

Certificate of Analysis

DYRK1A, 10 µg

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

ThermoFisher
SCIENTIFIC

Part Number: PV3785

Lot Number: 1783084P

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:

1,900 nmoles of phosphate transferred to DYRKtide peptide substrate (RRRFRPASPLRGPPK) per minute per mg of total protein at 30°C. Activity determined at a final protein concentration of 0.83 µg/mL.

Concentration:

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

Calculated **2,040 nM**.

Aliases:

DYRK1, DYRK, MNBH, HP86

Storage and Handling:

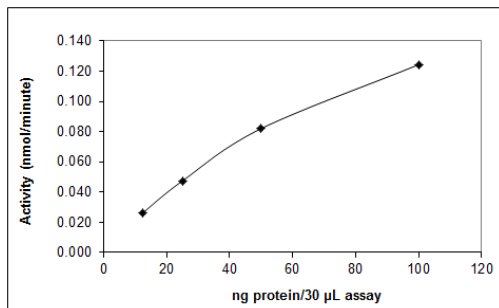
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 µg, 10 µg and 20 µg sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below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

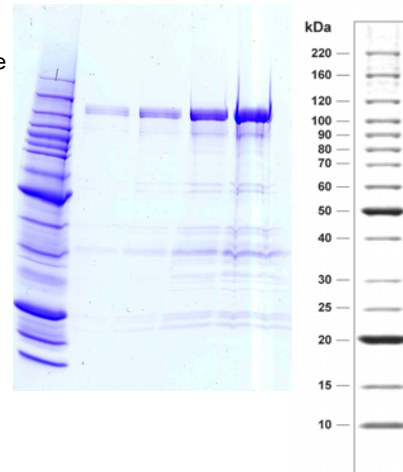
Lane 1: Invitrogen™ BenchMark™ Protein Ladder (Catalog #: 10747-012).

Lane 2: 0.5 µg DYRK1A

Lane 3: 1 µg DYRK1A

Lane 4: 2.5 µg DYRK1A

Lane 5: 5 µg DYRK1A



Purity:

70% 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	LEFPNLPPYI	DGDVKLTQSM	AIIRYIADKH	NMLGGCPKER	AEISMLEGAV	GST TAG
1	MAPILGYWK	IKGLVQPTRL	LLEYLEEKYE	EHLYERDEGD	KWRNKKFELG	LEFPNLPPYI	DGDVKLTQSM	AIIRYIADKH	NMLGGCPKER	AEISMLEGAV	IVGN DYRK1A
1											NP_001387
101	DIRYGVSR	AYS	KDFETLK	VD	FLSKLP	EM	LK	MFEDRLCH	KTY	LNGDHVT	HP
101	DIRYGVSR	AYS	KDFETLK	VD	FLSKLP	EM	LK	MFEDRLCH	KTY	LNGDHVT	HP
1											
201	WPLQGWQAT	FGGGDHPPKS	DLVPR								
201	WPLQGWQAT	FGGGDHPPKS	DLVPRHNQTS	LYKKAGTMHT	GGETSACKPS	SVRLAPSF	SVF	HAAGLQ	MAGQ	MPHSHQ	YS
1											
224											
301	PLTNQVMPD	IVMLQRRMPQ	TFRDPATAPL	RKLSVDLIKT	YKHINEVYYA	KKKRRHQ	Q	Q	G	D	S
65	PLTNQVMPD	IVMLQRRMPQ	TFRDPATAPL	RKLSVDLIKT	YKHINEVYYA	KKKRRHQ	Q	Q	G	D	S
224											
401	IGKGSFGQV	VKAYDRVEQE	WVAIKIKNK	KAFLNQAQIE	VRLLELMNKH	DTEMKYYIVH	LKRHF	MFRNH	LCLVF	EMLSY	NLYD
165	IGKGSFGQV	VKAYDRVEQE	WVAIKIKNK	KAFLNQAQIE	VRLLELMNKH	DTEMKYYIVH	LKRHF	MFRNH	LCLVF	EMLSY	NLYD
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	PGGRRAGESG	HTVADYLKFK	DLILRMLDYD	
365	NEVDQMNI	VEVLGIPPAH	ILDQAPKARK	FFEKLPDGTW	NLKKTKDGKR	EYKPPGTRKL	HNILGVETGG	PGGRRAGESG	HTVADYLKFK	DLILRMLDYD	
224											
701	KTRIOPYYA	LQHSFFKKTA	DEGTNTNSV	STSPAMEQSQ	SSGTTSSSTSS	SSGGSSGTSN	SGRARS	DP	TH	QHRHSGGHFT	AAVQAMDCET
465	KTRIOPYYA	LQHSFFKKTA	DEGTNTNSV	STSPAMEQSQ	SSGTTSSSTSS	SSGGSSGTSN	SGRARS	DP	TH	QHRHSGGHFT	AAVQAMDCET
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	SSTSSSSTG	NQGNQAYQNR	PVAANTLDFG	QNGAMDVNLT	VYSNPRQETG	IAGHPTYQFS	ANTGPAHYMT	EGHLTMRQGA	DREESPM	TG	CVQQSPVASS
665	SSTSSSSTG	NQGNQAYQNR	PVAANTLDFG	QNGAMDVNLT	VYSNPRQETG	IAGHPTYQFS	ANTGPAHYMT	EGHLTMRQGA	DREESPM	TG	CVQQSPVASS

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

Anita Targosz

Anita Targosz, Associate Director

Date: 11/Mar/2016

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