ELK Biotechnology

RAPH1 rabbit pAb

Cat No.:ES10102

For research use only

Overview

Product Name	RAPH1 rabbit pAb
Host species	Rabbit
Applications	WB;ELISA
Species Cross-Reactivity	Human;Rat;Mouse;
Recommended dilutions	WB 1:500-2000 ELISA 1:5000-20000
Immunogen	Synthesized peptide derived from human protein . at AA range: 370-450
Specificity	RAPH1 Polyclonal Antibody detects endogenous levels of protein.
Formulation	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.
Storage	Store at -20℃. Avoid repeated freeze-thaw cycles.
Protein Name	Ras-associated and pleckstrin homology domains-containing protein 1 (RAPH1) (Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 18 protein) (Amyotrophic lateral sclerosis 2 chromosomal
Gene Name	RAPH1 ALS2CR18 ALS2CR9 KIAA1681 LPD PREL2 RMO1
Cellular localization	Cell membrane ; Peripheral membrane protein ; Cytoplasmic side . Cell projection, lamellipodium . Cell projection, filopodium . Cytoplasm, cytoskeleton . Recruited to the membrane, via the PH domain, by the phosphoinositide, PI(3,4)P2. Colocalizes with ENAH/VASP at the tips of lamellipodia and filopodia. Also colocalizes with the pathogens, Vaccinia and Enteropathogenic E.coli (EPEC) at the interface between the pathogen and their actin.
Purification	The antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific immunogen.
Clonality	Polyclonal

Concentration	1 mg/ml
Observed band	137kD
Human Gene ID	65059
Human Swiss-Prot Number	Q70E73
Alternative Names	
Background	This gene encodes a protein that belongs to the Mig10/Rap1-interacting adaptor molecule/Lamellipodin family of adapter proteins, which function in cell migration. Members of this family contain pleckstrin-homology domains, Ras-association domains, and proline-rich C-termini. The protein encoded by this gene regulates actin dynamics through interaction with Ena/Vasodilator proteins as well as direct binding to filamentous actin to regulate actin network assembly. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jul 2016],