



YBC417Hu01 100µg

Recombinant Carnitine Palmitoyltransferase 2, Mitochondrial (CPT2)

Organism Species: Homo sapiens (Human)

Instruction manual

FOR IN VITRO USE AND RESEARCH USE ONLY

NOT FOR USE IN CLINICAL DIAGNOSTIC PROCEDURES

10th Edition (Revised in Jan, 2014)

[PROPERTIES]

Residues: Ala152~Ser658

Tags: Two N-terminal Tags, His-tag and GST-tag

Accession: P23786

Host: *E. coli*

Subcellular Location: Mitochondrion inner membrane. Peripheral membrane protein. Matrix side.

Purity: >90%

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

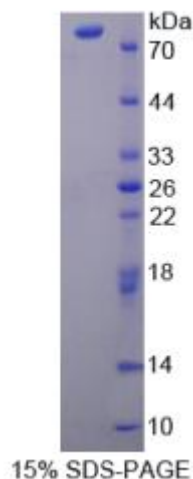
Formulation: Supplied as lyophilized form in PBS, pH7.4, containing 5% trehalose, 0.01% sarcosyl.

Predicted isoelectric point: 7.0

Predicted Molecular Mass: 86.6kDa

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 sequence of the target protein is listed below.

**ATNMTVSAI RFLKTLRAGL LEPEVFHLNP AKSDTITFKR LIRFVPSSLS WYGAYLVNAY
PLDMSQYFRL FNSTRLPKPS RDELFTDDKA RHLLVLRKGN FYIFDVLDQD GNVSPSEIQ
AHLKYILSDS SPAPEFPLAY LTSENEDIWA ELRQKLMSSG NEESLRKVDS AVFCLCLDDF
PIKDLVHLSH NMLHGDGTNR WFDKSFNLI AKDGSTAVHF EHSWGDGVAV LRRFNEVFKD
STQTPAVTPQ SQPATTDSTV TVQKLNFEIT DALKTGITAA KEKFDATMKT LTIDCVQFQR
GGKEFLKKQK LSPDAVAQLA FQMAFLRQYG QTVATYESCS TAAFKHGRTE TIRPASVYTK
RCSEAFVREP SRHSAGELQQ MMVECSKYHG QLTKEAAMGQ GFDRHLFALR HLAAAKGIIL
PELYLDPAYG QINHNVLSTS TLSSPAVNLG GFAPVSDGF GVGAVHDNW IGCNVSSYPG
RNAREFLQCV EKALEDMFDA LEGKSIKS**