32-13766: COMP Human

Format : The COMP solution (0. 5mg/1ml) contains phosphate buffered saline (pH7.4) and 10% glycerol.

Alternative Name : Cartilage Oligomeric Matrix Protein (pseudoachondroplasia epiphyseal dysplasia 1 multiple), MED, THBS5, TSP5, EDM1, PSACH, EPD1, Thrombospondin-5

Description

Source:HEK293 Cells.

Physical Appearance:Sterile filtered colorless solution.

Biological Activitynull

COMP is a non-collagenous glycoprotein and is belongs to the thrombospondin family of extracellular proteins. COMP is a calcium-binding protein of high molecular weight (>500kDa) found in the extracellular matrix of articular, nasal and tracheal cartilage. COMP is not only cartilage-derived but is common in other tissues, such as synovium and tendon. Intact COMP is pentameric, with 5 equal subunits and the carboxy-terminal globular domain of native COMP binds to collagens I, II, and IX. COMP molecules are vital for conserving the properties and integrity of collagen network. Moreover, COMP has a storage and delivery function for hydrophobic cellsignaling molecules such as vitamin D. Mutations of the COMP gene cause Pseudoachondroplasia and some forms of multiple epiphyseal dysplasia which implicates that it is vital that COMP develops and functions normally.

COMP Human Recombinant produced in HEK293 Cells is a single, glycosylated polypeptide chain containing 749 amino acids (21-757a.a) and having a molecular mass of 82.4kDa.COMP is expressed with a 6 amino acid His tag at C-Terminus and purified by proprietary chromatographic techniques.

Product Info

Amount : 10 μg / 2 μg

Purification : Greater than 85.0% as determined by SDS-PAGE.

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 : ADPDAHSLWY NFTIIHLPRH GQQWCEVQSQ VDQKNFLSYD CGSDKVLSMG HLEEQLYATD AWGKQLEMLR EVGQRLRLEL ADTELEDFTP SGPLTLQVRM SCECEADGYI RGSWQFSFDG RKFLLFDSNN RKWTVVHAGA RRMKEKWEKD SGLTTFFKMV SMRDCKSWLR DFLMHRKKRL EPTAPPTMAP GLEPKSCDKT HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP REPQVYTLPP SRDELTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGKHHHHHH