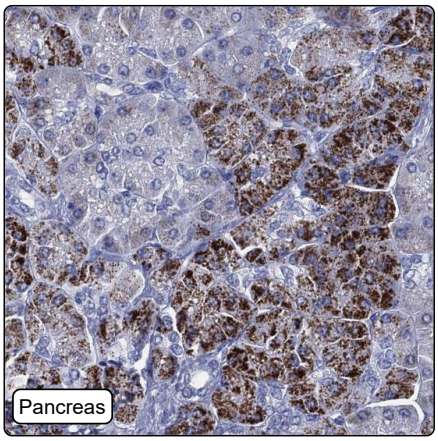
CPTC-PTGS2-1 (CAB079991)

Uniprot ID: P35354
Protein name: PGH2_HUMAN
Full name: Prostaglandin G/H synthase 2
Function: Dual cyclooxygenase and peroxidase in the biosynthesis pathway of prostanoids, a class of C20 oxylipins mainly derived from arachidonate, with a particular role in the inflammatory response (PubMed:7947975, PubMed:7592599, PubMed:9261177, PubMed:16373578, PubMed:22942274, PubMed:26859324, PubMed:27226593, PubMed:11939906, PubMed:19540099). The cyclooxygenase activity oxygenates arachidonate (AA, C20:4(n-6)) to the hydroperoxy endoperoxide prostaglandin G2 (PGG2), and the peroxidase activity reduces PGG2 to the hydroxy endoperoxide PGH2, the precursor of all 2-series prostaglandins and thromboxanes (PubMed:7947975, PubMed:7592599, PubMed:9261177, PubMed:16373578, PubMed:22942274, PubMed:26859324, PubMed:27226593). This complex transformation is initiated by abstraction of hydrogen at carbon 13 (with S-stereochemistry), followed by insertion of molecular O2 to form the endoperoxide bridge between carbon 9 and 11 that defines prostaglandins. The insertion of a second molecule of O2 (bis-oxygenase activity) yields a hydroperoxy group in PGG2 that is then reduced to PGH2 by two electrons (PubMed:7947975, PubMed:7592599, PubMed:9261177, PubMed:16373578, PubMed:22942274, PubMed:26859324, PubMed:27226593). Similarly catalyzes successive cyclooxygenation and peroxidation of dihomo-gamma-linoleate (DGLA, C20:3(n-6)) and eicosapentaenoate (EPA, C20:5(n-3)) to corresponding PGH1 and PGH3, the precursors of 1- and 3-series prostaglandins (PubMed:11939906, PubMed:19540099). In an alternative pathway of prostanoid biosynthesis, converts 2-arachidonoyl lysophopholipids to prostanoid lysophopholipids, which are then hydrolyzed by intracellular phospholipases to release free prostanoids (PubMed:27642067). Metabolizes 2-arachidonoyl glycerol yielding the glyceryl ester of PGH2, a process that can contribute to pain response (PubMed:22942274). Generates lipid mediators from n-3 and n-6 polyunsaturated fatty acids (PUFAs) via a lipoxygenase-type mechanism. Oxygenates PUFAs to hydroperoxy compounds and then reduces them to corresponding alcohols (PubMed:11034610, PubMed:11192938, PubMed:9048568, PubMed:9261177). Plays a role in the generation of resolution phase interaction products (resolvins) during both sterile and infectious inflammation (PubMed:12391014). Metabolizes docosahexaenoate (DHA, C22:6(n-3)) to 17R-HDHA, a precursor of the D-series resolvins (RvDs) (PubMed:12391014). As a component of the biosynthetic pathway of E-series resolvins (RvEs), converts eicosapentaenoate (EPA, C20:5(n-3)) primarily to 18S-HEPE that is further metabolized by ALOX5 and LTA4H to generate 18S-RvE1 and 18S-RvE2 (PubMed:21206090). In vascular endothelial cells, converts docosapentaenoate (DPA, C22:5(n-3)) to 13R-HDPA, a precursor for 13-series resolvins (RvTs) shown to activate macrophage phagocytosis during bacterial infection (PubMed:26236990). In activated leukocytes, contributes to oxygenation of hydroxyeicosatetraenoates (HETE) to diHETES (5,15-diHETE and 5,11-diHETE) (PubMed:22068350, PubMed:26282205). During neuroinflammation, plays a role in neuronal secretion of specialized preresolving mediators (SPMs) 15R-lipoxin A4 that regulates phagocytic microglia (By similarity).
Subcellular location:
Microsome membrane (*experimental evidence*) (Topo: Peripheral membrane protein)
Endoplasmic reticulum membrane (*experimental evidence*) (Topo: Peripheral membrane protein)
Nucleus inner membrane (*experimental evidence*) (Topo: Peripheral membrane protein)
Nucleus outer membrane (*experimental evidence*) (Topo: Peripheral membrane protein)
NOTE: Detected on the lumenal side of the endoplasmic reticulum and nuclear envelope.
Protein existence: Experimental evidence at protein level

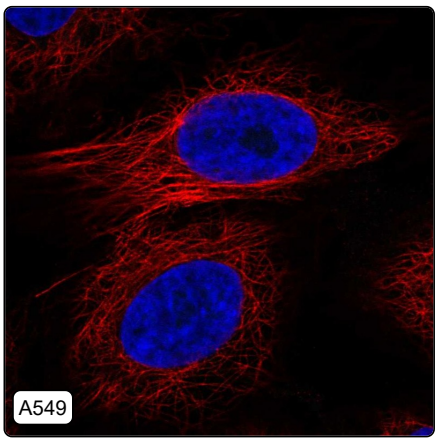
Comment:

Immunohistochemistry



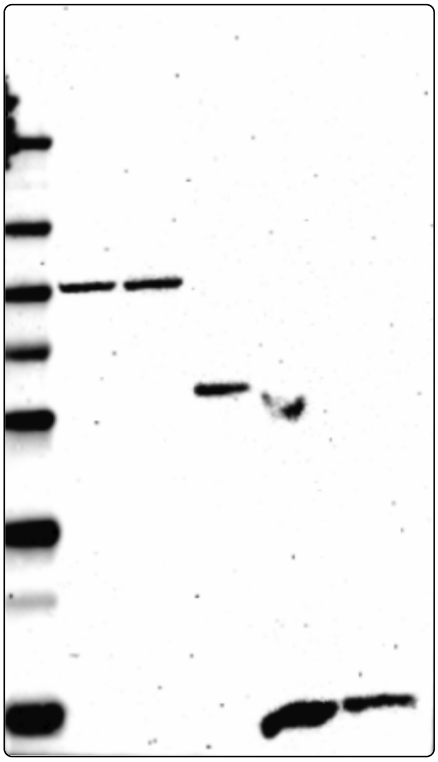
IHC protocol:	HIER pH6, Dilution 1:2000
IHC test staining:	Granular cytoplasmic positivity in pancreas and kidney. Additional positivity in erythrocytes and hematopoietic cells.
Literature conformance:	Not consistent with gene/protein characterization data
Literature significance:	
RNA consistency:	Not consistent with RNA expression data
IHC Sibling similarity:	Other antibody shows dissimilar IHC staining pattern
IHC fail comment:	ANTIBODY FAILED: Improbable histological location,Many parameters contradicts IHC,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 CACO-2:	Negative
IF in U-2 OS:	Negative

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):	69
WB Validation:	Uncertain (Weak band of predicted size but with additional bands of higher intensity also present.)