

Certificate of Analysis

PRKCG (PCK Gamma), 10 µg

Protein Kinase C Gamma, Recombinant human protein

ThermoFisher
SCIENTIFIC

Part Number: A41917

Lot Number: 2158974

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 PRKCG (PCK Gamma), full length, amino acids M₁ – M₆₉₇, K216N mutation, with an N-terminal GST-HIS₆ tag with a Thrombin cleavage site was expressed in insect cells. No special measures we taken to activate this kinase.

Accession Number:

The gene accession number for PRKCG (PCK Gamma) is NP_002730.1.

Specific Activity:

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

Concentration:

0.088 mg/mL total protein as measured using the Bradford protein assay with BSA as a standard. Calculated **784 nM**.

Aliases: MGC57564; PKCC; PKCG; SCA14

Storage and Handling:

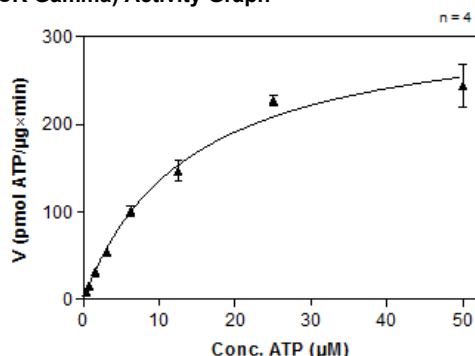
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 ug, 10ug and 20ug sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below 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, 15 mM glutathione and 20% Glycerol.

QUALITY ASSURANCE

PRKCG (PCK Gamma) Activity Graph



Assay Conditions:

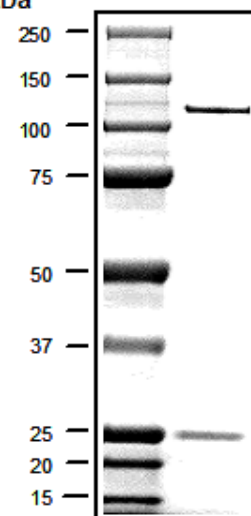
PRKCG (PCK Gamma) was assayed for activity at 0.4 µg/mL in 60 mM HEPES (pH 7.5), 3 mM MgCl₂, 3 mM MnCl₂, 3 µM Na₃VO₄, 1.2 mM DTT, 50 µg/mL PEG_{20,000}, ATP (titrated) using 20 µg/mL PKC-derived peptide

Gel Information for PRKCG (PCK Gamma)

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

Lane 1: Molecular Weight markers as labeled.

Lane 2: 2 µg PRKCG (PCK Gamma)



Molecular Weight:

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

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_002730.1

1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	GDVKLTQDMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	GST-H6
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	GDVKLTQDMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	LIFE PRKCG
1											NP_002730.1
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	PMGHHHHHHG	RRRASVAAGI	LVPRGSPGLD	GICSSGRQCD	GYLQNSPLA				
201	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHHG	RRRASVAAGI	LVPRGSPGLD	GICSSGRQCD	GYLQNSPLAM	AGLGPVGDS	EGGPRPLFCR	KGALRQKVH	
1											
245											
301	EVKSHKFTAR	FFKQPTFCSH	CTDFIWGIGK	QGLQCQVCSF	VVHRRCHEFV	TFECPGAGKG	PQTDDPRNKH	KFRLHSYSSP	TFCDHCGSLL	YGLVHQGMKC	
32	EVKSHKFTAR	FFKQPTFCSH	CTDFIWGIGK	QGLQCQVCSF	VVHRRCHEFV	TFECPGAGKG	PQTDDPRNKH	KFRLHSYSSP	TFCDHCGSLL	YGLVHQGMKC	
245											
401	SCCEMNVHRR	CVRSVPSLCG	VDHTERRGR	QLEIRAPTAD	EIHVTVGEAR	NLIPMDPNGL	SDPYVKLKI	PDPRLTKQK	TRTVNATLNP	VWNETFVFN	
132	SCCEMNVHRR	CVRSVPSLCG	VDHTERRGR	QLEIRAPTAD	EIHVTVGEAR	NLIPMDPNGL	SDPYVKLKI	PDPRLTKQK	TRTVKATLNP	VWNETFVFN	
245											
501	KPGDVERRLS	VEVWDWDRS	RNDFMGAMSF	GVSELLKAPV	DGWYKLLNQE	EGEYVNPVA	DADNCSLLQK	FEACNYPLEL	YERVRMGPS	SPIPSPSPS	
232	KPGDVERRLS	VEVWDWDRS	RNDFMGAMSF	GVSELLKAPV	DGWYKLLNQE	EGEYVNPVA	DADNCSLLQK	FEACNYPLEL	YERVRMGPS	SPIPSPSPS	
245											
601	TDPKRCFFGA	SPGRLHISDF	SFLMVLGKGS	FGKVMLEARR	GSDELYAIIKI	LKKDVIQDD	DVDCTLVEKR	VLALGGRGPG	GRPHFLTQLH	STFQTPDRLY	
332	TDPKRCFFGA	SPGRLHISDF	SFLMVLGKGS	FGKVMLEARR	GSDELYAIIKI	LKKDVIQDD	DVDCTLVEKR	VLALGGRGPG	GRPHFLTQLH	STFQTPDRLY	
245											
701	MVKRRDYLDL	AASTPSDSL	YDDGLSEET	PLVDCNNAPL	PRALPSTWIE	NKLYGMSDPN	WPGESPVPLT	RADGTNTGFP	RYPNDSVYAN	WMLSPSAAKL	
432	MVKRRDYLDL	AASTPSDSL	YDDGLSEET	PLVDCNNAPL	PRALPSTWIE	NKLYGMSDPN	WPGESPVPLT	RADGTNTGFP	RYPNDSVYAN	WMLSPSAAKL	
245											
801	FVMEYVTGGD	LMYHIQQLGK	FKEPAAAFYA	AEIAIGLFFL	HNQGIYRDL	KLDNVMLDAE	GHIKITDFGM	CKENVFPGTT	TRTFCTPDY	IAPEIIAYQP	
532	FVMEYVTGGD	LMYHIQQLGK	FKEPAAAFYA	AEIAIGLFFL	HNQGIYRDL	KLDNVMLDAE	GHIKITDFGM	CKENVFPGTT	TRTFCTPDY	IAPEIIAYQP	
245											
901	YGKSDVWWSF	GVLLEYMLAG	QPPFDGEDEE	ELFQAIMEQT	VTYPKSLSRE	AVAICKGFLT	KHPGKRLGSG	PDGEPTIRAH	GFFRWIDWER	LERLEIPPPF	
632	YGKSDVWWSF	GVLLEYMLAG	QPPFDGEDEE	ELFQAIMEQT	VTYPKSLSRE	AVAICKGFLT	KHPGKRLGSG	PDGEPTIRAH	GFFRWIDWER	LERLEIPPPF	
245											
1001	RPRPCGRSGE	NFDKFFTRAA	PALTPPDLRV	LASIDQADFQ	GFTYVNPDEFV	HPDARSPTSP	VPVPVMQGR	PAHWRPLLVD	PSSVPPGDLY	RLC	
732	RPRPCGRSGE	NFDKFFTRAA	PALTPPDLRV	LASIDQADFQ	GFTYVNPDEFV	HPDARSPTSP	VPVPVM				

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

Anita Targosz

Anita Targosz, Associate Director

Date: 03/Oct/2019

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