Recombinant Human MMP16 Protein (His Tag)

Catalog Number: PDEH101036

Note: *Centrifuge before opening to ensure complete recovery of vial contents.*

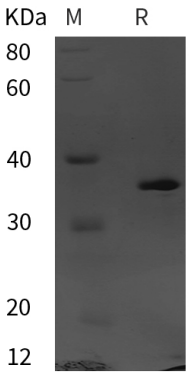
Description

Species	Human
Source	E.coli-derived Human MMP16 protein Ala151-Lys450, with an N-terminal His & C-terminal His
Calculated MW	32.9 kDa
Observed MW	35 kDa
Accession	P51512
Bio-activity	Not validated for activity

Properties

Purity	> 95% as determined by reducing SDS-PAGE.
Endotoxin	< 10 EU/mg of the protein as determined by the LAL method
Storage	Generally, lyophilized proteins are stable for up to 12 months when stored at -20 to -80°C. Reconstituted protein solution can be stored at 4-8°C for 2-7 days. Aliquots of reconstituted samples are stable at < -20°C for 3 months.
Shipping	This product is provided as lyophilized powder which is shipped with ice packs.
Formulation	Lyophilized from a 0.2 μm filtered solution in PBS with 5% Trehalose and 5% Mannitol.
Reconstitution	It is recommended that sterile water be added to the vial to prepare a stock solution of 0.5 mg/mL. Concentration is measured by UV-Vis.

Data



SDS-PAGE analysis of Human MMP16 proteins, 2 μg/lane of Recombinant Human MMP16 proteins was resolved with SDS-PAGE under reducing conditions, showing bands at 35 kDa.

Background

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Matrix metalloproteinases (MMPs) are a family of zinc and calcium dependent endopeptidases with the combined ability to degrade all the components of the extracellular matrix (ECM). MMP-16 (MT3-MMP) is found in brain, lung, placenta, smooth muscle cells, and malignant tumor tissues including oral melanoma and renal carcinoma . MMP-16 has been shown to activate proMMP-2 and degrade various ECM components including native collagens. MMP-16 has been proposed to possess the potential to directly enhance the growth and invasiveness of cells in vivo, two critical processes for development and carcinogenesis . Structurally, MMP-16 consists of the following domains: a pro domain containing the furin cleavage site, a catalytic domain containing the zinc-binding site, a hinge region, a hemopexin-like domain, a transmembrane domain, and a cytoplamasic tail . The structure of the catalytic domain in complex with a hydroxamate inhibitor has been solved . The rhMMP-16PC consists of the pro and catalytic domains, which can be activated by treatment with furin.

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