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YB93503Hu01 100µg Heat Shock 70kDa Protein 14 (HSPA14) **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: Met1~Ser509 (Accession # Q0VDF9),

with N-terminal His-Tag.

Host: E. coli

Subcellular Location: Cytoplasm, cytosol.

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: 5.8

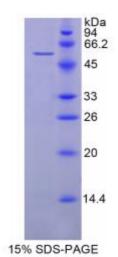
Predicted Molecular Mass: 56.0kDa

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 target protein is fused with N-terminal His-Tag, its sequence is listed below. MG H H H H H H S G S- M A A I G V H L G C TS A C VAV Y K D GR A G V VA N D A GD RV T PAV VA YSENEEIVGL AAKOSRIRNI SNTVMKVKOI LGRSSSDPOA OKYIAESKCL VIEKNGKLRY EIDTGEETKF VNPEDVARLI FSKMKETAHS VLGSDANDVV ITVPFDFGEK QKNALGEAAR AAGFNVLRLI HEPSAALLAY GIGQDSPTGK SNILVFKLGG TSLSLSVMEV NSGIYRVLST NTDDNIGGAH FTETLAQYLA SEFQRSFKHD VRGNARAMMK LTNSAEVAKH SLSTLGSANC FLDSLYEGOD FDCNVSRARF ELLCSPLFNK CIEAIRGLLD ONGFTADDIN KVVLCGGSSR IPKLQQLIKD LFPAVELLNS IPPDEVIPIG AAIEAGILIG KENLLVEDSL MIECSARDIL VKGVDESGAS RFTVLFPSGT PLPARRQHTL QAPGSISSVC LELYESDGKN SAKEETKFAQ VVLQDLDKKE NGLRDILAVLTMKRDGSLHV TCTDQETGKC EAISIEIAS