abcam

Product datasheet

Recombinant Human RAB7 protein ab103507

3 References 1 Image

Description

Product name Recombinant Human RAB7 protein

Purity > 90 % SDS-PAGE.

purified by using anion-exchange chromatography (DEAE sepharose resin) and gel-filtration

chromatography (Sephacryl S-200) with 20mM Tris pH 7.5, 2mM EDTA.

Expression system Escherichia coli

Accession P51149

Protein length Full length protein

Animal free No

Nature Recombinant

Species Human

Sequence MGSSHHHHHH SSGLVPRGSH MTSRKKVLLK

VIILGDSGVG KTSLMNQYVN KKFSNQYKAT IGADFLTKEV

MVDDRLVTMQ IWDTAGQERF QSLGVAFYRG ADCCVLVFDV TAPNTFKTLD SWRDEFLIQA SPRDPENFPF VVLGNKIDLE NRQVATKRAQ

AWCYSKNNIP YFETSAKEAI NVEQAFQTIA RNALKQETEV

ELYNEFPEPIKLDKNDRAKA SAESCSC

Predicted molecular weight 26 kDa including tags

Amino acids 1 to 207

Tags His tag N-Terminus

Specifications

Our Abpromise quarantee covers the use of ab103507 in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Applications SDS-PAGE

Mass Spectrometry

Mass spectrometry MALDI-TOF

Form Liquid

Preparation and Storage

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Stability and Storage

Shipped at 4°C. Upon delivery aliquot and store at -20°C or -80°C. Avoid repeated freeze / thaw cycles.

pH: 8.00

Constituents: 0.0154% DTT, 0.316% Tris HCl, 30% Glycerol (glycerin, glycerine), 0.58% Sodium chloride

General Info

Function

Key regulator in endo-lysosomal trafficking. Governs early-to-late endosomal maturation, microtubule minus-end as well as plus-end directed endosomal migration and positioning, and endosome-lysosome transport through different protein-protein interaction cascades. Plays a central role, not only in endosomal traffic, but also in many other cellular and physiological events, such as growth-factor-mediated cell signaling, nutrient-transportor mediated nutrient uptake, neurotrophin transport in the axons of neurons and lipid metabolism. Also involved in regulation of some specialized endosomal membrane trafficking, such as maturation of melanosomes, pathogen-induced phagosomes (or vacuoles) and autophagosomes. Plays a role in the maturation and acidification of phagosomes that engulf pathogens, such as S.aureus and M.tuberculosis. Plays a role in the fusion of phagosomes with lysosomes. Plays important roles in microbial pathogen infection and survival, as well as in participating in the life cycle of viruses. Microbial pathogens possess survival strategies governed by RAB7A, sometimes by employing RAB7A function (e.g. Salmonella) and sometimes by excluding RAB7A function (e.g. Mycobacterium). In concert with RAC1, plays a role in regulating the formation of RBs (ruffled borders) in osteoclasts. Controls the endosomal trafficking and neurite outgrowth signaling of NTRK1/TRKA. Regulates the endocytic trafficking of the EGF-EGFR complex by regulating its lysosomal degradation.

Tissue specificity

Involvement in disease

Widely expressed; high expression found in skeletal muscle.

Defects in RAB7A are the cause of Charcot-Marie-Tooth disease type 2B (CMT2B) [MIM:600882]; also known as hereditary motor and sensory neuropathy II (HMSN2). CMT2B is a form of Charcot-Marie-Tooth disease, the most common inherited disorder of the peripheral nervous system. Charcot-Marie-Tooth disease is classified in two main groups on the basis of electrophysiologic properties and histopathology: primary peripheral demyelinating neuropathy or CMT1, and primary peripheral axonal neuropathy or CMT2. Neuropathies of the CMT2 group are characterized by signs of axonal regeneration in the absence of obvious myelin alterations, normal or slightly reduced nerve conduction velocities, and progressive distal muscle weakness and atrophy. CMT2B is clinically characterized by marked distal muscle weakness and a high frequency of foot ulcers, infections and amputations of the toes. CMT2B inheritance is autosomal dominant.

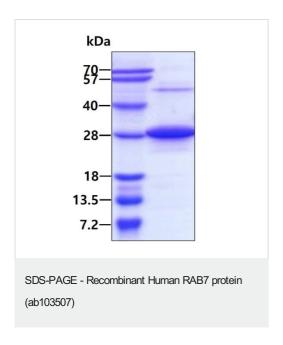
Sequence similarities

Cellular localization

Belongs to the small GTPase superfamily. Rab family.

Late endosome. Lysosome. Cytoplasmic vesicle > phagosome. Melanosome. Cytoplasmic vesicle > phagosome membrane. Co-localizes with OSBPL1A at the late endosome. Found in the ruffled border (a late endosomal-like compartment in the plasma membrane) of bone-resorbing osteoclasts. Recruited to phagosomes containing S.aureus or Mycobacterium.

Images



3ug by SDS-PAGE under reducing conditions and visualized by coomassie blue stain.

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