Human ERP72 / PDIA4 Protein (Fc Tag)

Catalog Number: **13333-H02H**

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Biological Solution Specialist

General Information

Gene Name Synonym:

ERp-72; ERP70; ERP72; AI987846; Cai; ERp-72; Erp72

Protein Construction:

A DNA sequence encoding the human PDIA4 (P13667) (Met1-Thr641) was expressed, fused with the Fc region of human IgG1 at the C-terminus.

Source: Human

Expression Host: Human Cells

QC Testing

Purity: > 90 % as determined by SDS-PAGE

Endotoxin:

< 1.0 EU per μg of the protein as determined by the LAL method

Stability:

Samples are stable for up to twelve months from date of receipt at -70 ℃

Predicted N terminal: Val 21

Molecular Mass:

The recombinant human PDIA4/Fc is a disulfide-linked homodimer. The reduced monomer comprises 862 amino acids and has a predicted molecular mass of 97.2 kDa. The apparent molecular mass of the protein is approximately 96 kDa in SDS-PAGE under reducing conditions

Formulation:

Lyophilized from sterile PBS, pH 7.4

Normally 5 % - 8 % trehalose, mannitol and 0.01% Tween80 are added as protectants before lyophilization. Specific concentrations are included in the hardcopy of COA. Please contact us for any concerns or special requirements.

Usage Guide

Storage:

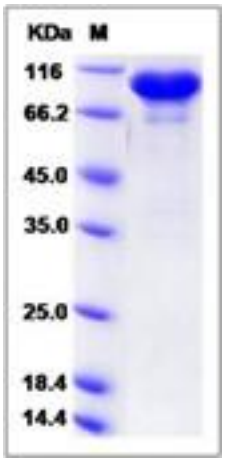
Store it under sterile conditions at -20℃ to -80℃ upon receiving. Recommend to aliquot the protein into smaller quantities for optimal storage.

Avoid repeated freeze-thaw cycles.

Reconstitution:

Detailed reconstitution instructions are sent along with the products.

SDS-PAGE:



Protein Description

ERP72, also known as PDIA4, is an endoplasmic reticulum luminal protein which belongs to the protein disulfide isomerase family. ERP72 is a stress protein and participates in the catalysis of protein-S-S-bond rearrangement. Both of PDIA4 and PDIA3 function as proteases, protein disulfide isomerases, phospholipases or an arrangement of these. ERP72 compose part of a large chaperone multiprotein complex comprising CABP1, DNAJB11, HSP90B1, HSPA5, HYOU, PDIA2, PDIA4, PPIB, SDF2L1, UGT1A1 and very small amounts of ERP29, but not, or at very low levels, CALR nor CANX.

References

1.Tsai YC, *et al*. (2012) Functional proteomics establishes the interaction of SIRT7 with chromatin remodeling complexes and expands its role in regulation of RNA polymerase I transcription. Mol Cell Proteomics. 11(5):60-76.
2.Kim W, *et al*. (2011) Systematic and quantitative assessment of the ubiquitin-modified proteome. Mol Cell. 44(2):325-40.
3.Vinayagam A, *et al*. (2011) A directed protein interaction network for investigating intracellular signal transduction. Sci Signal. 4(189):rs8.