

Human Latent TGF-beta 1 / TGFB1 Protein (His Tag)

Catalog Number: 10804-H08H



Sino Biological
Biological Solution Specialist

General Information

Gene Name Synonym:

CED; DPD1; LAP; TGF-beta 1; TGFB; TGFbeta

Protein Construction:

A DNA sequence encoding the full length of human TGFβ1 (NP_000651.3) (Met 1-Ser 390) was fused with a C-terminal polyhistidine tag.

Source: Human

Expression Host: HEK293 Cells

QC Testing

Purity: > 95 % as determined by SDS-PAGE

Bio Activity:

1. Measured by its binding ability in a functional ELISA.
2. Immobilized Human TGFβ1-His at 10 µg/mL (100 µl/well) can bind biotinylated human TGFβR2-Fch, The EC₅₀ of biotinylated human TGFβR2-Fch is 50-200 ng/mL.

Endotoxin:

< 1.0 EU per µg of the protein as determined by the LAL method

Stability:

Samples are stable for up to twelve months from date of receipt at -70 °C

Predicted N terminal: Leu 30 & Ala 279

Molecular Mass:

The recombinant human latent TGFβ1 consists of 370 amino acids and has a calculated molecular mass of 42.4 kDa. In SDS-PAGE under reducing conditions, the apparent molecular mass of rh TGFβ1 is approximately 16, 38 and 55 kDa corresponding to mature TGFβ1, LAP protein and inactive latent TGFβ1 respectively due to glycosylation. In non-reduced SDS-PAGE, it migrates as an approximately 110 kDa protein consisting of a TGFβ1 homodimer non-covalently linked to a LAP homodimer.

Formulation:

Lyophilized from sterile PBS, pH 7.4

Normally 5 % - 8 % trehalose, mannitol and 0.01% Tween80 are added as protectants before lyophilization. Specific concentrations are included in the hardcopy of COA. Please contact us for any concerns or special requirements.

Usage Guide

Storage:

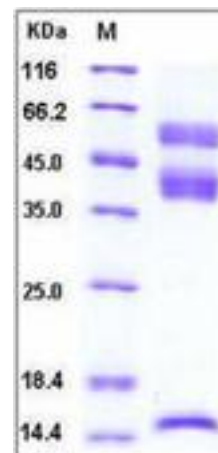
Store it under sterile conditions at -20°C to -80°C upon receiving. Recommend to aliquot the protein into smaller quantities for optimal storage.

Avoid repeated freeze-thaw cycles.

Reconstitution:

Detailed reconstitution instructions are sent along with the products.

SDS-PAGE:



Protein Description

TGF-beta 1 is a member of the transforming growth factor beta (TGF-beta) family. The transforming growth factor-beta family of polypeptides are involved in the regulation of cellular processes, including cell division, differentiation, motility, adhesion and death. TGF-beta 1 positively and negatively regulates many other growth factors. It inhibits the secretion and activity of many other cytokines including interferon-γ, tumor necrosis factor-alpha and various interleukins. It can also decrease the expression levels of cytokine receptors. Meanwhile, TGF-beta 1 also increases the expression of certain cytokines in T cells and promotes their proliferation, particularly if the cells are immature. TGF-beta 1 also inhibits proliferation and stimulates apoptosis of B cells, and plays a role in controlling the expression of antibody, transferrin and MHC class II proteins on immature and mature B cells. As for myeloid cells, TGF-beta 1 can inhibit their proliferation and prevent their production of reactive oxygen and nitrogen intermediates. However, as with other cell types, TGF-beta 1 also has the opposite effect on cells of myeloid origin. TGF-beta 1 is a multifunctional protein that controls proliferation, differentiation and other functions in many cell types. It plays an important role in bone remodeling as it is a potent stimulator of osteoblastic bone formation, causing chemotaxis, proliferation and differentiation in committed osteoblasts. Once cells lose their sensitivity to TGF-beta1-mediated growth inhibition, autocrine TGF-beta signaling can promote tumorigenesis. Elevated levels of TGF-beta1 are often observed in advanced carcinomas, and have been correlated with increased tumor invasiveness and disease progression.

References

1. Ghadami M, *et al.* (2000) Genetic Mapping of the Camurati-Engelmann Disease Locus to Chromosome 19q13.1-q13.3. *Am J Hum. Genet.* 66(1):143-7.
2. Letterio J, *et al.* (1998) Regulation of immune responses by TGF-beta. *Annu Rev Immunol.* 16:137-61.
3. Vaughn SP, *et al.* (2000) Confirmation of the mapping of the Camurati-Engelmann locus to 19q13.2 and refinement to a 3.2-cM region. *Genomics.* 66(1):119-21.

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