SHANGHAI GENOMICS

Recombinant Human Adenomatosis Polyposis Coli2

rHuApc2

Catalog number: 3132-01

Specifications and Use

Source	● *Sf9 insect cell*
Molecular Mass	● 100 kDa
Purity	● ≥ 85% as determined by SDS-PAGE
Tag	● 6×His
Formulation	● 20mM Tris-HCl, 150mM NaCl, 0.5mM EDTA, pH7.9, 10% glycerol
Stability	● Store at -80°C. Avoid repeated freezing and thawing
Usage	● FOR RESEARCH USE ONLY. NOT FOR HUMAN USE.

Human APC2

The adenomatous polyposis syndromes, familial adenomatous polyposis (FAP) and Gardner's syndrome (GS), are characterized by numerous adenomatous polyps throughout the entire colon. These polyps invariably progress to colon cancer in addition to other extracolonic manifestations. The cloning of the APC gene revealed a ubiquitously expressed protein, 2843 amino acids in length, with a molecular weight of 300 kDa, which is frequently mutated in patients suffering from FAP and GS. APC has been found to be associated with structural components of intracellular junctions. β-catenin and γ-catenin (also called plakoglobin) are involved in the regulation of cellular adhesion. APC and E cadherin compete for binding to specific internal regions of both β- and γ-catenin. Interactions between cytoskeleton and the APC, E cadherin, β/γ catenin complex are mediated by α-catenin. Like APC, APC2 contains SAMP domains, which are required for conductin binding. Both APC and APC2 regulate the formation of active β-catenin-Tcf complexes.

Protein Sequence:

HHHHHHDYDIPTTENLYFQAAMDPEFRANPAMAAAVVVAEGDSDSRPGQELLVAWNTVSTGLVPP
AALGLVSSRTSGAVPPKEEELRAAVEVLRGHGLHSVLEEWFVEVLQNDLQANISPEFWNAISQCEN
SADEPQCLLLLLDAFGLLESRLDPYLRSLELLEKWTRLGLLMGTGAQGLREEVHTMLRGVLFFSTP
RTFQEMIQRLYGCFLRVYMQSKRKGEGGTDPELEGELDSRYARRRYYRLLQSPLCAGCSSDKQQ
CWCRQALEQFHQLSQVLHRLSLLERVSAEAVTTTLHQVTRERMEDRCRGEYERSFLREFHKWIER
VVGWLGKVFLQDGPARPASPEAGNTLRRWRCHVQRFFYRIYASLRIEELFSIVRDFPDSRPAIEDLK
YCLERTDQRQQLLVSLKAALETRLLHPGVNTCDIITLYISAIKALRVLDPSMVILEVACEPIRRYLRTRE
DTVRQIVAGLTGDSDGTGDLAVELSKTDPASLETGQDSEDDSGEPEDWVPDPVDADPGKSSSKRR
SSDIISLLVSIYGSKDLFINEYRSLLADRLLHQFSFSPEREIRNVELLKLRFGEAPMHFCEVMLKDMA
DSRRINANIREEDEKRPAEEQPPFGVYAVILSSEFWPPFKDEKLEVPEDIRAALEAYCKKYEQLKAM
RTLSWKHTLGLVTMDVELADRTLSVAVTPVQAVILLYFQDQASWTLEELSKAVKMPVALLRRRMSV
WLQQGVLREEPPGTFSVIEEERPQDRDNMVLIDSDDESDSGMASQADQKEEELLLFWTYIQAMLT
NLESLSLDRIYNMLRMFVVTGPALAEIDLQELQGYLQKKVRDQQLVYSAGVYRLPKNCS

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