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YB92342Hu01 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).

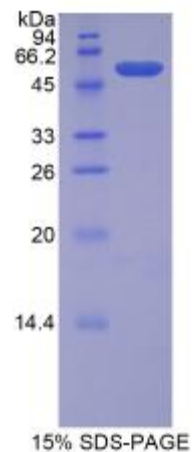
Formulation: Supplied as lyophilized form in PBS, pH7.4, containing 5% sucrose, 0.01% sarcosyl.

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.)





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[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.

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MRNKKFELGL EFPNLPYYID GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL
DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD
VVLYMDPMCL DAFPKLVCFK KRIAIPQID KYLKSSKYIA WPLQGWQATF GGDHPPKSD
G S T S G S G H H H H H S A G L V P R G S T A I G M K E T A A A K F E R Q H M D S P D L G T L E V
LFQG PLGSEF-DLPV MIWIYGG AFL MGSG HGAN FL NNYLYDG EEI ATRGN VIVVT
FN YRVG PLGF LSTGDANLPG NYGLRDQHMA IAWVKRNIAA FGGDPNNITL FGESAGGASV
SLQTLSPY NK GLIRRAISQS GVALSPWVIQ KNPLFWAKKV AEKVGCPVGD AARMAQCLKV
TDPRAL TLAY KVPLAGLEYP MLHYVGFVPV IDGDFIPADP INLYANAADI DYIAGTNNMD
GHIFASIDMP AINKGNKKVT E
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