



FGFR1 (Phospho-Tyr766) Antibody

#12186

Catalog Number: 12186-1 12186-2

Amount: 50µg/100µl 100µg/100µl

Swiss-Prot No. : P11362

Form of Antibody: Rabbit IgG in phosphate buffered saline (without Mg²⁺ and Ca²⁺), pH 7.4, 150mM NaCl, 0.02% sodium azide and 50% glycerol.

Storage/Stability: Store at -20°C/1 year

Immunogen: The antiserum was produced against synthesized phosphopeptide derived from human FGFR1 around the phosphorylation site of Tyr766

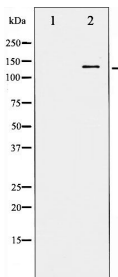
Purification: The antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific phosphopeptide. The antibody against non-phosphopeptide was removed by chromatography using non-phosphopeptide corresponding to the phosphorylation site.

Specificity/Sensitivity: FGFR1(Phospho-Tyr766) Antibody detects endogenous levels of FGFR1 only when phosphorylated at Tyr766 .

Reactivity: Human, Mouse, Rat

Applications:

Predicted MW: 140 kd WB: 1:500~1:1000 IHC : 1:50~1:100



Western blot analysis of FGFR1 phosphorylation expression in EGF treated HepG2 whole cell lysates. The lane on the left is treated with the antigen-specific peptide.

Background : The protein encoded by this gene is a member of the fibroblast growth factor receptor family, where amino acid sequence is highly conserved between members and throughout evolution. FGFR family members differ from one another in their ligand affinities and tissue distribution. A full-length representative protein consists of an extracellular region, composed of three immunoglobulin-like domains, a single hydrophobic membrane-spanning segment and a cytoplasmic tyrosine kinase domain. The extracellular portion of the protein interacts with fibroblast growth factors, setting in motion a cascade of downstream signals, ultimately influencing mitogenesis and differentiation. This particular family member binds both acidic and basic fibroblast growth factors and is involved in limb induction. Mutations in this gene can lead to Pfeiffer syndrome and Jackson-Weiss syndrome. The genomic organization of this gene is very similar to family members 2-4, encompassing 19 exons that are subject to complex alternative splicing, which allows for structural, tissue expression and ligand affinity variations among the isoforms.