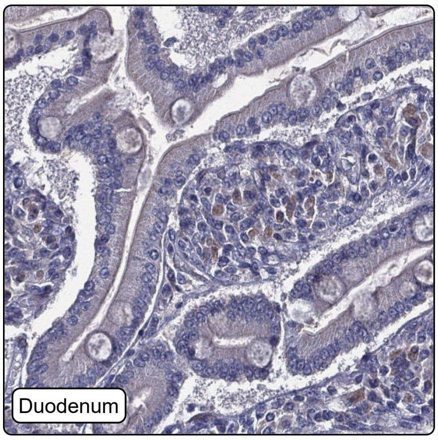
CPTC-SNAI2-1 (CAB080399)

Uniprot ID: O43623
Protein name: SNAI2_HUMAN
Full name: Zinc finger protein SNAI2
Tissue specificity: Expressed in most adult human tissues, including spleen, thymus, prostate, testis, ovary, small intestine, colon, heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas. Not detected in peripheral blood leukocyte. Expressed in the dermis and in all layers of the epidermis, with high levels of expression in the basal layers (at protein level). Expressed in osteoblasts (at protein level). Expressed in mesenchymal stem cells (at protein level). Expressed in breast tumor cells (at protein level).
Function: Transcriptional repressor that modulates both activator-dependent and basal transcription. Involved in the generation and migration of neural crest cells. Plays a role in mediating RAF1-induced transcriptional repression of the TJ protein, occludin (OCLN) and subsequent oncogenic transformation of epithelial cells (By similarity). Represses BRCA2 expression by binding to its E2-box-containing silencer and recruiting CTBP1 and HDAC1 in breast cells. In epidermal keratinocytes, binds to the E-box in ITGA3 promoter and represses its transcription. Involved in the regulation of ITGB1 and ITGB4 expression and cell adhesion and proliferation in epidermal keratinocytes. Binds to E-box2 domain of BSG and activates its expression during TGFB1-induced epithelial-mesenchymal transition (EMT) in hepatocytes. Represses E-Cadherin/CDH1 transcription via E-box elements. Involved in osteoblast maturation. Binds to RUNX2 and SOC9 promoters and may act as a positive and negative transcription regulator, respectively, in osteoblasts. Binds to CXCL12 promoter via E-box regions in mesenchymal stem cells and osteoblasts. Plays an essential role in TWIST1-induced EMT and its ability to promote invasion and metastasis.
Subcellular location:
Nucleus (*experimental evidence*)
Cytoplasm
NOTE: Observed in discrete foci in interphase nuclei. These nuclear foci do not overlap with the nucleoli, the SP100 and the HP1 heterochromatin or the coiled body, suggesting SNAI2 is associated with active transcription or active splicing regions.
Protein existence: Experimental evidence at protein level

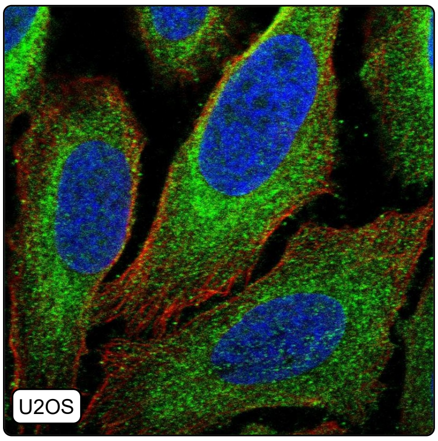
Comment:

Immunohistochemistry



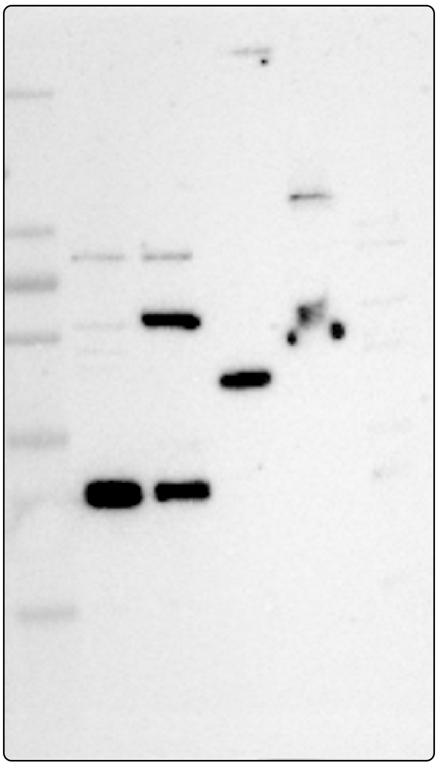
IHC protocol:	HIER pH6, Dilution 1:500
IHC test staining:	Cytoplasmic positivity was observed in peripheral nerve.
Literature conformance:	Not consistent with gene/protein characterization data
Literature significance:	
RNA similarity:	Very low consistency between antibody staining and RNA expression data
RNA tissue specificity:	Low tissue specificity
RNA tissue distribution:	Detected in many
IHC Sibling similarity:	Other antibody shows dissimilar IHC staining pattern

Immunofluorescence



IF Overlay:	antibody (green), anti-tubulin (red) and DAPI (blue)
IF main location:	Endoplasmic reticulum - 5: **Approved** (auto)
IF additional location:	Vesicles - 5: **Approved** (auto)
IF approved for publication on HPA:	No
IF in THP-1:	Vesicles
IF in U2OS:	ER

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):	10, 30
WB Validation:	Supported (Band of predicted size in kDa (+/-20%) with additional bands present.)