ELK Biotechnology

c-Abl (phospho-Thr735) rabbit pAb

Cat No.:ES17898

For research use only

Overview

Product Name	c-Abl (phospho-Thr735) rabbit pAb
Host species	Rabbit
Applications	WB
Species Cross-Reactivity	Human;Rat;Mouse;
Recommended dilutions	WB 1:1000-2000
Immunogen	Synthesized phosho peptide around human c-Abl (Thr735)
Specificity	This antibody detects endogenous levels of Human c-Abl (phospho-Thr735)
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	c-Abl (Thr735)
Gene Name	ABL1 ABL JTK7
Cellular localization	Cytoplasm, cytoskeleton. Nucleus. Mitochondrion . Shuttles between the nucleus and cytoplasm depending on environmental signals. Sequestered into the cytoplasm through interaction with 14-3-3 proteins. Localizes to mitochondria in response to oxidative stress (By similarity). .; [Isoform IB]: Nucleus membrane; Lipid-anchor. The myristoylated c-ABL protein is reported to be nuclear.
Purification	The antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific immunogen.
Clonality	Polyclonal
Concentration	1 mg/ml
Observed band	140(200kd BCR-ABL complex）
Human Gene ID	25
Human Swiss-Prot Number	P00519
Alternative Names	Tyrosine-protein kinase ABL1 (EC 2.7.10.2) (Abelson murine leukemia viral oncogene homolog 1) (Abelson tyrosine-protein kinase 1) (Proto-oncogene

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Background

c-Abl) (p150)
This gene is a protooncogene that encodes a protein tyrosine kinase involved in a variety of cellular processes, including cell division, adhesion, differentiation, and response to stress. The activity of the protein is negatively regulated by its SH3 domain, whereby deletion of the region encoding this domain results in an oncogene. The ubiquitously expressed protein has DNA-binding activity that is regulated by CDC2-mediated phosphorylation, suggesting a cell cycle function. This gene has been found fused to a variety of translocation partner genes in various leukemias, most notably the t(9;22) translocation that results in a fusion with the 5' end of the breakpoint cluster region gene (BCR; MIM:151410). Alternative splicing of this gene results in two transcript variants, which contain alternative first exons that are spliced to the remaining common exons. [pr

+86-27-59760950 ELKbio@ELKbiotech.com www.elkbiotech.com
23-2, No.388 Gaoxin 2nd Road,Wuhan East Lake Hi-tech Development Zone, Hubei , P.R.C