RPA822Mu01 100μg

Recombinant Heat Shock 60kD Protein 1, Chaperonin (HSPD1)

Organism Species: Mus musculus (Mouse)

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: Lys28~Phe573 (Accession # P63038), with two N-terminal Tags, His-tag and T7-tag.

Host: *E. coli*

Subcellular Location: Mitochondrion matrix.

Purity: >95%

Endotoxin Level: <1.0EU per 1μg (determined by the LAL method).
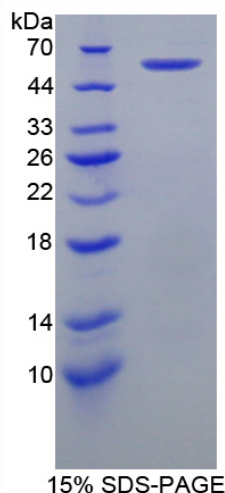
Formulation: Supplied as lyophilized form in PBS, pH7.4, containing 5% sucrose, 0.01% sarcosyl.

Predicted isoelectric point: 5.9

Predicted Molecular Mass: 61.4kDa

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

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

kDa
70
44
33
26
22
18
14
10

15% SDS-PAGE

[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 T7-tag, its sequence is listed below.

MGSSHHHHHH SSGLVPRGSH MASMTGGQQM GRGS- KDV KFGADARALM LQGVDLLADA
VAVTMGPKGR TVIIEQSWGS PKVTKDGVTV AKSIDLKDKY KNIGAKLVQD VANNTNEEAG
DGTTTATVLA RSIAKEGFEK ISKGANPVEI RRGVMLAVDA VIAELKKQSK PVTTPEEIAQ
VATISANGDK DIGNIISDAM KKVGRKGVIT VKDGKTLNDE LEIIEGMKFD RGYISPYFIN
TSKGQKCEFQ DAYVLLSEKK ISSVQSIVPA LEIANAHRKP LVIIAEDVDG EALSTLVLNR
LKVGLQVVAV KAPGFGDNRK NQLKDMAIAT GGAVFGEEGL NLNLEDVQAH DLGKVGEVIV
TKDDAMLLKG KGDKAHIEKR IQEITEQLDI TTSEYEKEKL NERLAKLSDG VAVLKVGGTS
DVEVNEKKDR VTDALNATRA AVEEGIVLGG GCALLRCIPA LDSLKPANED QKIGIEIIKR
ALKIPAMTIA KNAGVEGSLI VEKILQSSSE VGYDAMLGDF VNMVEKGIID PTKVVRTALL
DAAGVASLLT TAEAVVTEIP KEEKDPGMGA MGGMGGGMGG GMF