

## PIK3CD/PIK3R1

phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta

**Recombinant Human Active Lipid Kinase**

**HGNC Symbol:** PIK3CD

**Synonyms PIK3CD:** p110D, P110DELTA, PI3K, PI3K-delta

**Synonyms PIK3R1:** GRB1, p85, p85-ALPHA,

**Lipid Kinase Family:** PI3K Class I

(according to: Phylogenomics of phosphoinositide lipid kinases: perspectives on the evolution of second messenger signaling and drug discovery: James R Brown & Kurt R Auger; BMC Evolutionary Biology 11, 4-14 (2011))

**Product No.:** 1162-1165-1

**Lot:** 004

**Description:** Human PIK3CD, full length, amino acids M<sub>1</sub>-Q<sub>1044</sub> (as in [NCBI/Protein](#) entry NP\_005017.3), N-terminal GST-HIS<sub>6</sub> fusion protein with a 3C cleavage site and PIK3R1, full length, amino acids M<sub>1</sub>-R<sub>724</sub> (as in [NCBI/Protein](#) entry NP\_852664.1), N-terminally fused to a MYC-tag, coexpressed in Sf9 insect cells

**Product identity:** PIK3CD/PIK3R1 Lot 004, was confirmed as PIK3CD/PIK3R1 by mass spectroscopy LC-ESI-MS/MS

**Theoretical MW<sub>GST-PIK3CD</sub>** : 147,998 Da

**Theoretical MW<sub>PIK3R1</sub>** : 85,371 Da

**Expression host:** Sf9 insect cells

**Purification:** GST-Affinity Chromatography

**Activation:** This kinase was not activated by special procedures

**Storage buffer:** 50 mM HEPES pH 7.5, 100 mM NaCl, 5 mM DTT, 15 mM reduced glutathione, 0.1 % Triton X-100, 20% glycerol

**Storage temperature:** -80°C

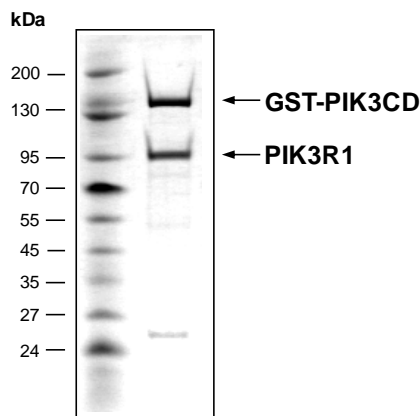
For complete recovery, mix well and spin before use. Product must not be stored in diluted solutions, aliquots below 10µl are not advisable. Avoid repeated freeze-thaw cycles!

**Protein concentration:** 0.250 µg/µl (Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

**Biochemical Parameters:**

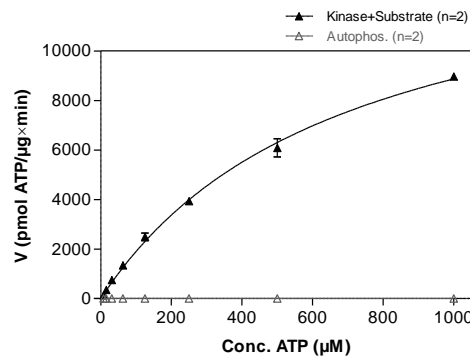
Specific kinase activity (P<sub>i</sub> transfer): 14967pmol/µg × min  
ATP-K<sub>M</sub>: 688 µM

**PIK3CD/PIK3R1 Lot 004:  
Coomassie stain**



4 µg GST-PIK3CD/PIK3R1

**PIK3CD/PIK3R1 Lot 004:  
Determination of V<sub>max</sub> and K<sub>M</sub> value for ATP**



**Determination of K<sub>M</sub> value & Specific activity:**

- Assay conditions:
  - 50 mM HEPES-NaOH, pH 7.5
  - 3 mM MgCl<sub>2</sub>
  - 1 mM EGTA
  - 100 mM NaCl
  - 0.03% CHAPS
  - 2 mM DTT
  - ATP (variable)
  - 1 % (v/v) DMSO
  - Substrate: PIP2: 50 µM / PS: 950 µM
  - PIP2: 08:0 PI(4,5)P2 (1,2-Dioctanoyl-sn-Glycero-3-(Phosphoinositol-4,5-Bisphosphate)
  - PS: 1-Palmitoyl-2-Oleoyl-sn-Glycero-3-[Phospho-L-Serine]
  - PIK3CD/PIK3R1: 1 µg/ml
- Assay technology: ADP-Glo (Promega)

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# PIK3CD/PIK3R1

Product No.: 1162-1165-1

GST-PIK3CD Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP EML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI PQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHG	RDSLEVLFCG	240
241	PLAMLMPGGV	DCPMEFWTKE	ENQSVVDFL	LPTGVYLNFP	VSRNANLSTI	KQLLWHRAQY	300
301	EPLFHMLSGP	EAYVFTCINQ	TAEQCELEDE	QRRLCDVQPF	LPVLRVARE	GDRVKCLINS	360
361	QISLLIGKGL	HEFDSLCDPE	VNDFRAKMCQ	FCEEEAARRQ	QLGWEAWLQY	SFPLQLEPSA	420
421	QTWPGTTLRL	PNRALLVNK	FEGSEESFTF	QVSTKDVPLA	LMACALRKA	TVFRQPLVEQ	480
481	PEDYTLQVNG	RHEYLYGSYP	LCQFQYICSC	LHSGLTPHLT	MVHSSSILAM	RDEQSNPAPQ	540
541	VQKPRAKPPP	IPAKKPSSVS	LWSLEQPFRI	ELIQGSKVNA	DERMKLVVQA	GLFHGNEMLC	600
600	KTVSSSEVSV	CSEPVMKQRL	EFDINICDLP	RMARLCFALY	AVIEKAKKAR	STKKKSKKAD	660
661	CPIAWANLML	FDYKDLKGTG	ERCLYMWPSV	PDEKCELLNP	TGTVRSNPNT	DSAAALLICL	720
721	PEVAPHV VY	PALEKILELG	RHSECVHVTE	EEQLQREIL	ERRGSGELYE	HEKDLVWKL R	780
781	HEVQEHFPEA	LARLLLVTWK	NKHEDVAQML	YLLCSWPELP	VLSALELLDF	SFPDCHVGSF	840
841	AIKSLRKLTD	DELFOYLLQL	VQVLKYESYL	DCELTKFLLD	RALANRKIGH	FLFWHLRSEM	900
901	HVPSVALRFG	LILEAYCRGS	THHMKVLKMQ	GEALSCLKAL	NDFVKLSSQK	TPKPQTKELM	960
961	HLCMRQEAYL	EALSHLQSP	DPSTLLAEVC	VEQCTFMDSK	MKPLWIMYSN	EEAGSGG SVG	1020
1021	IIFKNGDDL R	QDMLTLQMIQ	LMDVLWKQEG	LDLRMTPYGC	LPTGDRGTGLI	EVVLRSDTIA	1080
1081	NIQLNKS NMA	ATAAFNKDAL	LNWLKSNPGE	EALDRAIEEF	TLSCAGYCA	TYVLGIGDRH	1140
1141	SDNIMIRESG	QLFHIDFGHF	LGNFKTKFGI	NRERVPFILT	YDFVHVIIQQG	KTNNSEKFER	1200
1201	FRGYCERAYT	ILRRHGLLFL	HLFALMRAAG	LPELSCSKDI	OYLKDSLALG	KTEEEALKHF	1260
1261	RVKFNEALRE	SWKTKVNWLA	HNVSKDNRQ				1320

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: PIK3CD

PIK3CD wt <sup>1</sup> Amino Acid Sequence							
1	MPPGVDCPME	FWTKEENQSV	VVDFLLPTGV	YLNFPVSRNA	NLSTIKQLLW	HRAQYEPLFH	60
61	MLSGPEAYVF	TCINQTAEQQ	ELEDEQRRLC	DVQPFPLVLR	LVAREGDRVK	KLINSQISLL	120
121	IGKGLHEFDS	LCDPEVNDFR	AKMCQFCEEA	AARRQQLGWE	AWLQYSFPLQ	LEPSAQTWGP	180
181	GTLRLPNRAL	LVNVKFEGSE	ESFTFQVSTK	DVPLALMACA	LRKKATVFRQ	PLVEQPEDYT	240
241	LQVNGRHEYL	YGSYPLCQFQ	YICSCLSHSL	TPHLTMVHSS	SILAMRDEQS	NPAPQVQKPR	300
301	AKPPPIPAK	PSSVSLWSLE	QPFRIELIQG	SKVNADERMK	LVVQAGLFHG	NEMLCKTVSS	360
361	SEVSVCS EPG	WKQRLEFDIN	ICDLPRMARL	CFALYAVIEK	AKKARSTKKK	SKKADCP IAW	420
421	ANLMLFDYKD	QLKTGERCLY	MWPSVPDEKG	ELLNPTGTVR	SNPNTDSAAA	LLICLPEVAP	480
481	HPVYYPALEK	ILELGRHSEC	VHVTEEEQLQ	LREILERRGS	GELYEHEKDL	VWKL RHEVQE	540
541	HFPEALARLL	LVTKWNKHED	VAQMLYLLCS	WPELPVLSAL	ELLD FSFPDC	HVGSFAIKSL	600
600	RKLTDEL FQ	YLLQLVQVLK	YESYLDCELT	KFLLDRALAN	RKIGHFLFWH	LRSEMHVPSV	660
661	ALRFG LILEA	YCRGSTHMK	VLMKQGEALS	KLKALNDFVK	LSSQKTPKPQ	TKELMHLCMR	720
721	QEAYLEALSH	LQSPLDPSTL	LAEVCVEQCT	FMDSKMKPLW	IMYSNEEAGS	GGSVGII FKN	780
781	GDDL RQDMLT	LQMIQLMDVL	WKQEGLDLRM	TPYGC LPTGD	RTGLIEV VLR	SDTIANIQLN	840
841	KSNMAATAAF	NKDALLNWLK	SKNPGEALDR	AIEEFTLSCA	GYCVATYVLG	IGDRHSDNIM	900
901	IRESGQLFHI	DFGHFLGNFK	TKFGINRERV	PFILTYDFVH	VIQQGKTNNS	EKFERFRGYC	960
961	ERAYTILRRH	GLLFLHLFAL	MRAAGLPELS	CSKDIQY LK	SLALGKTEEE	ALKHFRVKFN	1020
1021	EALRESWKTK	VNWLAHNVSK	DNRQ				1080

blue: PIK3CD sequence expressed in recombinant protein

<sup>1</sup>NCBI/Protein accession number NP\_005017.3

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**MYC-PIK3R1 Recombinant Fusion Protein Amino Acid Sequence**

1	MEEQKLISEE	DL	PMVMSAEG	YQYRALYDYK	KEREEDIDLH	LGDILTVNKG	SLVALGFSDG	60
61	QEARPEEIGW		LNGYNETTGE	RGDFPGTYVE	YIGRKKISPP	TPKPRPPRPL	PVAPGSSKTE	120
121	ADVEQQALTL		PDLAEQFAPP	DIAPPLLIK	VEAIEKKGLE	CSTLYRTQSS	SNLAELRQLL	180
181	DCDTPSVGLE		MIDVHVLADA	FKRYLLDLPN	PVIPAAYVSE	MISLAPEVQS	SEEYIQLLKK	240
241	LIRSPSIPHQ		YWLTLQYLLK	HFFKLSQTSS	KNLLNARVLS	EIFSPMLFRF	SAASSDNTEN	300
301	LIKVIEILIS		TEWNERQPAP	ALPPKPPKPT	TVANNGMNNN	MSLQDAEWYW	GDISREEVNE	360
361	KLRDTADGTF		LVRDASTKMH	GDYTLTLRKG	GNNKLIKIFH	RDGKYGFSDP	LTFSVVVELI	420
421	NHYRNESLAQ		YNPKLDVKLL	YPVSKYQQDQ	VVKEDNIEAV	GKKLHKYNTQ	FQEKRSREYDR	480
481	LYEEYTRTSQ		EIQMKRTAIE	AFNETIKIFE	EQCQTQERY	KEYIEKFKRE	GNEKEIQRIM	540
541	HNYDKLKSRI		SEIIDSRRRL	EEDLKKQAAE	YREIDKRMNS	IKPDLIQLRK	TRDQYLMWLT	600
601	QGVVRQKKNL		EYLVNTEDED	QYSLVEDDED	LPHHDEKTN	VGSSNRNKAE	NLLRKRDRGT	660
661	FLVRESSKQG		CYACSVVDG	EVKHCVINKT	ATGYGFAEY	NLYSSLKELV	LHYQHTSLVQ	720
721	HNDLNLVTLA		YPVYAQQRR					780

1-218: GST Red: MYC-tag blue: PIK3R1 boxed: variation from RefSeq

**PIK3R1 wt<sup>2</sup> Amino Acid Sequence**

1	MSAEGYQYRA	LYDYKKEREE	DIDLHLGDIL	TVNKGSLVAL	GFSQGQEARP	EEIGWLNQYN	60
61	ETTGERGDFP	GTIVEYIGRK	KISPPTPKPR	PPRPLPVAPG	SSKTEADVEQ	QALTLPLDLAE	120
121	QFAPPDIAPP	LLIKLVEAIE	KGLEECSTLY	RTQSSSNLAE	LRQLLDCDTP	SVDLEMIDVH	180
181	VLADAFKRYL	LDLNPVPIPA	AVYSEMISLA	PEVQSSEEYI	QLLKKLIRSP	SIPHQYWLT	240
241	QYLLKHFFKL	SQTSSKNLLN	ARVLSEIFSP	MLFRFSAASS	DNTENLIKVI	EILISTEWNE	300
301	RQPAPALPPK	PPKPTTVANN	GMNNMSLQD	AEWYWGDISR	EEVNEKLRDT	ADGTFLVRDA	360
361	STKMHGDYTL	TLRKGGNKLN	IKIFHRDGKY	GFSQDPLTFSS	VVELINHYRN	ESLAQYNPKL	420
421	DVKLLYPVSK	YQQDQVVKED	NIEAVGKKLH	EYNTQFQEK	REYDRLYEY	TRTSQEIOMK	480
481	RTAIEAFNET	IKIFEEQCQT	QERYKEYIE	KFKREGNEKE	IQRIMHNYDK	LKSRISEIID	540
541	SRRLEEDLK	QAAEYREID	KRMNSIKPDL	IQLRKRTRDQY	LMWLTQKQV	QKKLNEWLGN	600
601	ENTEDQYSLV	EDDEDLPHHD	EKTWNVGSN	RNKAENLLRG	KRDGTFLVRE	SSKQGCYACS	660
661	VVDGGEVVKH	VINKTATGYG	FAEPYNLYSS	LKELVLHYQH	TSLVQHNDL	NVTLAYPVYA	720
721	QQRR						780

blue: PIK3R1 sequence expressed in recombinant protein Red: variant in recombinant protein

<sup>2</sup>NCBI/Protein accession number NP\_852664.1  
E451K: SNP variation see NCBI/dbSNP ID: rs17852841