

**RPA301Mu01 100µg**  
**Recombinant Heat Shock 70kDa Protein 1B (HSPA1B)**  
**Organism Species: *Mus musculus* (Mouse)**  
***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:** Met1~Asp642 (Accession # P17879),  
with N-terminal His-Tag.

**Host:** *E. coli*

**Subcellular Location:** Cytoplasm.

**Purity:** >95%

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

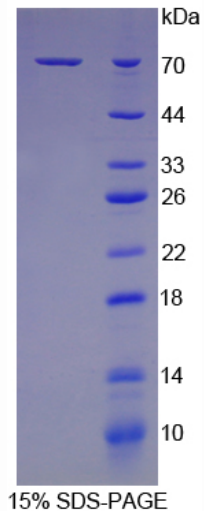
**Formulation:** Supplied as lyophilized form in PBS,  
pH7.4, containing 5% trehalose, 0.01% sarcosyl.

**Predicted isoelectric point:** 5.7

**Predicted Molecular Mass:** 71.7kDa

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

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



**[ 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 N-terminal His-Tag, its sequence is listed below.

MGHHHHHHSGSEF- MAKNTAIGID LGTTYSCVGV FQHGKVEIIA NDQGNRTTPS  
YVAFTDTERL IGDAAKNQVA LNPQNTVFDA KRLIGRKFGD AVVQSDMKHW PFQVVNDGDK  
PKVQVNYKGE SRSFFPEEIS SMVLTKMKEI AEAYLGHPVT NAVITVPAYF NDSQRQATKD  
AGVIAGLNVL RIINEPTAAA IAYGLDRTGK GERNVLIFDL GGGTFDVSIL TIDDGIFEVK  
ATAGDTHLGG EDFDNRLVSH FVEEFKRKHK KDISQNKRAV RRLRTACERA KRTLSSSTQA  
SLEIDSLFEG IDFYTSITRA RFEELCSDLF RGTLEPVEKA LRDAKMDKAQ IHDLVLVGGG  
TRIPKVQKLL QDFFNGRDLN KSINPDEAVA YGAAVQAAIL MGDKSENVQD LLLLDVAPLS  
LGLETAGGVM TALIKRNSTI PTKQTQFTT YSDNQPGVLI QVYEGERAMT RDNNLLGRFE  
LSGIPPAPRG VPQIEVTFDI DANGILNVTA TDKSTGKANK ITITNDKGRL SKEEIERMVQ  
EAERYKAEDE VQRDRVAANK ALESYAFNMK SAVEDEGLKG KLSEADKKKV LDKCQEIVISW  
LDSNTLADKE EFVHKREELE RVCSPHISGL YQGAGAPGAG GFGAQAPPKG ASGSGPTIEE  
VD