

**rP92342Hu01 100µg**  
**Lipase, Bile Salt Dependent (BSDL)**  
**Organism: Homo sapiens (Human)**  
*Instruction manual*

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

7th Edition (Revised in May, 2013)

## [ **PROPERTIES** ]

**Residues:** Asp117~Glu361 (Accession # P19835),  
with two N-terminal Tags, His-tag and GST-tag.

**Host:** *E. coli*

**Subcellular Location:** Secreted.

**Purity:** >95%

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

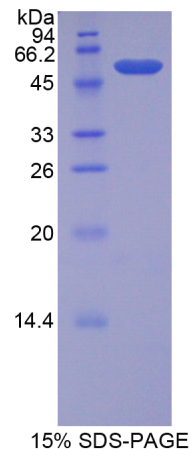
**Formulation:** Supplied as lyophilized form in PBS,  
pH7.4, containing 5% sucrose, 0.01% sarcosyl.

**Predicted isoelectric point:** 6.5

**Predicted Molecular Mass:** 53.4kDa

**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.

MRNKKFELGL EFPNLPYYID GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL  
DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD  
VVLYMDPMCL DAFPKLVCVK KRIEAIPQID KYLKSSKYIA WPLQGWQATF GGGDHPPKSD  
GSTSGSGHHH HHSAGL VPR GSTAIGMKET AAKFERQHM DSPDLGTLEV  
LFQGPLGSEF-DLPV MIWIYGG AFL MGS GHGANFL NNYLYD GEEI ATRGNVIVVT  
FNYRVGPLGF LSTGDANLPG NYGLRDQHMA IAWVKRNIAA FGGDPNNITL FGESAGGASV  
SLQTLSPY NK GLIRRAISQS GVALSPWVIQ KNPLFWAKKV AEKVGCPVGD AARMAQCLKV  
TDPRALTLAY KVPLAGLEYP MLHYVGFVPV IDGDFIPADP INLYANAADI DYIAGTNMMD  
GHIFASIDMP AINKGNKKVT E