

**YBA890Ra01 100µg**  
**Recombinant Surfactant Associated Protein A (SPA)**  
**Organism Species: Rattus norvegicus (Rat)**  
***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:** Asn21~Phe248 (Accession # P08427), with two N-terminal Tags, His-tag and GST-tag.

**Host:** *E. coli*

**Subcellular Location:** Secreted, extracellular space, extracellular matrix. Surface film.

**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:** 5.6

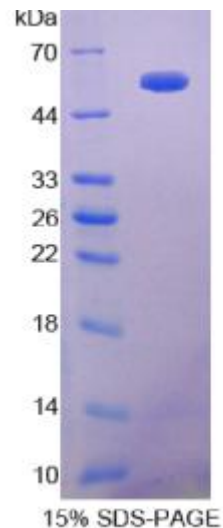
**Predicted Molecular Mass:** 56.6kDa

**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 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 DIRYGVSRIA YSKDFETLKV  
DFLSKLP EML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK  
KRIEAI PQID KYLKSSKYIA WPLQG WQATF GGGDHPPKSD GSTSGSGHHH HHSAGLVPR  
GSTAIGKET AA AKFERQH M DSPDLGTGGG SGIEGRGSMG YRGSEF-NVTDVCAGSP  
G I P G A P G N H G L P G R D G R D G V K G D P G P P G P M G P P G M P G L P G R D G L P G A P G  
APGERGDKGE PGERGLPGFP AYLDEELQTE LYEIKHQILQ TMGVLSLQGS MLSVGDKVFS  
TNGQSVNFD T IKEMCTRAGG NIAVPRTPEE NEAIASIAKK YNNYVYLGMI EDQTPGDFHY  
LDGASVNYTN WYPGEPRGQG KEKCVEMYTD GTWNRGCLQ YRLAVCEF**