

## FGFR1/2 Polyclonal Antibody

Catalog No. E-AB-31438

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

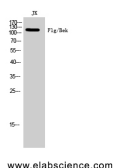
### Description

<b>Reactivity</b>	Human,Mouse,Rat
<b>Immunogen</b>	Synthesized peptide derived from human Flg/Bek around the non-phosphorylation site of Tyr463/466.
<b>Host</b>	Rabbit
<b>Isotype</b>	IgG
<b>Purification</b>	Affinity purification
<b>Conjugation</b>	Unconjugated
<b>Buffer</b>	PBS with 0.02% sodium azide, 0.5% protective protein and 50% glycerol, pH7.4

### Applications Recommended Dilution

<b>WB</b>	1:500-1:2000
<b>ELISA</b>	1:10000

### Data



Western Blot analysis of Jurkat cells with FGFR1/2  
Polyclonal Antibody  
**Observed Mw:120kDa**  
**Calculated Mw:92kDa**

### Preparation & Storage

**Storage** Store at -20°C. Avoid freeze / thaw cycles.

### Background

FGFR1 encoded by this gene is a member of the fibroblast growth factor receptor (FGFR) 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 have been associated with Pfeiffer syndrome, Jackson-Weiss syndrome, Antley-Bixler syndrome, osteoglophonic dysplasia, and autosomal dominant Kallmann syndrome 2. Chromosomal aberrations involving this gene are associated

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with stem cell myeloproliferative disorder and stem cell leukemia lymphoma syndrome. Alternatively spliced variants which encode different protein isoforms have been described; however, not all variants have been fully characterized.