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

**Catalog Number:PKSH031178**

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

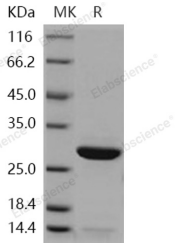
## Description

| | |
|---|---|
| **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 |
| **Species** | Human |
| **Expression Host** | E.coli |
| **Sequence** | Met 1-Pro 224 |
| **Accession** | P30041 |
| **Calculated Molecular Weight** | 26.5 kDa |
| **Observed molecular weight** | 26.5 kDa |
| **Tag** | N-His |

## 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℃. 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<br>Normally 5 % - 8 % trehalose, mannitol and 0.01% Tween80 are added as protectants before lyophilization.<br>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

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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.



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