

Certificate of Analysis

PRKCE, (PKC Epsilon), 10 µg

Protein Kinase C Epsilon, Recombinant human

ThermoFisher
SCIENTIFIC

Part Number: A41914

Lot Number: 77731515A

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 active PRKCE, (PKC Epsilon), full length, amino acids M₁ - P₇₃₇, with an N-terminal GST-HIS₆ tag with a Thrombin cleavage site was expressed in insect cells. No special measures were taken to activate this kinase.

Accession Number:

The gene accession number for PRKCE, (PKC Epsilon) is NP_005391.1.

Specific Activity:

184 nmoles of phosphate transferred to PKC-derived peptide per minute per mg of total protein at saturating ATP.

Concentration:

0.366 mg/mL total protein as measured using the Bradford protein assay with BSA as a standard. Calculated **3,230 nM**.

Aliases:

PKCE

Storage and Handling:

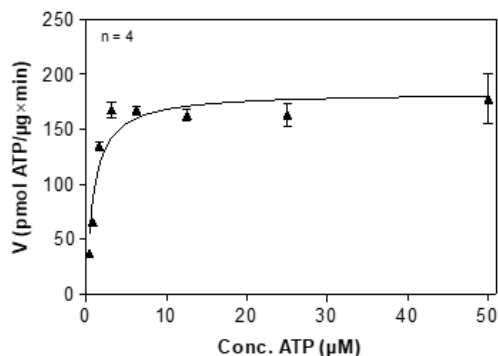
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 µg, 10 µg and 20 µg sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below 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-HCl (pH 8.0), 100 mM NaCl, 5 mM DTT, 4 mM glutathione and 20% Glycerol.

QUALITY ASSURANCE

PRKCE, (PKC Epsilon) Activity Graph



Assay Conditions:

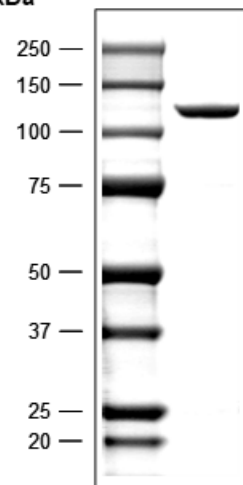
PRKCE, (PKC Epsilon) was assayed for activity at 1.0 µg/mL in 60 mM HEPES (pH 7.5), 3 mM MgCl₂, 3 mM MnCl₂, 1 mM CaCl₂, 4 mM EDTA, 3 µM Na₃VO₄, 5 µg/mL Phosphatidylserine, 1 µg/mL 1,2 Dioleoyl-glycerol, 1.2 mM DTT, 50 µg/mL PEG_{20,000}, ATP (titrated) using 10 µg/mL PKC-derived peptide

Gel Information for PRKCE, (PKC Epsilon)

Page Description: Run on an SDS-PAGE gel and stained with Coomassie®.

Lane 1: Molecular Weight markers as labeled.

Lane 2: 2 µg PRKCE, (PKC Epsilon)



Molecular Weight:

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

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_006246.2

1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HYERDEGDK	WRNKKFELGL	EFPNLPYYID	GDVKLTQDMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	GST-H6
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HYERDEGDK	WRNKKFELGL	EFPNLPYYID	GDVKLTQDMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	LIFE PRKCE
1											NP_006246.2
101	DIRYGVSRIA	YSKDFETLKV	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	KRIEAIQID	KYLKSSSKYIA	
101	DIRYGVSRIA	YSKDFETLKV	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	KRIEAIQID	KYLKSSSKYIA	
1											
201	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHHG	RRRASVAAGI	LVPRGSPGLD	GICSRNS					
201	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHHG	RRRASVAAGI	LVPRGSPGLD	GICSRNSMSS	GTMKFNGYLR	VRIGEAVGLQ	PTRWSLRHSL	FKKGHQLLDP	
1						-----MSS	GTMKFNGYLR	VRIGEAVGLQ	PTRWSLRHSL	FKKGHQLLDP	
245											
301	YLTVSVDQVR	VGQTSTKQKT	NKPTYNEEFC	ANVTGGHLE	LAVFHETPLG	YDHFVANCTL	QFQELLRTTG	ASDTFEGWVD	LEPEGKVFFV	ITLTGSFTEA	
41	YLTVSVDQVR	VGQTSTKQKT	NKPTYNEEFC	ANVTGGHLE	LAVFHETPLG	YDHFVANCTL	QFQELLRTTG	ASDTFEGWVD	LEPEGKVFFV	ITLTGSFTEA	
245											
401	TLQRDRIFKH	FTRKRQRAMR	RRVHQINGHK	FMATYLRQPT	YCSHCREFIW	GVFGKQGYQC	QVCTCVVHKR	CHHLIVTACT	CQNNINKVDS	KIAEQRFGIN	
141	TLQRDRIFKH	FTRKRQRAMR	RRVHQINGHK	FMATYLRQPT	YCSHCREFIW	GVFGKQGYQC	QVCTCVVHKR	CHHLIVTACT	CQNNINKVDS	KIAEQRFGIN	
245											
501	IPHKFSIHNY	KVPTFCDHCG	SLWGIMRQG	LQCKICKMNV	HIRCQANVAP	NCGVNAVELA	KTLAGMGLQP	GNISPTSKLV	SRSTLRRQ GK	ESSKEGNGIG	
241	IPHKFSIHNY	KVPTFCDHCG	SLWGIMRQG	LQCKICKMNV	HIRCQANVAP	NCGVNAVELA	KTLAGMGLQP	GNISPTSKLV	SRSTLRRQ GK	ESSKEGNGIG	
245											
601	VNSSNRLGID	NFEFIRVLGK	GSFGKVMRLAR	VKETGDLYAV	KVLKKDVILQ	DDDVECTMTE	KRILSLARNH	PFLTQLFCCF	QTPDRLFFVM	EFVNGGDLMF	
341	VNSSNRLGID	NFEFIRVLGK	GSFGKVMRLAR	VKETGDLYAV	KVLKKDVILQ	DDDVECTMTE	KRILSLARNH	PFLTQLFCCF	QTPDRLFFVM	EFVNGGDLMF	
245											
701	HIQSRRFDE	ARARFYAAEI	ISALMFLHDK	GIYRDLKLD	NVLDDHEGHC	KLADFGMCKE	GICNGVTTAT	FCGTPDYIAP	EILQEMLYGP	AVDWWAMGVL	
441	HIQSRRFDE	ARARFYAAEI	ISALMFLHDK	GIYRDLKLD	NVLDDHEGHC	KLADFGMCKE	GICNGVTTAT	FCGTPDYIAP	EILQEMLYGP	AVDWWAMGVL	
245											
801	LYEMLCGHAP	FEAENEDDLF	EAILNDEVVY	PTWLHEDATG	ILKSFMTKNP	TMRLGSLTQG	GEHAILRHFP	FKEIDWAQLN	HRQIEPPFRP	RIKSREDVSN	
541	LYEMLCGHAP	FEAENEDDLF	EAILNDEVVY	PTWLHEDATG	ILKSFMTKNP	TMRLGSLTQG	GEHAILRHFP	FKEIDWAQLN	HRQIEPPFRP	RIKSREDVSN	
245											
901	FDPDFIKEEP	VLTPIDEGLH	PMINQDEFNR	FSYVSPQLQP							
641	FDPDFIKEEP	VLTPIDEGLH	PMINQDEFNR	FSYVSPQLQP							

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

Rachel Smith

Rachel Smith, Manager, QA/QC

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