Recombinant Human Peroxiredoxin 6/PRDX6 Protein (His Tag)

Catalog Number: PKSH031178

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

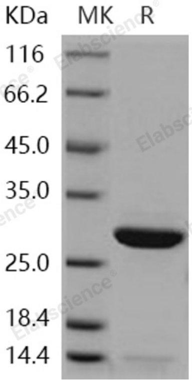
Description

Species	Human
Source	E.coli-derived Human Peroxiredoxin 6/PRDX6 protein Met 1-Pro 224, with an N-terminal His
Calculated MW	26.5 kDa
Observed MW	26.5 kDa
Accession	P30041
Bio-activity	Not validated for activity

Properties

Purity	> 95 % as determined by reducing SDS-PAGE.
Endotoxin	Please contact us for more information.
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 sterile PBS, pH 7.4 Normally 5% - 8% trehalose, mannitol and 0.01% Tween 80 are added as protectants before lyophilization. Please refer to the specific buffer information in the printed manual.
Reconstitution	Please refer to the printed manual for detailed information.

Data



> 95 % as determined by reducing SDS-PAGE.

Background

acid phosphatase-like protein 2; also known as ACPL2; is a secreted protein which belongs to thehistidine acid phosphatase family. A large-scale effort; termed the Secreted Protein Discovery Initiative (SPDI); was undertaken to identify novel secreted and transmembrane proteins. In the first of several approaches; a biological signal sequence trap in yeast cells was utilized to identify cDNA clones encoding putative secreted proteins. A second strategy utilized various algorithms that recognize features such as the hydrophobic properties of signal sequences to identify putative proteins encoded by expressed sequence tags (ESTs) from human cDNA libraries. A third approach surveyed ESTs for protein sequence similarity to a set of known receptors and their ligands with the BLAST algorithm. Finally; both signal-sequence prediction algorithms and BLAST were used to identify single exons of potential genes from within human genomic sequence.