

P92738Hu02
Pancreas Specific Transcription Factor 1a (PTF1a)
Organism: Homo sapiens (Human)
Instruction manual

FOR IN VITRO USE AND RESEARCH USE ONLY
NOT FOR USE IN DIAGNOSTIC OR THERAPEUTIC PROCEDURES

5th Edition (Revised in January, 2013)

[DESCRIPTION]

Protein Names: Pancreas Specific Transcription Factor 1a

Synonyms: PTF1a, BHLHA29, PTF1P48

Species: Human

Size: 100µg

Source: *Escherichia coli*-derived

Subcellular Location: Nucleus. Cytoplasm.

[PROPERTIES]

Residues: Gln177~Ser328 (Accession # Q7RTS3), with two N-terminal Tags, His-tag and GST-tag.

Grade & Purity: >95%, 45kDa as determined by SDS-PAGE reducing conditions.

Formulation: Supplied as lyophilized form in PBS, pH 7.4, containing 5% sucrose.

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

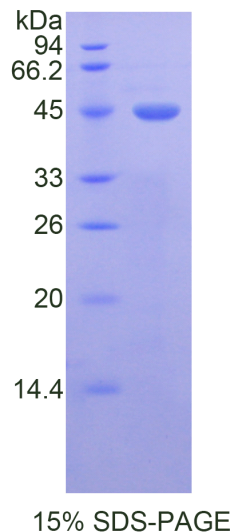
Applications: SDS-PAGE; WB; ELISA; IP.

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

Predicted Molecular Mass: 43.4kDa

Predicted isoelectric point: 6.6

Human PTF1a



[PREPARATION]

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
VVL YM DPMCL DAFPKLVCFK KRIEAIQID KYLKSSKYIA WPLQGWQATF GGGDHPPKSD
GSTSGSGHHH HHHSAGLVPR GSTAIGMKET AAKFERQHM DSPDLGTLEV
LFQGPLGSEF- QSIN DAFEGLRSHI PTLPYEKRLS KVDTLRLAIG YINFLSELVQ
ADLPLRGGGA GGCGGPGGGG RLGGDSPGSQ AQKVIICHRG TRSPSPSDPD
YGLPPLAGHS LSWTDEKQLK EQNIIRTAKV WTPEDPRKLN SKSSFNNIEN EPPFEFVS