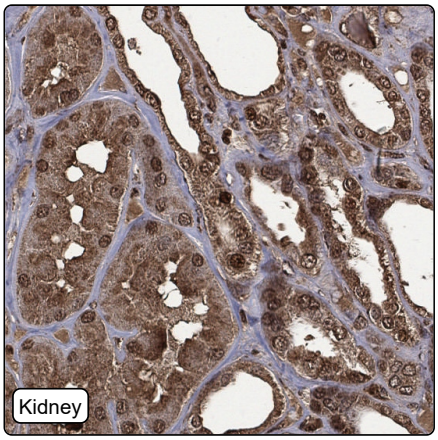
CPTC-SNAI1-1 (CAB080398)

Uniprot ID: O95863
Protein name: SNAI1_HUMAN
Full name: Zinc finger protein SNAI1
Tissue specificity: Expressed in a variety of tissues with the highest expression in kidney. Expressed in mesenchymal and epithelial cell lines.
Function: Involved in induction of the epithelial to mesenchymal transition (EMT), formation and maintenance of embryonic mesoderm, growth arrest, survival and cell migration. Binds to 3 E-boxes of the E-cadherin/CDH1 gene promoter and to the promoters of CLDN7 and KRT8 and, in association with histone demethylase KDM1A which it recruits to the promoters, causes a decrease in dimethylated H3K4 levels and represses transcription (PubMed:20389281, PubMed:20562920). The N-terminal SNAG domain competes with histone H3 for the same binding site on the histone demethylase complex formed by KDM1A and RCOR1, and thereby inhibits demethylation of histone H3 at 'Lys-4' (in vitro) (PubMed:20389281, PubMed:21300290, PubMed:23721412). During EMT, involved with LOXL2 in negatively regulating pericentromeric heterochromatin transcription (By similarity). SNAI1 recruits LOXL2 to pericentromeric regions to oxidize histone H3 and repress transcription which leads to release of heterochromatin component CBX5/HP1A, enabling chromatin reorganization and acquisition of mesenchymal traits (By similarity). Associates with EGR1 and SP1 to mediate tetradecanoyl phorbol acetate (TPA)-induced up-regulation of CDKN2B, possibly by binding to the CDKN2B promoter region 5'-TCACA-3. In addition, may also activate the CDKN2B promoter by itself.
Subcellular location:
Nucleus (*experimental evidence*)
Cytoplasm (*experimental evidence*)
NOTE: Once phosphorylated (probably on Ser-107, Ser-111, Ser-115 and Ser-119) it is exported from the nucleus to the cytoplasm where subsequent phosphorylation of the destruction motif and ubiquitination involving BTRC occurs.
Protein existence: Experimental evidence at protein level

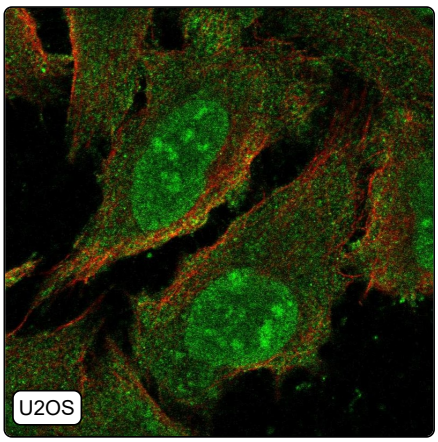
Comment:

Immunohistochemistry



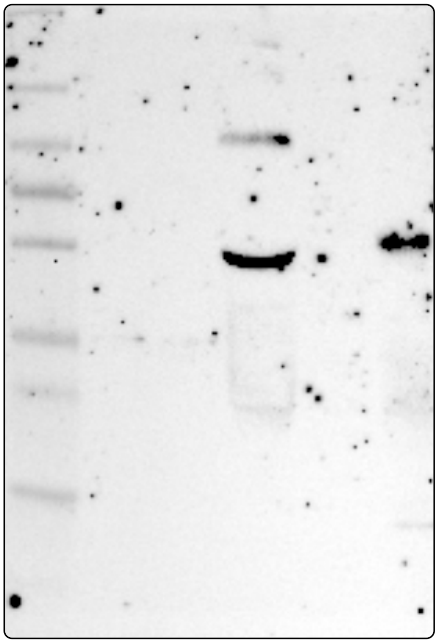
IHC protocol:	HIER pH6, Dilution 1:250
IHC test staining:	Nuclear positivity in most tissues, additional cytoplasmic staining in several.
Literature conformance:	Consistent with extensive gene/protein characterization data
Literature significance:	
RNA similarity:	Low consistency between antibody staining and RNA expression data
RNA tissue specificity:	Tissue enhanced (adipose tissue)
RNA tissue distribution:	Detected in many
IHC Sibling similarity:	Other antibody shows partly similar IHC staining pattern

Immunofluorescence



IF Overlay:	antibody (green), anti-tubulin (red) and DAPI (blue)
IF main location:	Plasma membrane - 12: **Uncertain** (auto)
IF additional location:	Nucleoli - 3: **Supportive** (auto) Nucleoplasm - 3: **Supportive** (auto) Micronucleus - 12: **Uncertain** (auto)
IF approved for publication on HPA:	No
IF in THP-1:	Nucleoli Plasma membrane (Protrusions)
IF in U2OS:	Nucleoplasm Nucleoli Micronucleus Plasma membrane

Western blot



WB Size markers (kDa):	250, 130, 100, 70, 55, 35, 25, 15, 10
WB Lanes:	Marker (1), RT-4 (2), U-251MG (3), Plasma (4), Liver (5), Tonsil (6)
WB Target weight (kDa):	29
WB Validation:	Uncertain (Only bands not corresponding to the predicted size.)