

TGF β Receptor II (Phospho Tyr284) Rabbit pAb

CatalogNo: YP1698 Orthogonal Validated 

Key Features

Host Species

- Rabbit

Reactivity

- Human, Mouse, Rat

Applications

- WB

MW

- 62kD (Calculated)
- 75kD (Observed)

Isotype

- IgG

Storage

Storage* -15°C to -25°C/1 year (Do not lower than -25°C)

Formulation Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.

Recommended Dilution Ratios

WB 1:500-2000

Basic Information

Clonality Polyclonal

Immunogen Information

Immunogen Synthesized peptide derived from human TGFBR2 (Phospho-Tyr284)

Specificity This antibody detects endogenous levels of TGFBR2 (Phospho-Tyr284) at Human, Mouse, Rat. The name of modified sites may be influenced by many factors, such as species (the modified site was not originally found in human samples) and the change of protein sequence (the previous protein sequence is incomplete, and the protein sequence may be prolonged with the development of protein sequencing technology). When naming, we will use the "numbers" in historical reference to keep the sites consistent with the reports. The antibody binds to the following modification sequence (lowercase letters are modification sites):EEyAS

| Target Information

Gene name TGFBR2

Protein Name TGFBR2 (Phospho-Tyr284)

Organism	Gene ID	UniProt ID
Human	7048 ;	P37173 ;
Mouse	21813 ;	Q62312 ;
Rat	81810 ;	P38438 ;

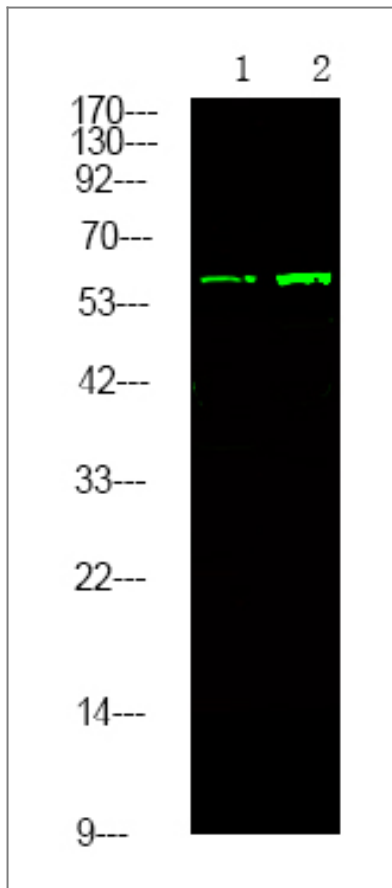
Cellular Localization Cell membrane ; Single-pass type I membrane protein . Membrane raft . ; [Isoform 3]: Secreted .

Tissue specificity Cerebellum,Colon,Epithelium,Glial cell,Liver,

Function

Catalytic activity:ATP + [receptor-protein] = ADP + [receptor-protein] phosphate.,cofactor:Magnesium or manganese.,Disease:Defects in TGFBR2 are a cause of esophageal cancer [MIM:133239].,Disease:Defects in TGFBR2 are the cause of aortic aneurysm familial thoracic type 3 (AAT3) [MIM:610380]. Aneurysms and dissections of the aorta usually result from degenerative changes in the aortic wall. Thoracic aortic aneurysms and dissections are primarily associated with a characteristic histologic appearance known as 'medial necrosis' or 'Erdheim cystic medial necrosis' in which there is degeneration and fragmentation of elastic fibers, loss of smooth muscle cells, and an accumulation of basophilic ground substance. AAT3 is an autosomal dominant disorder with reduced penetrance and variable expression.,Disease:Defects in TGFBR2 are the cause of hereditary non-polyposis colorectal cancer type 6 (HNPCC6) [MIM:190182]. Mutations in more than one gene locus can be involved alone or in combination in the production of the HNPCC phenotype (also called Lynch syndrome). Most families with clinically recognized HNPCC have mutations in either MLH1 or MSH2 genes. HNPCC is an autosomal, dominantly inherited disease associated with marked increase in cancer susceptibility. It is characterized by a familial predisposition to early onset colorectal carcinoma (CRC) and extra-colonic cancers of the gastrointestinal, urological and female reproductive tracts. HNPCC is reported to be the most common form of inherited colorectal cancer in the Western world, and accounts for 15% of all colon cancers. Cancers in HNPCC originate within benign neoplastic polyps termed adenomas. Clinically, HNPCC is often divided into two subgroups. Type I: hereditary predisposition to colorectal cancer, a young age of onset, and carcinoma observed in the proximal colon. Type II: patients have an increased risk for cancers in certain tissues such as the uterus, ovary, breast, stomach, small intestine, skin, and larynx in addition to the colon. Diagnosis of classical HNPCC is based on the Amsterdam criteria: 3 or more relatives affected by colorectal cancer, one a first degree relative of the other two; 2 or more generation affected; 1 or more colorectal cancers presenting before 50 years of age; exclusion of hereditary polyposis syndromes. The term "suspected HNPCC" or "incomplete HNPCC" can be used to describe families who do not or only partially fulfill the Amsterdam criteria, but in whom a genetic basis for colon cancer is strongly suspected. HNPCC6 is a type of colorectal cancer complying with the clinical criteria of HNPCC, except that the onset of cancer was beyond 50 years of age in all cases.,Disease:Defects in TGFBR2 are the cause of Loeys-Dietz syndrome type 1B (LDS1B) [MIM:610168]. LDS1 is an aortic aneurysm syndrome with widespread systemic involvement. The disorder is characterized by arterial tortuosity and aneurysms, craniosynostosis, hypertelorism, and bifid uvula or cleft palate. Other findings include exotropia, micrognathia and retrognathia, structural brain abnormalities, intellectual deficit, congenital heart disease, translucent skin, joint hyperlaxity and aneurysm with dissection throughout the arterial tree.,Disease:Defects in TGFBR2 are the cause of Loeys-Dietz syndrome type 2B (LDS2B) [MIM:610380]; formerly Marfan syndrome type 2. LDS2 is an aortic aneurysm syndrome with widespread systemic involvement. Physical findings include prominent joint laxity, easy bruising, wide and atrophic scars, velvety and translucent skin with easily visible veins, spontaneous rupture of the spleen or bowel, diffuse arterial aneurysms and dissections, and catastrophic complications of pregnancy, including rupture of the gravid uterus and the arteries, either during pregnancy or in the immediate postpartum period. LDS2 is characterized by the absence of craniofacial abnormalities with the exception of bifid uvula that can be present in some patients.,Function:On ligand binding, forms a receptor complex consisting of two type II and two type I transmembrane serine/threonine kinases. Type II receptors phosphorylate and activate type I receptors which autophosphorylate, then bind and activate SMAD transcriptional regulators. Receptor for TGF-beta.,PTM:Phosphorylated on a Ser/Thr residue in the cytoplasmic domain.,similarity:Belongs to the protein kinase superfamily.,similarity:Belongs to the protein kinase superfamily. TKL Ser/Thr protein kinase family. TGFB receptor subfamily.,similarity:Contains 1 protein kinase domain.,subunit:Binds to DAXX. Interacts with TCTEX1D4.,

Validation Data



Western Blot analysis of 1 A549 cell, 2 LPS 100ng/mL 30min treated ,using primary antibody at 1:1000 dilution. Secondary antibody(catalog#:RS23920) was diluted at 1:10000

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