

**RPB441Hu01 100µg**

**Recombinant Lysosomal Associated Membrane Protein 1 (LAMP1)**

**Organism Species: Homo sapiens (Human)**

***Instruction manual***

FOR IN VITRO USE AND RESEARCH USE ONLY  
NOT FOR USE IN CLINICAL DIAGNOSTIC PROCEDURES

9th Edition (Revised in Jul, 2013)

## **[ PROPERTIES ]**

**Residues:** Ala49~Ser297 (Accession # P11279),  
with two N-terminal Tags, His-tag and GST-tag.

**Host:** *E. coli*

**Subcellular Location:** Cell membrane; Lysosome  
membrane; Single-pass type I membrane protein.  
Endosome membrane; Late endosome.

**Purity:** >95%

**Endotoxin Level:** <1.0EU per 1µg  
(determined by the LAL method).

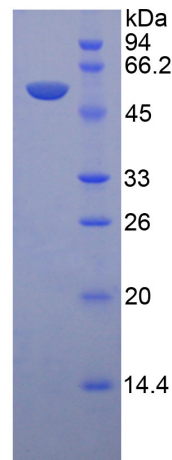
**Formulation:** Supplied as lyophilized form in PBS,  
pH7.4, containing 5% sucrose, 0.01% sarcosyl.

**Predicted isoelectric point:** 6.6

**Predicted Molecular Mass:** 58.9kDa

**Applications:** SDS-PAGE; WB; ELISA; IP.

(May be suitable for use in other assays to be determined by the end user.)



15% SDS-PAGE

## **[ USAGE ]**

Reconstitute in sterile PBS, pH7.2-pH7.4.

## **[ STORAGE AND STABILITY ]**

### **Storage: Avoid repeated freeze/thaw cycles.**

Store at 2-8°C for one month.

Aliquot and store at -80°C for 12 months.

**Stability Test:** The thermal stability is described by the loss rate of the target protein. The loss rate was determined by accelerated thermal degradation test, that is, incubate the protein at 37°C for 48h, and no obvious degradation and precipitation were observed. (Referring from China Biological Products Standard, which was calculated by the Arrhenius equation.) The loss of this protein is less than 5% within the expiration date under appropriate storage condition.

## **[ SEQUENCES ]**

The target protein is fused with two N-terminal Tags, His-tag and GST-tag, its sequence is listed below.

MSPILGYWKI KGLVQPTRL L LEYLEEKYEE HLYERDEGDK WRNKKFELGL EFPNLPYYID  
GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL DIRYGVSR IA YSKDFETLKV  
DFLSKLP EML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFP KLVCFK  
KRIEAI PQID KYLKSSKYIA WPLQG WQATF GGGDHPPKSD GSTSGSGHHH HHSAGLVPR  
GSTAIGMKET AAKFERQHM DSPDLGTLEV LFQG PLGSEF-AF SVNYDTKSGP  
KNMTFDLPSD ATVVLNRSS GKENTS DPSL VIAFGRGHTL TLNFTRNATR YSVQLMSFVY  
NLS DTHLFPN ASSKEIKTVE SITDIRADID KKYRCVSGTQ VHMNNVT VTL HDATI QAYLS  
NSSFSRGETR CEQDRPSPTT APPAPPSPSP SPVPKSPSVD KYNVSGTNGT CLLAS MGLQL  
NLTYERKDNT TVTRLLNINP NKTSASGSCG AHLVTLELHS EGTTVLLFQF GMNASSS