SunLong Biotech Co.,LTD
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[Marker Primary Antibody]

Rabbit Anti-phospho-RAC1 + RAC2 (Ser71)/AF647 Conjugated antibody

Catalog Number: SL5698R-AF647

FOR RESEARCH USE ONLY

[DATASHEET]

Host:	Rabbit
Isotype:	IgG
Clonality:	Polyclonal
Target:	Anti-phospho-RAC1 + RAC2 (Ser71)/AF647
Immunogen:	KLH conjugated Synthesised phosphopeptide derived from human RAC1 around the phosphorylation site of Ser71
Purification:	affinity purified by Protein A
Concentration:	1mg/ml
Storage:	Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. The lyophilized antibody is stable at room temperature for at least one month and for greater than a year when kept at -20°C. When reconstituted in sterile pH 7.4 1M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.
Applications:	ICC/IF=1:100-500 not yet tested in other applications. optimal dilutions/concentrations should be determined by the end user.
Reactivity:	Human(predicted:Mouse,Rat,Dog,Pig,Cow,Horse,Rabbit,Sheep)
Background:	background: The protein encoded by this gene is a GTPase which belongs to the RAS superfamily of small GTP-binding proteins. Members of this superfamily appear to regulate a diverse array of cellular events, including the control of cell growth, cytoskeletal reorganization, and the activation of protein kinases. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Mar 2009] **Function:** Plasma membrane-associated small GTPase which cycles between active GTP-bound and inactive GDP-bound states. In its active state, binds to a variety of effector proteins to regulate cellular responses such as secretory processes, phagocytosis of apoptotic cells, epithelial cell polarization and growth-factor induced formation of membrane ruffles. Rac1 p21/rho GDI heterodimer is the active component of the cytosolic factor sigma 1, which is involved in stimulation of the NADPH oxidase activity in macrophages. Essential for the SPATA13-mediated regulation of cell migration and adhesion

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	assembly and disassembly. Stimulates PKN2 kinase activity. In concert with RAB7A, plays a role in regulating the formation of RBs (ruffled borders) in osteoclasts. In glioma cells, promotes cell migration and invasion. In podocytes, promotes nuclear shuttling of NR3C2; this modulation is required for a proper kidney functioning. Required for atypical chemokine receptor ACKR2-induced LIMK1-PAK1-dependent phosphorylation of cofilin (CFL1) and for up-regulation of ACKR2 from endosomal compartment to cell membrane, increasing its efficiency in chemokine uptake and degradation. Isoform B has an accelerated GEF-independent GDP/GTP exchange and an impaired GTP hydrolysis, which is restored partially by GTPase-activating proteins. It is able to bind to the GTPase-binding domain of PAK but not full-length PAK in a GTP-dependent manner, suggesting that the insertion does not completely abolish effector interaction. **Subunit:** Interacts with NISCH. Interacts with PIP5K1A. Interacts with the GTP-bound form of RAB7A. Interacts with SRGAP2. Interacts with CYFIP1/SRA-1. Interacts with PLXNB3. Interacts with ARHGDIA; the interaction is induced by SEMA5A, mediated through PLXNB3 and inactivates and stabilizes RAC1. Interacts (GTP-bound form preferentially) with PKN2 (via the REM repeats); the interaction stimulates autophosphorylation and phosphorylation of PKN2. Interacts with the GEF proteins PREX1, RASGRF2, FARP1, FARP2, DOCK1, DOCK2 and DOCK7, which promote the exchange between GDP and GTP, and therefore activate it. Interacts with PARD6A, PARD6B and PARD6G in a GTP-dependent manner. Part of a quaternary complex containing PARD3, some PARD6 protein (PARD6A, PARD6B or PARD6G) and some atypical PKC protein (PRKCI or PRKCZ), which plays a central role in epithelial cell polarization. Found in a trimeric complex composed of DOCK1 and ELMO1, which plays a central role in phagocytosis of apoptotic cells. Interacts with RALBP1 via its effector domain. Interacts with PLXNB1. Probably found in a ternary complex composed of DSCAM, PAK1 and RAC1. Interacts with DSCAM; the interaction requires PAK1. Part of a complex with MAP2K3, MAP3K3, CCM2 and DEF6. Interacts with BAIAP2, BAIAP2L1 and DEF6. Interacts with Y.pseudotuberculosis YPKA and PLCB2. Interacts with NOXA1. Interacts with ARHGEF2. Interacts with TBC1D2. Interacts with UNKL. Interacts with USP6. Interacts with SPATA13. Interacts with ARHGEF16; mediates activation of

	RAC1 by EPHA2. Interacts with ITGB4. Interacts with S100A8 and calprotectin (S100A8/9). Interacts with PACSIN2. Interacts with ITGB1BP1. Interacts (when active) with PPP5C (via TPR repeats); activates PPP5C phosphatase activity and translocates PPP5C to the cell membrane. **Subcellular Location:** Cell membrane; Lipid-anchor; Cytoplasmic side. Melanosome. Cytoplasm. Note=Inner surface of plasma membrane possibly with attachment requiring prenylation of the C-terminal cysteine. Identified by mass spectrometry in melanosome fractions from stage I to stage IV. Found in the ruffled border (a late endosomal-like compartment in the plasma membrane) of bone-resorbing osteoclasts. **Tissue Specificity:** Isoform B is predominantly identified in skin and epithelial tissues from the intestinal tract. Its expression is elevated in colorectal tumors at various stages of neoplastic progression, as compared to their respective adjacent tissues. **Post-translational modifications:** AMPylation at Tyr-32 and Thr-35 are mediated by bacterial enzymes in case of infection by H.somnus and V.parahaemolyticus, respectively. AMPylation occurs in the effector region and leads to inactivation of the GTPase activity by preventing the interaction with downstream effectors, thereby inhibiting actin assembly in infected cells. It is unclear whether some human enzyme mediates AMPylation; FICD has such ability in vitro but additional experiments remain to be done to confirm results in vivo. GTP-bound active form is ubiquitinated by HACE1, leading to its degradation by the proteasome. **Similarity:** Belongs to the small GTPase superfamily. Rho family. **Database links:** **Entrez Gene:** 5879 Human **Entrez Gene:** 5880 Human **Entrez Gene:** 19353 Mouse **Entrez Gene:** 19354 Mouse **Entrez Gene:** 363875 Rat **Entrez Gene:** 366957 Rat Omim: 602048 Human Omim: 602049 Human **SwissProt:** P15153 Human **SwissProt:** P63000 Human **SwissProt:** P63001 Mouse **SwissProt:** Q05144 Mouse **SwissProt:** Q6RUV5 Rat

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