MAPK10 (JNK3) [GST-tagged]

Kinase

Alternate Names: Mitogen-Activated Protein Kinase 10, PRKM10, SAPK1b, C-Jun Kinase 3

Cat. No.	**66-0030-050**	Quantity:	50 µg
Lot. No.	**30309**	Storage:	-70˚C

FOR RESEARCH USE ONLY

NOT FOR USE IN HUMANS

CERTIFICATE OF ANALYSIS Page 1 of 2

Background

Protein ubiquitylation and protein phosphorylation are the two major mechanisms that regulate the functions of proteins in eukaryotic cells. However, these different posttranslational modifications do not operate independently of one another, but are frequently interlinked to enable biological processes to be controlled in a more complex and sophisticated manner. Studying how protein phosphorylation events control the ubiquitin system and how ubiquitylation regulates protein phosphorylation has become a focal point of the study of cell regulation and human disease. MAP kinases are serine, threonine, and tyrosine specific protein kinases that regulate proliferation, gene expression, differentiation, mitosis, cell survival, and apoptosis in response to stimuli, such as mitogens, osmotic stress, heat shock and pro-inflammatory cytokines. Cloning of human Mitogen Activated Protein kinase 10 (MAPK10 or JNK3) was first described by Gupta *et al.* (1996). An example of such interplay between phosphorylation and ubiquitylation (more specifically SUMOylation) has been highlighted in a recent study uncovering a link between SUMO1 (small ubiquitin-like modifier 1) modification of glutamatergic kainate receptor subunit GluK2 and MLK3–JNK3 signaling cascades (Zhu *et al.*, 2012).

References:

Gupta S, Barrett T, Whitmarsh AJ, Cavanagh J, Sluss HK, Derijard B, *et al.* (1996) Selective interaction of JNK protein kinase isoforms with transcription factors. *Embo J* **15**, 2760-2770.

Hastie CJ, McLauchlan HJ, Cohen P (2006) Assay of protein kinases using radiolabeled ATP: a protocol. *Nat Protoc* **1**, 968-71.

Zhu QJ, Xu Y, Du CP and Hou XY (2012) SUMOylation of the kainate receptor subunit GluK2 contributes to the activation of the MLK3-JNK3 pathway following kainate stimulation. *FEBS Lett* **586**, 1259-1264.

Physical Characteristics

Species: human

Source: *E. coli*

Quantity: 50 µg

Concentration: 1.88 mg/ml

Formulation: 50 mM Tris/HCl pH7.5, 0.1 mM EGTA, 150 mM NaCl, 0.1% ß-Mercaptoethanol, 270 mM sucrose, 0.03% Brij-35, 1 mM Benzamidine, 0.2 mM PMSF

Molecular Weight: ~71.5 kDa

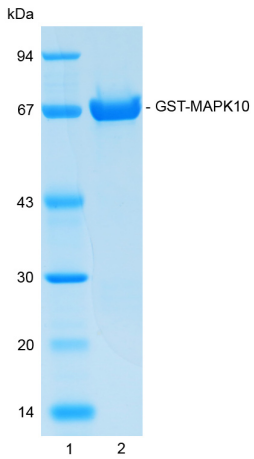
Purity: >95% by InstantBlue™ SDS-PAGE

Stability/Storage: 12 months at -70˚C; aliquot as required

Protein Sequence: Please see page 2

Quality Assurance

Purity:
4-12% gradient SDS-PAGE
InstantBlue™ staining
Lane 1: MW markers
Lane 2: 2.5 µg GST-MAPK10



Protein Identification:
Confirmed by mass spectrometry.

Activity Assay:
The specific activity of GST-MAPK10 was determined using the method described by Hastie *et al.* (2006) with the enzyme being assayed at several concentrations. GST-MAPK10 was incubated for 10 minutes at 30˚C in kinase reaction buffer in the presence of GST-ATF2 [19-96] substrate (0.2 mg/ml) and [γ-32P]ATP (100 µM). Duplicate reactions were stopped by spotting the assay mixture onto Whatman P81 paper – capturing the phosphorylated substrate.The radioactivity incorporated was measured on a scintillation counter and the enzyme's mean specific activity was calculated.

GST-MAPK10 specific activity:
50.06 Units/mg (94.12 Units/ml)

1 Unit = 1 nmole of phosphate incorporated into the substrate in 1 minute

Substrate: GST-ATF2 [residues 19-96]

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Email: tech.support@ubiquigent.com

Email **services@ubiquigent.com** for enquiries regarding compound profiling and/or custom assay development services.

Lot-specific COA version tracker: v1.0.0

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Physical Characteristics

Continued from page 1

Protein Sequence:

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEH
LYERDEGDKWRNKKFELGLEFPNLPYYIDGD
VKLTQSMAIIRYIADKHNMLGGCPKERAEISM
LEGAVLDIRYGVSRIAYSKDFETLKVDFL
SKLPEMLKMFEDRLCHKTYLNGDHVTHPD
FMLYDALDVVLYMDPMCLDAFPKLVCFK
KRIEAIPQIDKYLKSSKYIAWPLQGWQATF
GGGDHPPKSDLEVLFQGPLGS***S***KSKVDNQ
FYSVEVGDSTFTVLKRYQNLKPIGSGAQGIV
CAAYDAVLDRNVAIKKLSRPFQNQTHAKRAY
RELVLMKCVNHKNIISLLNVFTPQKTLEEFQD
VYLVMELMDANLCQVIQMELDHERMSYL
LYQMLCGIKHLHSAGIIHRDLKPSNIV
VKSDCTLKILDFGLARTAGTSFMMTPYV
VTRYYRAPEVILGMGYKENVDIWSVGCIMGEM
VRHKILFPGRDYIDQWNKVIEQLGTPCPEFM
KKLQPTVRNYVENRPKYAGLTFPKLFPDSLF
PADSEHNKLKASQARDLLSKMLVIDPAKRIS
VDDALQHPYINVWYDPAEVEAPPPQIYDKQL
DEREHTIEEWKELIYKEVMNSEEKTKNGVVK
GQPSPSAQVQQ**HHHHHH**

Tag (**bold text**): N-terminal GST and C-terminal 6His
Protease cleavage site: PreScission™ (LEVLFQ▼GP)
MAPK10 (regular text): Start ***bold italics*** (amino acid residues 40-422).
Accession number: NP_002744.1

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Email **services@ubiquigent.com** for enquiries regarding compound profiling and/or custom assay development services.

Lot-specific COA version tracker: v1.0.0