

Certificate of Analysis

PIP5K1B, 20 µg

PIP5K1B, full-length, recombinant human, GST-tagged



Part Number: A33521

Lot Number: 1954392

Immediate Storage: -80°C

Shipping Conditions: dry ice

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Description:

Recombinant human full-length active PIP5K1B was expressed in insect cells using a N-terminal GST tag.

PIP5K1B recombinant human full length was expressed in insect cells. PIP5K1B lipid kinase or phosphatidylinositol-4-phosphate 5-kinase, type I, beta is a member of the phosphatidylinositol-4-phosphate 5-kinase family. PIP5K1B gene contains 17 exons and spans more than 300 kb. The seventeenth exon was found by RT-PCR, and are derived from the 3-prime untranslated region of the PRKACG gene which is located on 9q13 approximately 3 kb downstream of the STM7.1 3-prime untranslated region. The overexpression of PIP5K1B in COS-7 cells induces an increase in short actin fibers and a decrease in actin stress fibers.

Accession Number:

The gene accession number for PIP5K1B is NP_003549.1.

Specific Activity:

3,400 nmoles of phosphate transferred to PI(4)P:PS substrate per minute per mg of total protein at 30°C.

Concentration:

0.05 mg/mL as determined by densitometry of the kinase gel band(s).

Calculated **573 nM**.

Aliases:

MSS4, STM7

Storage and Handling:

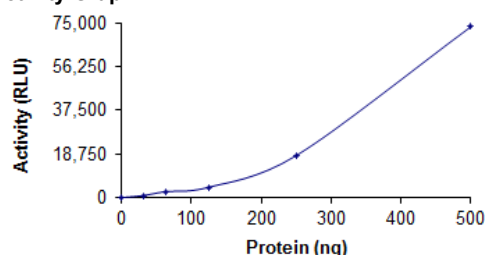
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 ug, 10ug and 20ug sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below 20 µL are not recommended. **Please never store a kinase diluted.** If properly stored at -80°C, this product is guaranteed for 6 months from date of purchase.

Storage Buffer:

50 mM Sodium Phosphate (pH 7.0), 300 mM NaCl, 150 mM Imidazole, 0.1 mM PMSF, 0.25 mM DTT and 25% Glycerol.

QUALITY ASSURANCE

PIP5K1B Activity Graph



Dilution Buffer:

5 mM MOPS (pH 7.2), 2.5 mM β-glycerol-phosphate, 5 mM MgCl₂, 1 mM EGTA, 0.4 mM EDTA and 50 ng/µL BSA.

Assay Conditions:

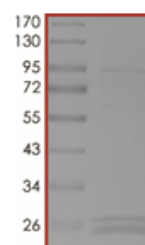
PIP5K1B was pre-diluted in enzyme dilution buffer and assayed in 5 mM MOPS (pH 7.2), 2.5 mM β-glycerol-phosphate, 5 mM MgCl₂, 0.4 mM EDTA, 1 mM EGTA, 0.05 mM DTT, with 50 µM ATP in an ADP accumulation assay using PI(4)P:PS substrate at 50 & 200 µM for 15 minutes at 30°C.

Gel Information for PIP5K1B

Page Description: Run on an SDS-PAGE gel and stained with Coomassie®.

Lane 1: Molecular Weight markers as labeled.

Lane 2: PIP5K1B



Purity:

> 70% as determined by a Coomassie® blue stained SDS-PAGE gel, excluding endogenous GST.

Molecular Weight:

87.3 kDa. Calculated from the protein sequence(s).

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_003549.1

1 MSPILGYWKIKGLVQPTRLLLEYLEEKYEHLVERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAISMLEGAVL GST
1 MSPILGYWKIKGLVQPTRLLLEYLEEKYEHLVERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAISMLEGAVL Life PIP5K1B
1 MS-----NP_003549.1

101 DIRYGVSRIAYS~~K~~FETLKVD~~F~~LSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAF~~P~~KLVC~~F~~KKRIE~~A~~IPQIDKYLKSSKYIA
101 DIRYGVSRIAYS~~K~~FETLKVD~~F~~LSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAF~~P~~KLVC~~F~~KKRIE~~A~~IPQIDKYLKSSKYIA
3 -----

201 WPLQGWQATFGGGDHPKSD
201 WPLQGWQATFGGGDHPKSDLVPRGSMSSAAENGEAAPGKQNEEKTYKKTASSAIGKAIQLGIGYTVGNLTSKPERDVLMDQFYVVEVSVFLPSEGSNLTP
3 -----SAAENGEAAPGKQNEEKTYKKTASSAIGKAIQLGIGYTVGNLTSKPERDVLMDQFYVVEVSVFLPSEGSNLTP

220
301 AHHPYDFRFKTYAPLAFRYFRELFGIKPDDYLYSICSEPLIELSNPGASGSLFFVTSDDDEFI~~I~~KT~~V~~QHKEA~~E~~FLQKLLPGYYMNLNQNPR~~T~~LLPKFYGLY
75 AHHPYDFRFKTYAPLAFRYFRELFGIKPDDYLYSICSEPLIELSNPGASGSLFFVTSDDDEFI~~I~~KT~~V~~QHKEA~~E~~FLQKLLPGYYMNLNQNPR~~T~~LLPKFYGLY

220
401 CMQSGGINIRIVVMNNVLP~~R~~SMRMHFTYDLKGSTYKRRASRKEREKSNPTFKDLDFLQDMHEGLYFDTETYNALMKTLQRDCRVLESF~~K~~IMDYSLLGIH
175 CMQSGGINIRIVVMNNVLP~~R~~SMRMHFTYDLKGSTYKRRASRKEREKSNPTFKDLDFLQDMHEGLYFDTETYNALMKTLQRDCRVLESF~~K~~IMDYSLLGIH

220
501 FLDHSLKEKEEETPNV~~P~~DAKRTGMQKVL~~Y~~STAMESIQGPGKSGDGIITENPDTMGGIPAKSHRGEKLLLFMGII~~I~~DLQSYRLMKKLEH~~S~~WKALVYDGD~~T~~
275 FLDHSLKEKEEETPNV~~P~~DAKRTGMQKVL~~Y~~STAMESIQGPGKSGDGIITENPDTMGGIPAKSHRGEKLLLFMGII~~I~~DLQSYRLMKKLEH~~S~~WKALVYDGD~~T~~

220
601 VSVHRPSFYADRFLKFMNSRVFKKI~~Q~~ALKASPSKKRCNSIAALKATSQEIVSSISQEWKDEKRDLLTEGQSFSSLDEEALGSRHRPDLVPSTPSLFEAAS
375 VSVHRPSFYADRFLKFMNSRVFKKI~~Q~~ALKASPSKKRCNSIAALKATSQEIVSSISQEWKDEKRDLLTEGQSFSSLDEEALGSRHRPDLVPSTPSLFEAAS

220
701 LATTISSSSLYVNEHYPHDRPTLYSNSKGLPSSSTFTLEEGTIYLTAE~~P~~NTLEVQDDNASVLDVYL
475 LATTISSSSLYVNEHYPHDRPTLYSNSKGLPSSSTFTLEEGTIYLTAE~~P~~NTLEVQDDNASVLDVYL

* highlighted residues denote differences from the reference protein sequence(s).

Anita Targosz

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