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**YBA301Bo01 100μg**  
**Heat Shock 70kDa Protein 1B (HSPA1B)**  
**Organism Species: Bos taurus; Bovine (Cattle)**  
***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~Asp641 (Accession # Q27965), with**  
**N-terminal His-Tag.**

**Host: *E. coli***

**Purity: >95%**

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

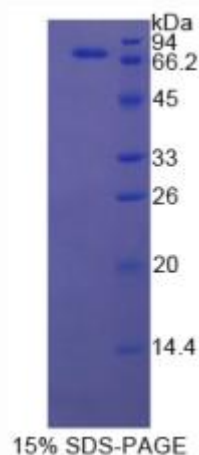
**Formulation: Supplied as lyophilized form in PBS, pH7.4,**  
**containing 5% sucrose, 0.01% sarcosyl.**

**Predicted isoelectric point: 5.9**

**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.**



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## **[ 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.**

MG H H H H H H SG SE F -MAK N TA I G ID LG TT Y S C VG V FQ H G K V E II A ND Q G N RT TP S  
YVAFTDTERL IGDAAKNQVA LNPQNTVFDA KRLIGRKFGD PVVQSDMKHW PFRVINDGDK  
PKVQVSYKGE TKAFYP EEISSMVLTKMKEI AEAYLGHPVT NAVITVPAYF NDSQRQATKD  
AGVIAGLNVL RIINEPTAAA IAYGLDRTGK GERNVLIFDL GGGTFDVSIL TIDDGIFEVK  
ATAGDTHLGG EDFDNLNVH FVEEFKRKHK KDISQNKRAV RRLRTACERA KRTLSSSTQA  
SLEIDSLFEG IDFYTSITRA RFEELCSDLF RSTLEPVEKA LRDAKLDKAQ IHDVLVLVGG S  
TRIPKVQKLL QDFFNGRDLN KSINPDEAVA YGA AVQAAIL MGDKSENVQD LLLLDVAPLS  
LGLETAGGVM TALIKRNSTI PTKQTQIFTT YSDNQPGVLI QVYEGERAMT RDNNLLGRFE  
LSGIPPAPRG VPQIEVTFDI DANGILNVTA TDKSTGKANK ITITNDKGRL SKEEIERMVQ  
EAEKYKAEDE VQRERSAKN ALESYAFNMK SAVEDEGLKG KISEADKKKV LDKCQEVISW  
LDANTLAEKD EFEHKRKELE QVCNPIISRL YQGAGGPGAG GFGAQGPKGG SGSGPTIEEV  
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