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32-13410: SERPIND1 Human

Alternative Name :	Serpin Family D Member 1, Cysteine Proteinase Inhibitor Clade D Member 1, Serpin Peptidase Inhibitor Clade D Member 1, Protease Inhibitor Leuserpin-2, Serpin D1, HCF2, HLS2, Leuserpin 2, D22S673, THPH10, HC-II, HCII, HC2, LS2.

Description

Source: Escherichia Coli.
Sterile Filtered colorless solution.
Serpin Peptidase Inhibitor, Clade D Member 1 (SERPIND1) is a serine proteinase inhibitor which rapidly inhibits thrombin in the presence of dermatan sulfate. SERPIND1 gene is a member of the serpin gene superfamily. SERPIND1 protein contains 5 exons and 4 introns. SERPIND1 shares homology with antithrombin III and other members of the alpha 1-antitrypsin superfamily. SERPIND1 gene mutations are linked with cofactor II deficiency. SERPIND1 protein is activated by dermatan sulfate, and glycosaminoglycans. Allelic variations in the SERPIND1 gene are linked with cofactor II deficiency.
SERPIND1 Human Recombinant produced in E.coli is a single, non-glycosylated polypeptide chain containing 465 amino acids (58-499) and having a molecular mass of 53.3kDa.SERPIND1 is fused to a 23 amino acid His-Tag at N-terminus and purified by proprietary chromatographic techniques.

Product Info

Amount :	5 µg / 20 µg
Purification :	Greater than 85% as determined by SDS-PAGE.
Content :	The SERPIND1 solution (1mg/ml) contains 20mM Tris-HCl buffer (pH 8.0), 10% glycerol and 0.4M Urea.
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 MGSDFHKENT VTNDWIPEGE EDDDYLDLEK IFSEDDDYID IVDSLSVSPT DSDVSAGNIL QLFHGKSRIQ RLNILNAKFA FNLYRVLKDQ VNTFDNIFIA PVGISTAMGM ISLGLKGETH EQVHSILHFK DFVNASSKYE ITTIHNLFRK LTHRLFRRNF GYTLRSVNDL YIQKQFPILL DFKTKVREYY FAEAQIADFS DPAFISKTNN HIMKLTKGLI KDALENIDPA TQMMILNCIY FKGSWVNKFP VEMTHNHNFR LNEREVVKVS MMQTKGNFLA ANDQELDCDI LQLEYVGGIS MLIVVPHKMS GMKTLEAQLT PRVVERWQKS MTNRTREVLL PKFKLEKNYN LVESLKLMGI RMLFDKNGNM AGISDQRIAI DLFKHQGTIT VNEEGTQATT VTTVGFMPLS TQVRFTVDRP FLFLIYEHRT SCLLFMGRVA NPSRS.