Recombinant Protein Technical Manual

Recombinant Human Peroxiredoxin 6/PRDX6 Protein (His Tag)
RPES1679

Product Data:

Product SKU: RPES1679

Size: 20µg

Species: Human

Expression host: E. coli

Uniprot: P30041

Protein Information:

Molecular Mass:	26.5 kDa
AP Molecular Mass:	26.5 kDa
Tag:	N-His
Bio-activity:	
Purity:	> 95 % as determined by reducing SDS-PAGE.
Endotoxin:	Please contact us for more information.
Storage:	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℃ for 2-7 days. Aliquots of reconstituted samples are stable at < -20℃ 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
Reconstitution:	Please refer to the printed manual for detailed information.
Application:	
Synonyms:	Peroxiredoxin-6; 1-Cys Peroxiredoxin; 1-Cys PRX; 24 kDa Protein; Acidic Calcium-Independent Phospholipase A2; aiPLA2; Antioxidant Protein 2; Liver 2D PAGE Spot 40; Non-Selenium Glutathione Peroxidase; NSGPx; Red Blood Cells Page Spot 12; PRDX6; AOP2; KIAA0106; p29

Sequence: Met 1-Pro 224

acid phosphatase-like protein 2, also known as ACPL2, is a secreted protein which belongs to the histidine 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.