YBF163Mu01 100ug

Recombinant Death Associated Protein Kinase 3 (DAPK3)

Organism Species: Mus musculus (Mouse)

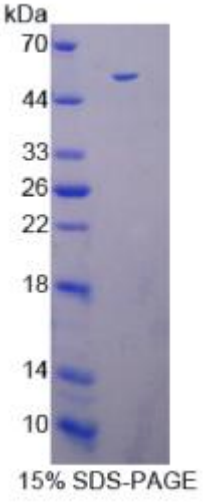
Instruction manual

FOR IN VITRO USE AND RESEARCH USE ONLY

NOT FOR USE IN CLINICAL DIAGNOSTIC PROCEDURES

10th Edition (Revised in Jan, 2014)

[PROPERTIES]



Residues: Met1~Arg448

Tags: Two N-terminal Tags, His-tag and T7-tag

Accession: O54784

Host: *E. coli*

Subcellular Location: Nucleus. Cytoplasm. Chromosome, centromere, cytoskeleton, microtubule organizing center.

Purity: >90%

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

Formulation: Supplied as lyophilized form in 20mM Tris, 150mM NaCl, pH8.0, containing 1mM EDTA, 1mM DTT, 0.01% sarcosyl, 5% trehalose, and preservative.

Predicted isoelectric point: 8.9

Predicted Molecular Mass:

55.1kDa

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 ddH_2O.

[STORAGE AND STABILITY]

Storage: Avoid repeated freeze/thaw cycles.

Store at 2-8^{o}C for one month.

Aliquot and store at -80^{o}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^{o}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.

MSTFRQEDVE DHYEMGEELG SGQFAIVRKC QQKGTGMEYA AKFIKKRRLP SSRRGVSREE
IEREVSILRE IRHPNIITLH DVFENKTDVV LILELVSGGE LFDFLAEKES LTEDEATQFL
KQILDGVHYL HSKRIAHFDL KPENIMLLDK HAASPRIKLI DFGIAHRIEA GSEFKNIFGT
PEFVAPEIVN YEPLGLEADM WSIGVITYIL LSGASPFLGE TKQETLTNIS AVNYDFDEEY
FSSTSELAKD FIRRLLVKDP KRRMTIAQSL EHSWIKVRRR EDGARKPERR RLRAARLREY
SLKSHSSMPR NTSYASFERF SRVLEDVAAA EQGLRELQRG RRQCRERVCA LRAAAEQREA
RCRDGSAGLG RDLRRLRTEL GRTEALRTRA QEEARAALLG AGGLKRRLCR LENRYDALAA

QVAAEVQFVR DLVRALEQER LQAECGVR