from the interphase nucleus to the spindle poles and cell cortex (PubMed:1541636, PubMed:10811826). The localization to the spindle poles is regulated by AAS (PubMed:26246606). In interphase, resides in the nuclear matrix (PubMed:1541630, PubMed:1541636, PubMed:23921553). In prophase, restricted to the interchromatin or condensed chromosome space (PubMed:10811826). In prometaphase, after nuclear envelope disassembly, forms aggregates both in the spindle midzone and at duplicated centrosomes and astral microtubules (MTs) of the bipolar spindle apparatus (PubMed:10811826). Translocates from the spindle midzone towards the spindle poles along spindle fibers in a MT- and dynein-dynactin-dependent manner until the anaphase onset (PubMed:1541636, PubMed:10811826). In metaphase, recruited to the polar cortical region in a GPM2- and GNAI1-dependent manner (PubMed:23870127, PubMed:24109598, PubMed:24996901). Excluded from the metaphase equatorial cortical region in a RanGTP-dependent manner (PubMed:22327364, PubMed:23870127). Phosphorylation on Thr-2055 by CDK1 results in its localization at spindle poles in metaphase, but not at the cell cortex (PubMed:23921553). In anaphase, recruited and anchored at the cell membrane of the polar cortical region in a EPB41-, EPB41L2-, phosphatidylinositol-dependent and GPM2- and G(i) alpha proteins-independent manner (PubMed:23870127, PubMed:24996901, PubMed:24109598, PubMed:24371089). Excluded from the anaphase equatorial region of the cell cortex in a RACGAP1- and KIF23-dependent and RanGTP-independent manner (PubMed:24996901). Associated with astral MTs emanating from the spindle poles during anaphase (PubMed:12445386, PubMed:24996901). Nonphosphorylated Thr-2055 localizes at the cell cortex, weakly during metaphase and more prominently during anaphase in a phosphatase PPP2CA-dependent manner (PubMed:23921553). As mitosis progresses it reassociates with telophase chromosomes very early during nuclear reformation, before substantial accumulation of lamins on chromosomal surfaces is evident (PubMed:1541636). Localizes to the tips of cortical MTs in prometaphase (PubMed:26765568). Localizes along MTs and specifically to both MT plus and minus ends (PubMed:26765568). Accumulates also at MT tips near the cell periphery (PubMed:26765568). Colocalizes with GPM2 at mitotic spindle poles during mitosis (PubMed:11781568, PubMed:21816348). Colocalizes with SPAG5 at mitotic spindle at prometaphase and at mitotic spindle poles at metaphase and anaphase (PubMed:27462074). Colocalizes with ABRO1 at mitotic spindle poles (PubMed:26195665). Colocalized with TNKS from prophase through to anaphase in mitosis (PubMed:16076287). Colocalizes with tubulin alpha (PubMed:12445386). CCSAP is essential for its centrosomal localization (PubMed:26562023). In horizontally retinal progenitor dividing cells, localized to the lateral cortical region (By similarity).

**Isoform 3:**

Cytoplasm > Cytosol (*experimental evidence*)

Cytoplasm > Cytoskeleton > Microtubule organizing center > Centrosome (*experimental evidence*)

Cytoplasm > Cytoskeleton > Spindle pole (*experimental evidence*)

**NOTE:** During interphase, mainly clustered at the centrosomal region in the cytosol. After entry into mitosis, detected at mitotic spindle poles.

**Isoform 4:**

Cytoplasm > Cytosol (*experimental evidence*)

Cytoplasm > Cytoskeleton > Microtubule organizing center > Centrosome (*experimental evidence*)

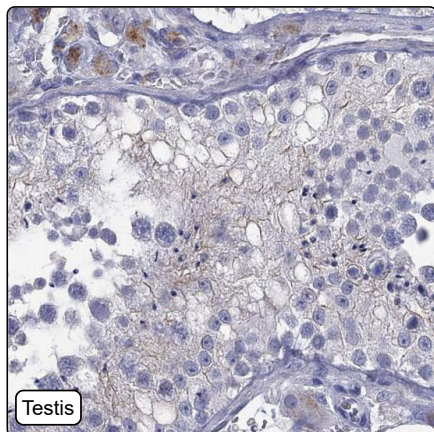
Cytoplasm > Cytoskeleton > Spindle pole (*experimental evidence*)

**NOTE:** During interphase, mainly clustered at the centrosomal region in the cytosol. After entry into mitosis, detected at mitotic spindle poles.

**Protein existence:** Experimental evidence at protein level

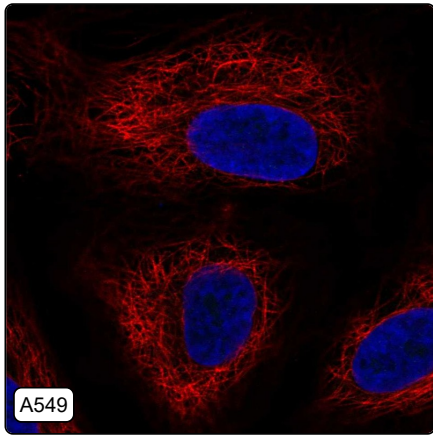
**Comment:**

## Immunohistochemistry



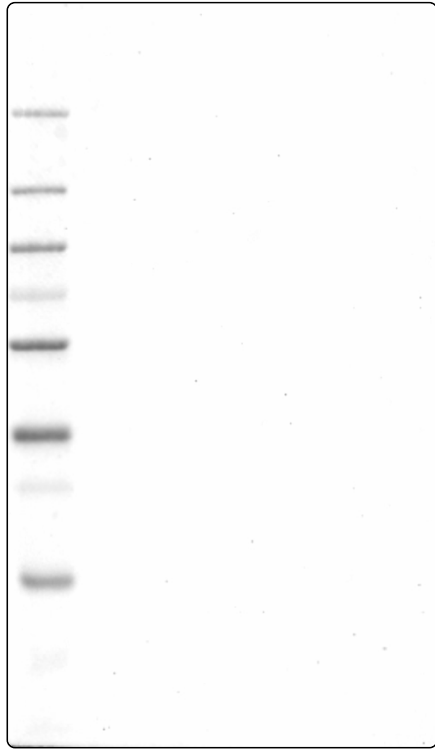
<b>IHC protocol:</b>	HIER pH6, Dilution 1:250
<b>IHC test staining:</b>	Cytoplasmic positivity in testis and neuronal processes.
<b>Literature conformance:</b>	Not consistent with gene/protein characterization data
<b>Literature significance:</b>	
<b>RNA consistency:</b>	Not consistent with RNA expression data
<b>IHC Sibling similarity:</b>	Other antibody shows dissimilar IHC staining pattern
<b>IHC fail comment:</b>	ANTIBODY FAILED: Improbable histological location, Not consistent with RNA

## Immunofluorescence



IF Overlay:	antibody (green), anti-tubuline (red) and DAPI (blue)
IF main location:	
IF additional location:	
IF Antibody score:	Failed IF
IF in A549:	Negative
IF in HEK 293:	Negative
IF in U-2 OS:	Negative

# Western blot



<b>WB Size markers (kDa):</b>	250, 130, 100, 70, 55, 35, 25, 15, 10
<b>WB Lanes:</b>	Marker (1), RT4 (2), U-251 MG (3), Plasma (4), Liver (5), Tonsil (6)
<b>WB Target weight (kDa):</b>	6, 7, 7, 8, 8, 9, 10, 12, 17, 18, 18, 20, 23, 25, 78, 97, 107, 109, 109, 236, 237, 237, 238
<b>WB Validation:</b>	Uncertain (No bands detected.)