

Certificate of Analysis

DYRK1A, 10 µg

Dual Specificity Tyrosine Phosphorylation Regulated Kinase 1A, GST-tagged

ThermoFisher
SCIENTIFIC

Part Number: PV3785

Lot Number: 2639089B

Immediate Storage: -80°C

Shipping Conditions: dry ice

5781 Van Allen Way

Carlsbad, CA 92008

Phone: 760.603.7200

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Description:

Recombinant human full-length protein, GST-tagged, expressed in insect cells. No special measures were taken to activate this kinase.

Specific Activity:

1,850 nmoles of phosphate transferred to DYRKtide peptide substrate (RRFRPASPLRGPPK) per minute per mg of total protein at 30°C. Activity determined at a final protein concentration of 0.83 µg/mL.

Concentration:

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

Calculated **3,890 nM**.

Aliases:

DYRK1, DYRK, MNBH, HP86

Storage and Handling:

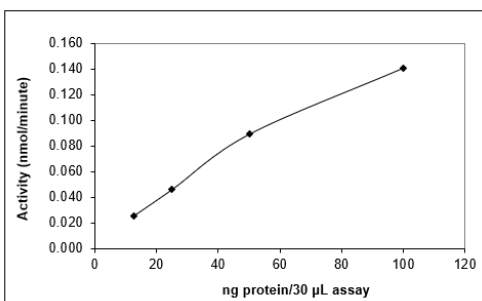
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 µg, 10 µg and 20 µg sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below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

DYRK1A 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:

DYRK1A 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, 200 µg/mL DYRKtide peptide substrate (RRFRPASPLRGPPK) and trace [³²P]-γ-ATP for 10 minutes at 30°C.

Gel Information for DYRK1A

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

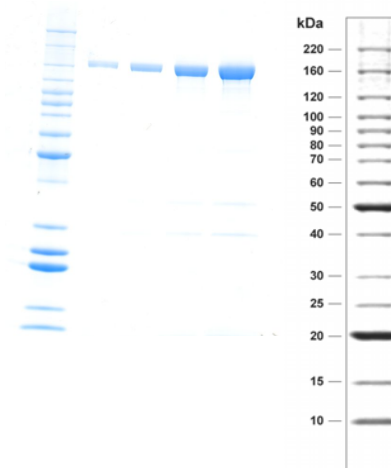
Lane 1: Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

Lane 2: 0.5 µg DYRK1A

Lane 3: 1.0 µg DYRK1A

Lane 4: 2.5 µg DYRK1A

Lane 5: 5.0 µg DYRK1A



Purity:

90% as determined by a SDS-PAGE gel stained with SimplyBlue™ SafeStain.

Molecular Weight:

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

Mass Spectrometry:

DYRK1A was subjected to proteolytic digest followed by mass spec analysis. The resulting MS/MS data verified DYRK1A identity by comparison against the amino acid sequence(s) of the recombinant protein.

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_001387

1	MAPILGYWK	IKGLVQPTRL	LLEYLEEKYE	EHLYERDEGD	KWRNKKFELG	LEFPNLPYYI	DGDVKLTQSM	AIIRYIADKH	NMLGGCPKER	AEISMLEGAV	GST TAG
1	MAPILGYWK	IKGLVQPTRL	LLEYLEEKYE	EHLYERDEGD	KWRNKKFELG	LEFPNLPYYI	DGDVKLTQSM	AIIRYIADKH	NMLGGCPKER	AEISMLEGAV	IVGN DYRK1A
1											NP_001387
101	DIRYGVSR	AYS	KDFETLK	VD	FLSKLPEM	LKMFEDRLCH	KTYLNGDHVT	HPDFMLYDAL	DV	VLYMDPMC	LDAFPKLVCF
101	DIRYGVSR	AYS	KDFETLK	VD	FLSKLPEM	LKMFEDRLCH	KTYLNGDHVT	HPDFMLYDAL	DV	VLYMDPMC	LDAFPKLVCF
1											
201	WPLQGQAT	FGGGDHPPKS	DLVPR								
201	WPLQGQAT	FGGGDHPPKS	DLVPRHNQTS	LYKKAGTMHT	GGETSACKPS	SVRLAPSF5F	HAAGLQMAQ	MPHSHQYSDR	RQPNISDQV	SALSYSDQIQ	
1				-----MHT	GGETSACKPS	SVRLAPSF5F	HAAGLQMAQ	MPHSHQYSDR	RQPNISDQV	SALSYSDQIQ	
224											
301	PLTNQVMPD	IVMLQRRMPQ	TFRDPATAPL	RKLSVDLIKT	YKHINEVYYA	KKKRRHQQGO	GDDSSHKKER	KVYNDGYDDD	NYDYIVKNGE	KWMDRYEIDS	
65	PLTNQVMPD	IVMLQRRMPQ	TFRDPATAPL	RKLSVDLIKT	YKHINEVYYA	KKKRRHQQGO	GDDSSHKKER	KVYNDGYDDD	NYDYIVKNGE	KWMDRYEIDS	
224											
401	IGKGSFGQV	VKAYDRVEQE	WVAIKIKNK	KAFLNQAQIE	VRLLELMNKH	DTEMKYYIVH	LKRHFMRNH	LCLVFEMLSY	NLYDLLRNTN	FRGVSLNLTR	
165	IGKGSFGQV	VKAYDRVEQE	WVAIKIKNK	KAFLNQAQIE	VRLLELMNKH	DTEMKYYIVH	LKRHFMRNH	LCLVFEMLSY	NLYDLLRNTN	FRGVSLNLTR	
224											
501	FAQMCTAL	LFLATPELSI	IHCCLKPENI	LLCNPKRSAI	KIVDFGSSCQ	LGQRIYQYIQ	SRFYRSPEVL	LGMPYDLAID	MWSLGCILVE	MHTGEPLFSG	
265	FAQMCTAL	LFLATPELSI	IHCCLKPENI	LLCNPKRSAI	KIVDFGSSCQ	LGQRIYQYIQ	SRFYRSPEVL	LGMPYDLAID	MWSLGCILVE	MHTGEPLFSG	
224											
601	NEVDQMNI	VEVLGIPPAH	ILDQAPKARK	FFEKLPDGTW	NLKKTKDGKR	EYKPPGTRKL	HNILGVETGG	PGRRRAGESG	HTVADYLFKF	DLILRMLDYD	
365	NEVDQMNI	VEVLGIPPAH	ILDQAPKARK	FFEKLPDGTW	NLKKTKDGKR	EYKPPGTRKL	HNILGVETGG	PGRRRAGESG	HTVADYLFKF	DLILRMLDYD	
224											
701	KTRIOPYYA	LQHSFFKKTA	DEGTNTNSV	STSPAMEQSQ	SSGTTSSSTSS	SSGGSSGTSN	SGRARSDPHT	QHRHSGGHFT	AAVQAMDCET	HSPQVRQQFP	
465	KTRIOPYYA	LQHSFFKKTA	DEGTNTNSV	STSPAMEQSQ	SSGTTSSSTSS	SSGGSSGTSN	SGRARSDPHT	QHRHSGGHFT	AAVQAMDCET	HSPQVRQQFP	
224											
801	PLGWSGTEA	PTQVTVETHP	VQETTFHVAP	QQNALHHHHG	NSSHHHHHHH	HHHHHHGQQA	LGNRTRPRVY	NSPTNSSSTQ	DSMEVGHSHH	SMTSLSSSTT	
565	PLGWSGTEA	PTQVTVETHP	VQETTFHVAP	QQNALHHHHG	NSSHHHHHHH	HHHHHHGQQA	LGNRTRPRVY	NSPTNSSSTQ	DSMEVGHSHH	SMTSLSSSTT	
224											
901	SSTSSSSSTG	NQGNQAYQNR	PVAANTLDFG	QNGAMDVNLT	VYSNPRQETG	IAGHPTYQFS	ANTGPAHYMT	EGHLTMRQGA	DREESPMGTG	CVQQSPVASS	
665	SSTSSSSSTG	NQGNQAYQNR	PVAANTLDFG	QNGAMDVNLT	VYSNPRQETG	IAGHPTYQFS	ANTGPAHYMT	EGHLTMRQGA	DREESPMGTG	CVQQSPVASS	

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



Chevoyn Joseph, Director, Quality

Date: 27/Apr/2023

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