



TEL:4006-871-227 Web:www.ybio.net Email:shybio@126.com

YB95506Mu01

**100µg Kinesin Family, Member 5A
(KIF5A) Organism: Mus musculus
(Mouse)**

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: Ala2~Ile211 (Accession # P33175), with two N-terminal Tags, His-tag and GST-tag.

Host: *E. coli*

Subcellular Location: Cytoplasm, perinuclear region.
Cytoplasm, cytoskeleton.

Purity: >95%

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

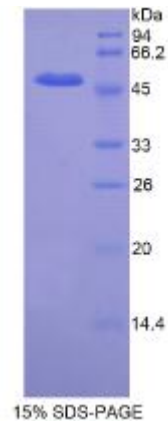
Formulation: Supplied as lyophilized form in PBS, pH7.4, containing 5% sucrose, 0.01% sarcosyl.

Predicted isoelectric point: 6.3

Predicted Molecular Mass: 50.7kDa

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 two N-terminal Tags, His-tag and GST-tag, its sequence is listed below.

MRNKKFELGL EFPNLPYYID GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL
DIRYGVSRIA YSKDFETLKV DFLSKLP EML KM FEDRLCHK TYLNGDHVTH PDFMLYDALD
VVLYMDPMCL DAFPKLVCFK KRIEAIPQID KYLKSSKYIA WPLQGWQATF GGGDHPPKSD
G S T S G S G H H H H H S A G L V P R G S T A I G M K E T A A A K F E R Q H M D S P D L G T L E V
LFQGPLGS-AETNNECSI KVL CRFRPLN QAEILRGDKF IPIFQGDDSV IIGGKPYVFD
RVFPPNTTQE QVYHACAMQI VKDVLGYNG TIFAYGQTSS GKTHMTEGKL HDPQLMGIIP
RIARDIFNHI YSM DENLEFH IKVSYFEIYL DKIRDLLDVT KTNLSVHEDK NRVPFVKGCT
ERFVSSPEEI LDVIDEGKSN RHVAVTMNE HSSRSHSIFL I