

32-5352: Recombinant Human HSP70 Interacting Protein

Alternative Name : AAG2,SNC6,HSPABP,FAM10A1,FAM10A4,HSPABP1,ST-13,Hsc70-interacting protein,Suppression of tumorigenicity protein 13,Putative tumor suppressor ST13,Protein FAM10A1,Progesterone receptor-associated p48 protein,Renal carcinoma antigen NY-REN-3

Description

Source : Escherichia Coli. Recombinant Human ST13 produced in E.Coli is a single,non-glycosylated polypeptide chain containing 369 amino acids (12-369 a.a.) and having a molecular mass of 41.3 kDa.ST13 human recombinant is purified by conventional chromatography techniques. ST13 is an adaptor protein (co-chaperone) that mediates the association of HSP70 & HSP90 and appears in early receptor complexes. ST13 plays a role in the assembly process of glucocorticoid receptor, which requires the assistance of multiple molecular chaperones. The expression of ST13 is downregulated in colorectal carcinoma tissue signifying that is candidate tumor suppressor gene. Through common binding to both Hsp70 and Hsp90, ST13 functions as an adaptor that can integrate Hsp70 and Hsp90 interactions. The expression of ST13 decreases in colorectal cancer tissue compared with that in adjacent normal tissue. ST13 is mostly expressed in colorectal epithelia and adenocarcinoma cells. ST13 functions to promote the efficiency of glucocorticoid receptor maturation in cells. The expression levels of the ST13 gene were significantly decreased in primary tumors compared with adjacent mucosa.

Product Info

Amount : 50 µg
Purification : Greater than 90.0% as determined by SDS-PAGE.
Content : The ST13 protein solution contains 20mM Tris-HCl, pH-8 1mM DTT, 0.1M NaCl & 10% Glycerol.
Storage condition : Store at 4°C if entire vial will be used within 2-4 weeks. Store, frozen at -20°C for longer periods of time. For long term storage it is recommended to add a carrier protein (0.1% HSA or BSA).Avoid multiple freeze-thaw cycles.
Amino Acid : MDPKRVNELR AFVKMCKQDP SVLHTEEMRF LREWVESMGK KVPPATQKAK SEENTKEEKP
DSKKVEEDLK ADEPSSEESD LEIDKEGVIEPDTDAPQEMG DENAEITEEM MDQANDKKVA AIEALNDGEL
QKAIDLFTDA IKLNRLAIL YAKRASVFK LQKPNAAIRD CDRAIEINPD SAQPYKWRGK AHRLLGHWEE
AAHDLALACK LDYDEDASAM LKEVQPRAQK IAEHRRKYER KREEREIKER IERVKKAREE
HERAQREEEARRQSGAQYGS FPGGFPGGMP GNFPGGMPGM GGGMPGMAGM PGLNEILSDP
EVLAAMQDPE VMVAFQDVAQ NPANMSKYQS NPKVMNLISK LSAKFGGQA.