32-4865: Recombinant Human SMAD Family Member 2

Alternative Name : JV18,MADH2,MADR2,JV18-1,hMAD-2,hSMAD2,MGC22139,MGC34440,SMAD2,Mothers against decapentaplegic homolog 2,Mothers against DPP homolog 2,Mad-related protein 2,SMAD 2,SMAD family member 2.

Description

Source : Escherichia Coli. SMAD2 Human Recombinant produced in E.Coli is a single, non-glycosylated polypeptide chain containing 487 amino acids (1-467) and having a molecular mass of 54.4 kDa. SMAD2 is fused to 20 amino acid His-Tag at N-Terminus and purified by standard chromatography techniques. SMAD2 is part of the SMAD family of proteins that mediate signal transduction by the TGF-beta/activin/BMP-2/4 cytokine superfamily from receptor Ser/Thr protein kinases at the cell surface to the nucleus. Phosphorylated SMAD2 is then able to form a complex with SMAD4 or SARA. These complexes accumulate in the cell nucleus, where they are directly participating in the regulation of gene expression. SMAD2 mediates the signal of the TGF-beta, and therefore regulates multiple cellular processes, such as cell proliferation, apoptosis, and differentiation. SMAD2 is recruited to the TGF-beta receptors through its interaction with the SMAD anchor for receptor activation (SARA) protein. TGF-beta 1 acts on adjacent stromal cells to turn on SMAD2 signalling that could lead to stromal decidualization. SMAD2 is the downstream signal transducers of TGF-beta-1 in human dental pulp cells.

Product Info

Amount :	10 µg
Purification :	Greater than 95.0% as determined by SDS-PAGE.
Content :	The SMAD2 protein solution contains 20mM Tris-HCl pH-8, and 100mM NaCl.
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 :	MGSSHHHHHH SSGLVPRGSH MSSILPFTPP VVKRLLGWKK SAGGSGGAGG GEQNGQEEKW CEKAVKSLVK KLKKTGRLDE LEKAITTQNC NTKCVTIPSTCSEIWGLSTP NTIDQWDTTG LYSFSEQTRS LDGRLQVSHR KGLPHVIYCR LWRWPDLHSH HELKAIENCE YAFNLKKDEV CVNPYHYQRV ETPVLPPVLVPRHTEILTEL PPLDDYTHSI PENTNFPAGI EPQSNYIPET PPPGYISEDG ETSDQQLNQS MDTGSPAELS PTTLSPVNHS LDLQPVTYSE PAFWCSIAYYELNQRVGETF HASQPSLTVD GFTDPSNSER FCLGLLSNVN RNATVEMTRR HIGRGVRLYY IGGEVFAECL SDSAIFVQSP NCNQRYGWHP ATVCKIPPGCNLKIFNNQEF AALLAQSVNQ GFEAVYQLTR MCTIRMSFVK GWGAEYRRQT VTSTPCWIEL HLNGPLQWLD KVLTQMGSPS VRCSSMS.