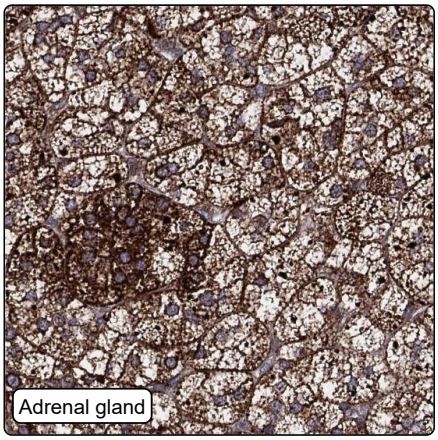
CPTC-MSH6-1 (CAB080005)

Uniprot ID: P52701
Protein name: MSH6_HUMAN
Full name: DNA mismatch repair protein Msh6
Function: Component of the post-replicative DNA mismatch repair system (MMR). Heterodimerizes with MSH2 to form MutS alpha, which binds to DNA mismatches thereby initiating DNA repair. When bound, MutS alpha bends the DNA helix and shields approximately 20 base pairs, and recognizes single base mismatches and dinucleotide insertion-deletion loops (IDL) in the DNA. After mismatch binding, forms a ternary complex with the MutL alpha heterodimer, which is thought to be responsible for directing the downstream MMR events, including strand discrimination, excision, and resynthesis. ATP binding and hydrolysis play a pivotal role in mismatch repair functions. The ATPase activity associated with MutS alpha regulates binding similar to a molecular switch: mismatched DNA provokes ADP-->ATP exchange, resulting in a discernible conformational transition that converts MutS alpha into a sliding clamp capable of hydrolysis-independent diffusion along the DNA backbone. This transition is crucial for mismatch repair. MutS alpha may also play a role in DNA homologous recombination repair. Recruited on chromatin in G1 and early S phase via its PWWP domain that specifically binds trimethylated 'Lys-36' of histone H3 (H3K36me3): early recruitment to chromatin to be replicated allowing a quick identification of mismatch repair to initiate the DNA mismatch repair reaction.
Subcellular location:
Nucleus (*experimental evidence*)
Chromosome (*experimental evidence*)
NOTE: Associates with H3K36me3 via its PWWP domain.
Protein existence: Experimental evidence at protein level

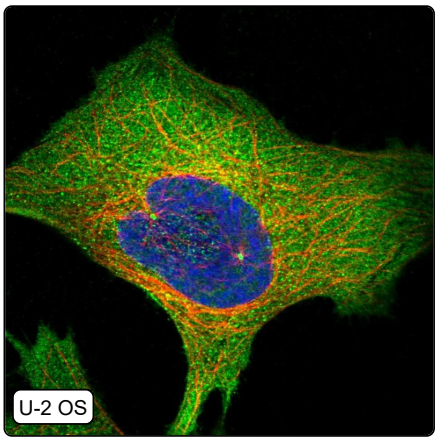
Comment:

Immunohistochemistry



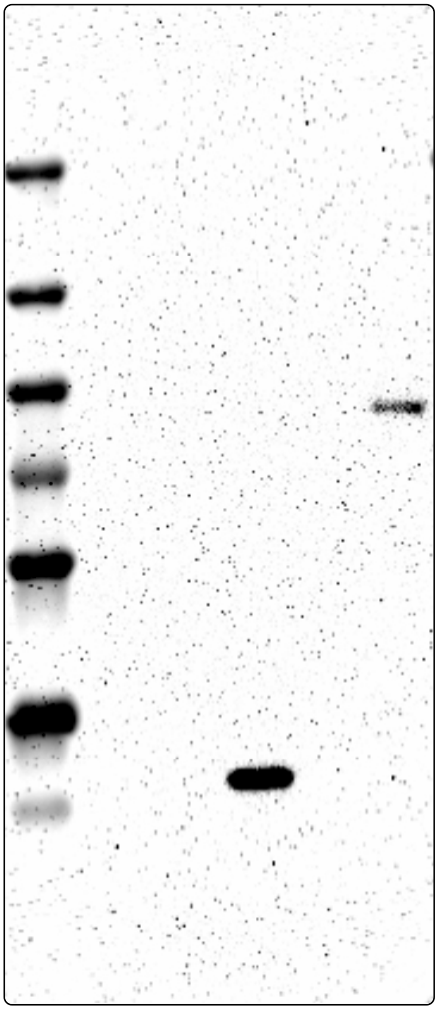
IHC protocol:	HIER pH6, Dilution 1:12000
IHC test staining:	Cytoplasmic positivity was observed in several tissues. Additional nuclear positivity in liver.
Literature conformance:	Not consistent with gene/protein characterization data
Literature significance:	
RNA consistency:	Mainly not consistent with RNA expression data
IHC Sibling similarity:	Other antibody shows dissimilar IHC staining pattern
IHC fail comment:	ANTIBODY FAILED: Improbable subcellular location

Immunofluorescence



IF Overlay:	antibody (green), anti-tubuline (red) and DAPI (blue)
IF main location:	Plasma membrane - 12: **Uncertain** (auto)
IF additional location:	Centrosome - 12: **Uncertain** (auto)
IF Antibody score:	Failed IF
IF in A549:	Plasma membrane
IF in HEK 293:	Negative
IF in U-2 OS:	Plasma membrane Centrosome

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):	6, 12, 13, 18, 37, 120, 120, 121, 138, 153
WB Validation:	Uncertain (Only bands not corresponding to the predicted size.)