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YB89122Hu02

Family With Sequence Similarity 132, Member A (FAM132A)

Organism: Homo sapiens (Human)

Instruction manual

FOR IN VITRO USE AND RESEARCH USE ONLY

NOT FOR USE IN DIAGNOSTIC OR THERAPEUTIC PROCEDURES

4th Edition (Revised in August, 2012)

[DESCRIPTION]

Protein Names: Family With Sequence Similarity 132, Member A

Synonyms: FAM132A, C1QDC2

Species: Human

Size: 100 μ g

Source: *Escherichia coli*-derived

Subcellular Location: Nucleus, nucleoplasm.

[PROPERTIES]

Residues: Arg2~Thr302 (Accession # Q5T7M4), with N-terminal His-Tag.

Grade & Purity: >95%, 33 kDa as determined by SDS-PAGE reducing conditions.

Formulation: Supplied as liquid form in Phosphate buffered saline(PBS), pH 7.4.

Endotoxin Level: <1.0 EU per 1 μ g (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: 33.8 kDa

Predicted isoelectric point: 9.2

[PREPARATION]

Reconstitute in sterile PBS, pH7.2-pH7.4.



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[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.

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MGHHHHHSG SEF-RRWAWAA VVLLGPQLV LLGGVGARRE AQRTPQPGQR ADPPNATASA SSREGLPEAP KPSQASGPEF  
SDAHMTWLN FVRRPDDGALR KRCGSRDKKP RDLFGPPGPP GAETVAETLL HEFQELLKEA TERRFSGLLD PLLPQAGLR  
LVGEAFHCR LQGPRRVDKRT LVELHGFQAP AAQGAFLRGS GLSLASGRFT APVSGIFQFS ASLHVDHSEL QGKARLRARD  
VVCVLICIES LCQRHTCLEA VSGLESNSRV FTLQVQGLLQ LQAGQYASVF VDNGSGAVLT IQAGSSFSGL LLGT
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