

rP93352Mu01 100μg**Hexokinase 2 (HK2)****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: Pro605~His868 (Accession # O08528),
with two N-terminal Tags, His-tag and GST-tag.

Host: *E. coli*

Purity: >95%

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

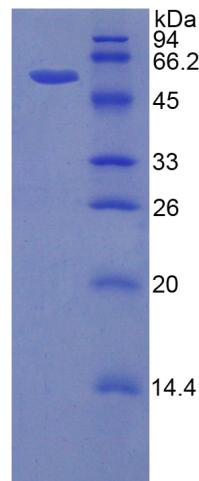
Formulation: Supplied as lyophilized form in PBS,
pH7.4, containing 5% sucrose, 0.01% sarcosyl.

Predicted Isoelectric point: 5.7

Predicted Molecular Mass: 56.4kDa

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

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



15% SDS-PAGE

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[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 EFPNLPPYYID GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTB PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPQID KYLKSSKYIA WPLQGWQATF GGGDHPPKSD GSTSGSGHHH HHHSAGLVPR GSTAIGMKET AAAKFERQHM DSPDLGTLEV LFQGPLGSEF-PCQQNS LDQSILLKWT KGFKASGCEG EDVVTLKEA IRRREEFDLD VVAVVNDTVGTMTCGYEDP HCEVGLIVGT GSNACYMEEM RNVELVDGEE GRMCVNMEWG AFGDNGCLDDLRTVFDVAVD ELSLNPGKQR FEKMISGMYL GEIVRNILID FTKRGLLFRG RISERLKTRGIFETKFLSQI ESDCLALLQV RAILRHLGLE STCDDSIIVK EVCTVVARRA AQLCGAGMAAVVDKIRENRG LDNLKVTVGV DGTLYKLH