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YBN942Hu01 100 μ g

Recombinant Autophagy Related Protein 16 Like Protein 1 (ATG16L1)

Organism Species: Homo sapiens (Human)

*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~Gly284 (Accession # Q676U5), with two N-terminal Tags, His-tag and GST-tag.

Host: *E. coli*

Subcellular Location: Cytoplasm.

Purity: >95%

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

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

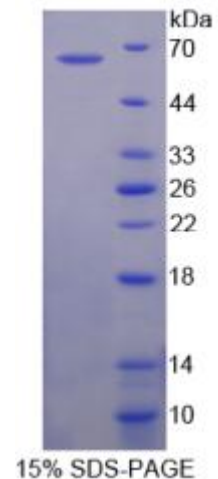
Predicted isoelectric point: 6.9

Predicted Molecular Mass: 65.4kDa

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

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

[USAGE]





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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 KGLVQPTRLL LEYLEEKYEE HLYERDEGDK WRNKKFELGL EFPNLPYYID
GDVKLTSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL DIRYGVSRIA YSKDFETLKV
DFLSKLP EML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK
KRIEAIPIQID KYLKSSKYIA WPLQGWAQTF GGGDHPPKSD GSTSGSGHHH HHSAGLVPR
GSTAIGMKET AAKFERQHM DSPDLGTGGG SGIEGRGSMG YRGSEF-MSSGLRAADF
PRWKRHISEQ LRRRDRLQRQ AFEEIILQYN KLEKSDLHS VLAQKLQAEK HDVPNRHEIS
P G H D G T W N D N Q L Q E M A Q L R I K H Q E E L T E L H K K R G E L A Q L V I D L N N Q M Q R K
DREM^QMNEAK IAELQTISD LETECLDLRT KLCDLERANQ TLKDEYDALQ ITFTALEGKL
RKTTEENQEL VTRWMAEKAQ EANRLNAENE KDSRRRQARL QKELAEAAKE PLPVEQDDDI
EVIVDETS^{DH} TEETSPVRAI SRAATKRLSQ PAGGLDSIT NIFG