

32-13273: ITGB4 Human

Alternative Name : Integrin beta-4, GP150, CD104, ITGB4, Integrin Subunit Beta 4, CD104 Antigen, Integrin, Beta 4, Integrin Beta-4.

Description

Source: Sf9, Baculovirus cells.

Sterile Filtered colorless solution.

ITGB4 (integrin beta-4 isoform 1) belongs to the Integrin beta family. ITGB4 forms noncovalent heterodimers with Integrin alpha 6 and takes part in the formation of epithelial hemidesmosomes. ITGB4 has a vital structural role in the hemidesmosome of epithelial cells and is needed for the regulation of keratinocyte motility & polarity. ITGB4 leans towards the association with alpha 6 subunit and is expected to take a key role in the biology of invasive carcinoma.

ITGB4 produced in Sf9 Baculovirus cells is a single, glycosylated polypeptide chain containing 691 amino acids (28-710a.a.) and having a molecular mass of 77.5kDa. (Molecular size on SDS-PAGE will appear at approximately 70-100kDa). ITGB4 is expressed with an 8 amino acid His tag at C-Terminus and purified by proprietary chromatographic techniques.

Product Info

Amount : 1 µg / 5 µg

Purification : Greater than 90.0% as determined by SDS-PAGE.

Content : ITGB4 protein solution (0.5mg/ml) contains Phosphate Buffered Saline (pH 7.4) & 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 : NRCKKAPVKS CTECVRVKD CAYCTDEMFR DRRCNTQAE LAAGCQRESI VMESSFQIT EETQIDTTLR
RSQMSPQGLR VRLRPGEERH FELEVFEPLE SPVDLYILMD FSNSMSDDLD NLKKMGQNLA RVLSQLTSDY
TIGFGKFVDK VSPQTDMPR EKLKEPWPNS DPPFSFKNVI SLTEDVDEFR NKLQGERISG NLDAPGGFD
AILQTAVCTR DIGWRPDSTH LLVFSTESAF HYEADGANVL AGIMSRNDER CHLDTTGTYT QYRTQDYPVS
PTLVRLAKH NIIPIFAVTN YSYSYEKLH TYFPVSSLGV LQEDSSNIVE LLEAFNRIR SNLDIRALDS
PRGLRTEVTS KMFQKTRTGS FHRRGEVGI YQVQLRALEH VDGTHVCQLP EDQKGNHLK PSFSDGLKMD
AGIICDVCTC ELQKEVRSAR CSFNGDFVCG QCVCSSEGWSG QTCNCSTGSL SDIQPCLREG EDKPCSGRGE
CQCGHCVCYG EGRYEGQFCE YDNFQCPRTS GFLCNDRGRC SMGQCVCEPG WTPSCDCPL
SNATCIDSNG GICNGRGHCE CGRCHCHQOS LYTDITICEIN YSAIHPLCE DLRSCVQCQA WGTGEKKGRT
CEEENFKVKM VDELKRAEEV VVRCSFRDED DDCTYSYME GDGAPGNST VLVHKKKDCP
PGSLEHHHHH H