Recombinant Stromal Interaction Molecule 1 Monoclonal Antibody

catalog number: AN300992L

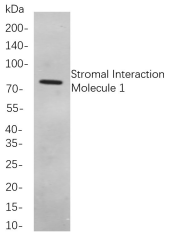
Note: *Centrifuge before opening to ensure complete recovery of vial contents.*

Description

Reactivity	Human;Mouse;Rat
Immunogen	Recombinant Human Stromal Interaction Molecule 1 protein
Host	Rabbit
Isotype	IgG,κ
Clone	B743
Purification	Protein A
Buffer	PBS, 50% glycerol, 0.05% Proclin 300, 0.05% protein protectant.

Applications	Recommended Dilution
IHC	1:200-1:1000
WB	1:1000-1:5000
IF	1:200-1:1000
ELISA	1:5000-1:20000
IP	1:50-1:200,

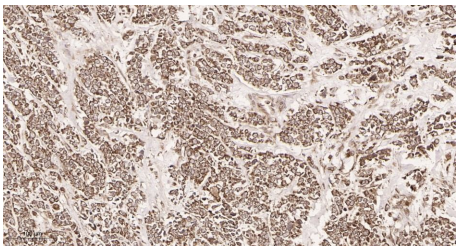
Data



Western Blot with Recombinant Stromal Interaction Molecule 1 Monoclonal Antibody at dilution of 1:1000 dilution. Lane A: C6 cells.

Observed-MW:77 kDa

Calculated-MW:77 kDa



Immunohistochemistry of paraffin-embedded human breast tissue using Recombinant Stromal Interaction Molecule 1 Monoclonal Antibody at dilution of 1:200.

Preparation & Storage

Storage	Store at -20°C Valid for 12 months. Avoid freeze / thaw cycles.
Shipping	Ice bag

Background

This gene encodes a type 1 transmembrane protein that mediates Ca2+ influx after depletion of intracellular Ca2+ stores by gating of store-operated Ca2+ influx channels (SOCs). It is one of several genes located in the imprinted gene domain of 11p15.5, an important tumor-suppressor gene region. Alterations in this region have been associated with the Beckwith-Wiedemann syndrome, Wilms tumor, rhabdomyosarcoma, adrenocrotical carcinoma, and lung, ovarian, and breast cancer. This gene may play a role in malignancies and disease that involve this region, as well as early hematopoiesis, by mediating attachment to stromal cells. Mutations in this gene are associated with fatal classic Kaposi sarcoma, immunodeficiency due to defects in store-operated calcium entry (SOCE) in fibroblasts, ectodermal dysplasia and tubular aggregate myopathy. This gene is oriented in a head-to-tail configuration with the ribonucleotide reductase 1 gene (RRM1), with the 3' end of this gene situated 1.6 kb from the 5' end of the RRM1 gene. Alternative splicing of this gene results in multiple transcript variants.

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