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Product datasheet for TP724296

Human CD142 Protein, hFc Tag

Product data:

Product Type:	Recombinant Proteins
Description:	Human CD142 Protein, hFc Tag
Expression Host:	HEK293
Tag:	C-Human Fc
Predicted MW:	The protein has a predicted molecular mass of 50.9 kDa after removal of the signal peptide. The apparent molecular mass of CD142-hFc is approximately 55-70kDa due to glycosylation.
Purity:	The purity of the protein is greater than 95% as determined by SDS-PAGE and Coomassie blue staining.
Reconstitution Method:	Lyophilized from sterile PBS, pH 7.4. Normally 5 % - 8% trehalose is added as protectants before lyophilization.
Storage:	Store at -20°C to -80°C for 12 months in lyophilized form. After reconstitution, if not intended for use within a month, aliquot and store at -80°C (Avoid repeated freezing and thawing). Lyophilized proteins are shipped at ambient temperature.
Stability:	12 months from date of despatch
Summary:	This gene encodes coagulation factor III which is a cell surface glycoprotein. This factor enables cells to initiate the blood coagulation cascades, and it functions as the high-affinity receptor for the coagulation factor VII. The resulting complex provides a catalytic event that is responsible for initiation of the coagulation protease cascades by specific limited proteolysis. Unlike the other cofactors of these protease cascades, which circulate as nonfunctional precursors, this factor is a potent initiator that is fully functional when expressed on cell surfaces, for example, on monocytes. There are 3 distinct domains of this factor: extracellular, transmembrane, and cytoplasmic. Platelets and monocytes have been shown to express this coagulation factor under procoagulatory and proinflammatory stimuli, and a major role in HIV-associated coagulopathy has been described. Platelet-dependent monocyte expression of coagulation factor III has been described to be associated with Coronavirus Disease 2019 (COVID-19) severity and mortality. This protein is the only one in the coagulation pathway for which a congenital deficiency has not been described. Alternate splicing results in multiple transcript variants.[provided by RefSeq, Aug 2020]

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