

P91391Hu01

Actin Gamma 1 (ACTg1)

Organism: Homo sapiens (Human)

Instruction manual

FOR IN VITRO USE AND RESEARCH USE ONLY
NOT FOR USE IN CLINICAL DIAGNOSTIC PROCEDURES

5th Edition (Revised in January, 2013)

[DESCRIPTION]

Protein Names: Actin Gamma 1

Synonyms: ACTg1, ACTB, ACTG

Species: Human

Size: 100µg

Source: *Escherichia coli*-derived

Subcellular Location: Cytoplasm, cytoskeleton.

[PROPERTIES]

Residues: Met1~Phe375 (Accession # P63261), with N-terminal His-Tag.

Grade & Purity: >95%, 45kDa as determined by SDS-PAGE reducing conditions.

Formulation: Supplied as lyophilized form in PBS, pH 7.4, containing 5% sucrose, 0.01% sarcosyl.

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

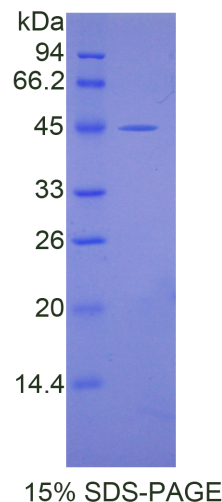
Applications: SDS-PAGE; WB; ELISA; IP.

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

Predicted Molecular Mass: 43.3kDa

Predicted isoelectric point: 5.6

Human ACTg1





[PREPARATION]

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.

MGHHHHHSGSEF- MEEIIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH
QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD DMEKIWHHTF YNELRVAPEE
HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRRTG IVMDSGDGVT
HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA
LDFEQEMATA ASSSSLEKSY ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN
SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL APSTMKIKII APPERKYSVW
IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF

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