

Certificate of Analysis

RPS6KA5 (MSK1), 10 µg

Ribosomal Protein S6 Kinase, 90 kDa, Polypeptide 5, GST-tagged

ThermoFisher
SCIENTIFIC

Part Number: PV3681

Lot Number: 1758877G

Immediate Storage: -80°C

Shipping Conditions: dry ice

5781 Van Allen Way

Carlsbad, CA 92008

Phone: 760.603.7200

www.thermofisher.com

Description:

Recombinant human full-length protein, GST-tagged, expressed in insect cells. Activated *in vitro* by MAPK1.

Specific Activity:

230 nmoles of phosphate transferred to Crosstide peptide substrate (GRPRSSFAEG) per minute per mg of total protein at 30°C. Activity determined at a final protein concentration of 3.33 µg/mL.

Concentration:

0.44 mg/mL total protein as measured using the Bradford protein assay with BSA as a standard.

Calculated **3,700 nM**.

Aliases:

MSK1, RLPK

Storage and Handling:

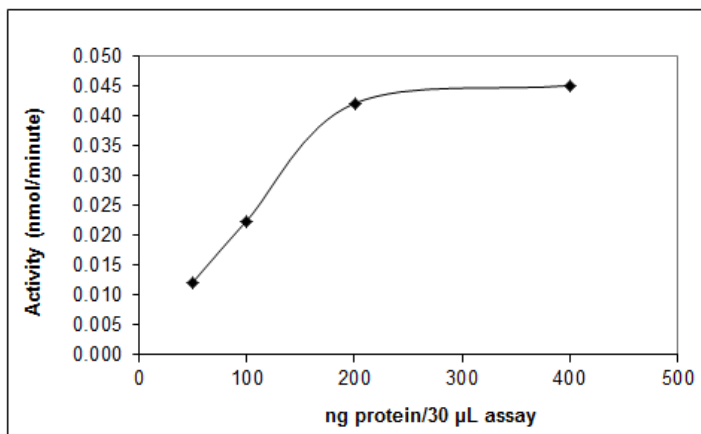
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 µg, 10 µg and 20 µg sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below 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 Tris (pH 7.5), 150 mM NaCl, 0.5 mM EDTA, 0.02% Triton® X-100, 2 mM DTT and 50% Glycerol.

QUALITY ASSURANCE

RPS6KA5 (MSK1) Activity Graph



Dilution Buffer:

20 mM Tris (pH 7.5), 0.02% Triton® X-100, 0.1 mg/mL BSA, 2 mM DTT, 0.5 mM Na₃VO₄ and 10% Glycerol.

Assay Conditions:

RPS6KA5 (MSK1) was pre-diluted in enzyme dilution buffer and assayed in 25 mM Tris (pH 7.5), 10 mM MgCl₂, 0.5 mM EGTA, 0.5 mM Na₃VO₄, 5 mM β-glycerophosphate, 2.5 mM DTT, 0.01% Triton® X-100, 200 µM ATP, 100 µM Crosstide peptide substrate (GRPRSSFAEG) and trace [³²P]-γ-ATP for 10 minutes at 30°C.

Gel Information for RPS6KA5 (MSK1)

Page Description: The SDS-PAGE and/or Native PAGE were run on 4-20% Tris-Glycine Novex™ gels (Catalog #: EC6025BOX).

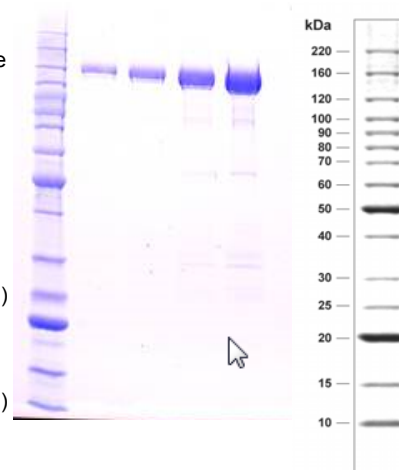
Lane 1: Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

Lane 2: 0.5 µg RPS6KA5 (MSK1)

Lane 3: 1 µg RPS6KA5 (MSK1)

Lane 4: 2.5 µg RPS6KA5 (MSK1)

Lane 5: 5 µg RPS6KA5 (MSK1)



Purity:

80% as determined by a SDS-PAGE gel stained with SimplyBlue™ SafeStain.

Molecular Weight:

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

Mass Spectrometry:

RPS6KA5 (MSK1) was subjected to proteolytic digest followed by mass spec analysis. The resulting MS/MS data verified RPS6KA5 (MSK1) identity by comparison against the amino acid sequence(s) of the recombinant protein.

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_004746.2

1	MAPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HYLERDEGDK	WRNKKFELGL	EFPNLPYYID	GDVKLTQDMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	GST TAG
1	MAPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HYLERDEGDK	WRNKKFELGL	EFPNLPYYID	GDVKLTQDMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	IVGN RPS6KA5
1											NP_004746.2
101	DIRYGVSRIA	YSKDFETLKV	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	KRIEAIQID	KYLKSSKYIA	
101	DIRYGVSRIA	YSKDFETLKV	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	KRIEAIQID	KYLKSSKYIA	
1											
201	WPLQGWQATF	GGGDHPPKSD	LVPR								
201	WPLQGWQATF	GGGDHPPKSD	LVPRHNTSL	YKKAGSAAAV	LEENLYFQGS	FTMEEEGGSS	GGAAGTSADG	GDGGEQLLTV	KHELRTANLT	GHAKEVGIEI	
1						--MEEEGGSS	GGAAGTSADG	GDGGEQLLTV	KHELRTANLT	GHAKEVGIEI	
224											
301	FELLKVLGTG	AYGKVFLVRK	ISGHDGTGKLY	AMKVLKKATI	VQKAKTTEHT	RTERQVLEHI	RQSPFLVTLH	YAFQTETKLH	LILDYINGGE	LFTHLSQRER	
49	FELLKVLGTG	AYGKVFLVRK	ISGHDGTGKLY	AMKVLKKATI	VQKAKTTEHT	RTERQVLEHI	RQSPFLVTLH	YAFQTETKLH	LILDYINGGE	LFTHLSQRER	
224											
401	FTEHEVQIYV	GEIVLALEHL	HKLGIYRDI	KLENILLDSN	GHVVLTDGFL	SKEFVADETE	RAYSFCGTIE	YMAPDIVRGG	DSGHDKAVDW	WSLGLVLMYEI	
149	FTEHEVQIYV	GEIVLALEHL	HKLGIYRDI	KLENILLDSN	GHVVLTDGFL	SKEFVADETE	RAYSFCGTIE	YMAPDIVRGG	DSGHDKAVDW	WSLGLVLMYEI	
224											
501	LTGASPFVTD	GEKNSQAEIS	RRILKSEPPY	PQEMSALAKD	LIQRLLMKDP	KKRLGCGPRD	ADEIKEHLFF	QKINWDDLAA	KKVPAPFKPV	IRDELVDVSNF	
249	LTGASPFVTD	GEKNSQAEIS	RRILKSEPPY	PQEMSALAKD	LIQRLLMKDP	KKRLGCGPRD	ADEIKEHLFF	QKINWDDLAA	KKVPAPFKPV	IRDELVDVSNF	
224											
601	AEFEETMDPT	YSPAALPQSS	EKLFGQYSFV	APSILFKRNA	AVIDPLQFHM	VERPGVTNV	ARSAMMKDSP	FYQHYDLDLK	DKPLGEGSFS	ICRKCVMHKS	
349	AEFEETMDPT	YSPAALPQSS	EKLFGQYSFV	APSILFKRNA	AVIDPLQFHM	VERPGVTNV	ARSAMMKDSP	FYQHYDLDLK	DKPLGEGSFS	ICRKCVMHKS	
224											
701	NQAFAVKIIS	KRMEANTQKE	ITALKLCEGH	PNIVKLHEVF	HDQLHTFLVM	ELLNGGELFE	RIKKKKHFSE	TEASYIMRKL	VSAVSHMHDV	GVVHRDLKPE	
449	NQAFAVKIIS	KRMEANTQKE	ITALKLCEGH	PNIVKLHEVF	HDQLHTFLVM	ELLNGGELFE	RIKKKKHFSE	TEASYIMRKL	VSAVSHMHDV	GVVHRDLKPE	
224											
801	NLLFTDENDN	LEIKIIDFGF	ARLKPDPNQ	LKTPCFTLHY	AAPELLNQNG	YDESCDLWSL	GVILYTMLSG	QVPFQSHDRS	LTCTSAVEIM	KKIKKGDFSF	
549	NLLFTDENDN	LEIKIIDFGF	ARLKPDPNQ	LKTPCFTLHY	AAPELLNQNG	YDESCDLWSL	GVILYTMLSG	QVPFQSHDRS	LTCTSAVEIM	KKIKKGDFSF	
224											
901	EGEAWKNVSQ	EAKDLIQGLL	TVDPNKRLKM	SGLRYNEWLQ	DGSQSSNPL	MTPDILGSSG	AAVHTCVKAT	FHAFNKYKRE	GFCLQNVDKA	PLAKRRKMKK	
649	EGEAWKNVSQ	EAKDLIQGLL	TVDPNKRLKM	SGLRYNEWLQ	DGSQSSNPL	MTPDILGSSG	AAVHTCVKAT	FHAFNKYKRE	GFCLQNVDKA	PLAKRRKMKK	
224											
1001	TSTSTETRSS	SSESSHSSSS	HSHGKTTPTK	TLQPSNPADS	NNPETLFQFS	DSVA.					
749	TSTSTETRSS	SSESSHSSSS	HSHGKTTPTK	TLQPSNPADS	NNPETLFQFS	DSVA					

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

Anita Targosz

Anita Targosz, Associate Director

Date: 11/Jan/2016

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