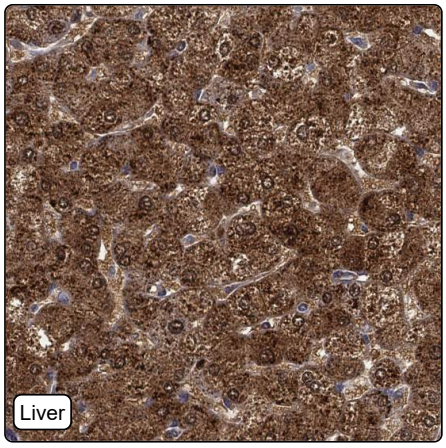
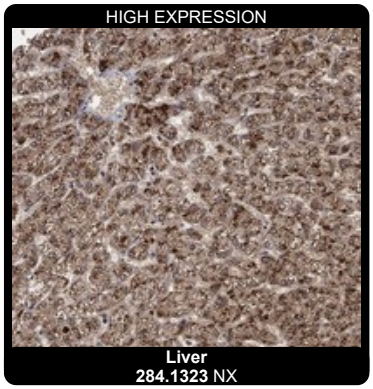
CPTC-ARG1-1 (CAB080011)

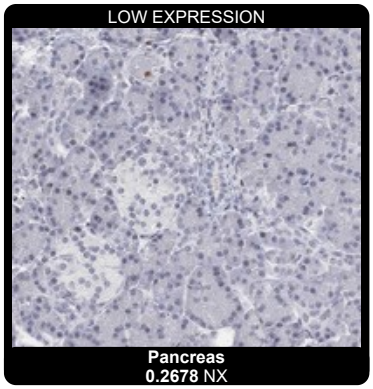
Uniprot ID: P05089
Protein name: ARGI1_HUMAN
Full name: Arginase-1
Tissue specificity: Within the immune system initially reported to be selectively expressed in granulocytes (polymorphonuclear leukocytes [PMNs]) (PubMed:15546957). Also detected in macrophages mycobacterial granulomas (PubMed:23749634). Expressed in group2 innate lymphoid cells (ILC2s) during lung disease (PubMed:27043409).
Function: Key element of the urea cycle converting L-arginine to urea and L-ornithine, which is further metabolized into metabolites proline and polyamides that drive collagen synthesis and bioenergetic pathways critical for cell proliferation, respectively; the urea cycle takes place primarily in the liver and, to a lesser extent, in the kidneys. Functions in L-arginine homeostasis in nonhepatic tissues characterized by the competition between nitric oxide synthase (NOS) and arginase for the available intracellular substrate arginine. Arginine metabolism is a critical regulator of innate and adaptive immune responses. Involved in an antimicrobial effector pathway in polymorphonuclear granulocytes (PMN). Upon PMN cell death is liberated from the phagolysosome and depletes arginine in the microenvironment leading to suppressed T cell and natural killer (NK) cell proliferation and cytokine secretion (PubMed:15546957, PubMed:16709924, PubMed:19380772). In group 2 innate lymphoid cells (ILC2s) promotes acute type 2 inflammation in the lung and is involved in optimal ILC2 proliferation but not survival (By similarity). In humans, the immunological role in the monocytic/macrophage/dendritic cell (DC) lineage is unsure.
Subcellular location:
Cytoplasm (*experimental evidence*)
Cytoplasmic granule (*experimental evidence*)
NOTE: Localized in azurophil granules of neutrophils (PubMed:15546957).
Protein existence: Experimental evidence at protein level

Comment:

Immunohistochemistry







IHC protocol:	HIER pH6, Dilution 1:3500
IHC test staining:	Cytoplasmic and nuclear positivity in liver and bone marrow.
Literature conformance:	Consistent with extensive gene/protein characterization data
Literature significance:	
RNA similarity:	High consistency between antibody staining and RNA expression data
RNA tissue specificity:	Tissue enriched (liver)
RNA tissue distribution:	Detected in some
IHC Sibling similarity:	Other antibody shows similar IHC staining pattern
Reliability score:	Supported
APE summary:	Selective expression in liver and subsets of bone marrow cells.
APE explanatory sentences:	High consistency between antibody staining and RNA expression data.
Orthogonal validation:	Yes
Independent validation:	No
IHC Annotation summary:	Strong cytoplasmic positivity was observed in liver, while bone marrow and spleen showed strong nuclear staining. Remaining normal tissues were negative. Strong cytoplasmic positivity was observed in liver cancers. Remaining cancers were negative.