E-Cadherin Polyclonal Antibody

catalog number: D-AB-10198L

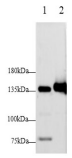
Note: *Centrifuge before opening to ensure complete recovery of vial contents.*

Description

Reactivity	Human;Mouse;Rat
Immunogen	Recombinant Human CDH1 protein expressed by E.coli
Host	Rabbit
Isotype	IgG
Purification	Antigen Affinity Purification
Buffer	PBS with 0.05% Proclin300, 1% protective protein and 50% glycerol, pH7.4

Applications	Recommended Dilution
WB	1:500-1:1000
IHC	1:100-1:200

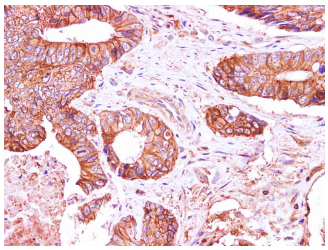
Data



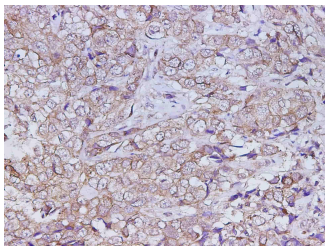
Western blot with E-Cadherin Polyclonal antibody at dilution of 1:1000.lane 1:Mouse spleen,lane 2:Rat brain

Observed-MW:135 kDa

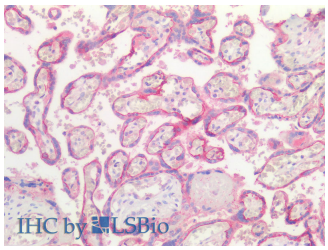
Calculated-MW:97 kDa



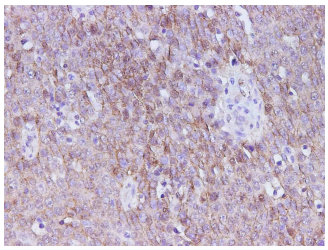
Immunohistochemistry of paraffin-embedded Human carcinoma of Colon using E-Cadherin Polyclonal Antibody at dilution of 1:100



Immunohistochemistry of paraffin-embedded Human breast cancer using E-Cadherin Polyclonal Antibody at dilution of 1:200



Immunohistochemistry of paraffin-embedded Human Placenta using E-Cadherin Polyclonal Antibody at dilution of 1:100(Elabscience Product)



Immunohistochemistry of paraffin-embedded Human ovarian cancer using E-Cadherin Polyclonal Antibody at dilution of 1:200

Preparation & Storage

Storage	Store at -20°C Valid for 12 months. Avoid freeze / thaw cycles.
Shipping	The product is shipped with ice pack, upon receipt, store it immediately at the temperature recommended.

Background

This gene is a classical cadherin from the cadherin superfamily. The encoded protein is a calcium dependent cell-cell adhesion glycoprotein comprised of five extracellular cadherin repeats,a transmembrane region and a highly conserved cytoplasmic tail. Mutations in this gene are correlated with gastric,breast,colorectal,thyroid and ovarian cancer. Loss of function is thought to contribute to progression in cancer by increasing proliferation,invasion,and/or metastasis. The ectodomain of this protein mediates bacterial adhesion to mammalian cells and the cytoplasmic domain is required for internalization. Identified transcript variants arise from mutation at consensus splice sites.

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