

Certificate of Analysis

STK23 (MSSK1), 10 µg

Serine/Threonine Kinase 23, GST-tagged

ThermoFisher
SCIENTIFIC

Part Number: PV3880

Lot Number: 2107211A

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. No special measures were taken to activate this kinase.

Specific Activity:

78 nmoles of phosphate transferred to myelin basic protein (MBP) per minute per mg of total protein at 30°C. Activity determined at a final protein concentration of 8.33 µg/mL.

Concentration:

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

Calculated **3,820 nM**.

Aliases:

MSSK1

Storage and Handling:

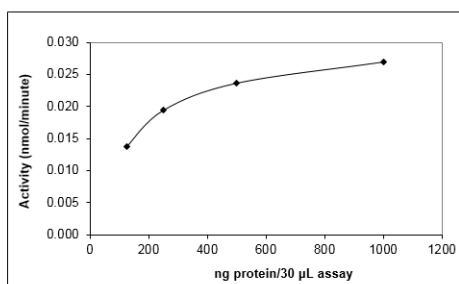
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 µg, 10 µg and 20 µg sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below 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

STK23 (MSSK1) 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:

STK23 (MSSK1) 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, 500 µg/mL myelin basic protein (MBP) and trace [³²P]-γ-ATP for 10 minutes at 30°C.

Gel Information for STK23 (MSSK1)

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

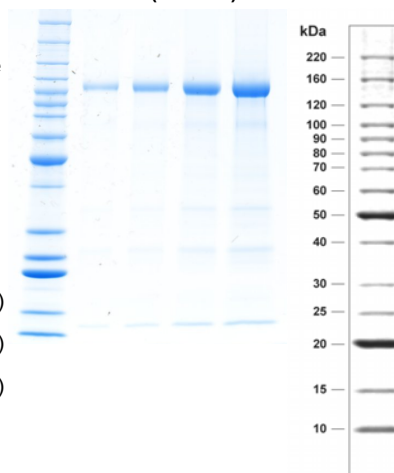
Lane 1: Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

Lane 2: 0.50 µg STK23 (MSSK1)

Lane 3: 1.0 µg STK23 (MSSK1)

Lane 4: 2.5 µg STK23 (MSSK1)

Lane 5: 5.0 µg STK23 (MSSK1)



Purity:

80% as determined by a Coomassie® blue stained SDS-PAGE gel.

Molecular Weight:

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

Mass Spectrometry:

STK23 (MSSK1) was subjected to proteolytic digest followed by mass spec analysis. The resulting MS/MS data verified STK23 (MSSK1) identity by comparison against the amino acid sequence(s) of the recombinant protein.

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_055185

1	MAPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	GDVKLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	GST TAG
1	MAPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	GDVKLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	IVGN STK23
1											NP_055185
101	DIRYGVSRIA	YSKDFETLKV	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	KRIEAIQID	KYLKSSSKYIA	
101	DIRYGVSRIA	YSKDFETLKV	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	KRIEAIQID	KYLKSSSKYIA	
1											
201	WPLQGQWATF	GGGDHPPKSD	LVPR								
201	WPLQGQWATF	GGGDHPPKSD	LVPRHNTSL	YKKAGTMSAS	TGGGDSGGG	GGSSSSSQAS	CGPSSSGSEL	ALATPVPQML	QGLLGSDDEE	QEDPKDYCKG	
1				-----MSAS	TGGGDSGGG	GGSSSSSQAS	CGPSSSGSEL	ALATPVPQML	QGLLGSDDEE	QEDPKDYCKG	
224											
301	GYHPVKIGDV	FNGRYHVVRK	LGWGHFSTVW	LCWDIQRKRF	VALKVVKSAG	HYTETAVDEI	KLLKCVRDSD	PSDPKRETIV	QLIDDFRISG	VNGVHVCML	
65	GYHPVKIGDV	FNGRYHVVRK	LGWGHFSTVW	LCWDIQRKRF	VALKVVKSAG	HYTETAVDEI	KLLKCVRDSD	PSDPKRETIV	QLIDDFRISG	VNGVHVCML	
224											
401	EVLGHQLLKW	IIKSNYQGLP	VPCVKISVRQ	VLHGLDYLHT	KCKIIHTDIK	PENILLCVGD	AYIRRLAAEA	TEWQQAGAPP	PSRSIVSTAP	QEVLTGKLSK	
165	EVLGHQLLKW	IIKSNYQGLP	VPCVKISVRQ	VLHGLDYLHT	KCKIIHTDIK	PENILLCVGD	AYIRRLAAEA	TEWQQAGAPP	PSRSIVSTAP	QEVLTGKLSK	
224											
501	NKRKKMRKR	KQKRLLEER	LRDLQRLEAM	EAATQAEDSG	LRLDGGSGST	SSSGFSGSLF	SPASCSILSG	SSNQRETGGL	LSPSTPFGAS	NLLVNPLEPQ	
265	NKRKKMRKR	KQKRLLEER	LRDLQRLEAM	EAATQAEDSG	LRLDGGSGST	SSSGFSGSLF	SPASCSILSG	SSNQRETGGL	LSPSTPFGAS	NLLVNPLEPQ	
224											
601	NADKIKIKIA	DLGNACVWHK	HFTEDIQTRQ	YRAVEVLIGA	EYGPADIWS	TACMAFELAT	GDYLFEPHSG	EDYSRDEDHI	AHIVELLGDI	PPAFALSGRY	
365	NADKIKIKIA	DLGNACVWHK	HFTEDIQTRQ	YRAVEVLIGA	EYGPADIWS	TACMAFELAT	GDYLFEPHSG	EDYSRDEDHI	AHIVELLGDI	PPAFALSGRY	
224											
701	SREFFNRRGE	LRHIHNLKHW	GLYEVLMEKY	EWPLEQATQF	SAFLLPMEY	IPEKRASAAD	CLQHPWLNPN				
465	SREFFNRRGE	LRHIHNLKHW	GLYEVLMEKY	EWPLEQATQF	SAFLLPMEY	IPEKRASAAD	CLQHPWLNPN				

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

Anita Targosz

Anita Targosz, Associate Director

Date: 22/Jul/2019

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