

## ProQinase™ PIK3CB wt/PIK3R1

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

### Recombinant Human Active Lipid Kinase

HGNC Symbol: PIK3CB

**Synonyms PIK3CB:** P110BETA, PI3K, PI3KBETA, PI3K-beta, PIK3C1

**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 discover: James R Brown & Kurt R Auger; BMC Evolutionary Biology 11, 4-14 (2011))

**Product No.:** 1168-1165-1

**Lot:** 005

**Description:** Human PIK3CB, full length, amino acids M<sub>1</sub>-S<sub>1070</sub> (as in [NCBI/Protein](#) entry NP\_006210.1), 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-terminal fused to a MYC-tag, coexpressed in Sf9 insect cells

**Product identity:** PIK3CB wt/PIK3R1 Lot 005, has been verified by mass spectrometry LC-ESI-MS/MS

**Theoretical MW<sub>PIK3CB</sub>:** 151267 Da  
**Theoretical MW<sub>PIK3R1</sub>:** 85371 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!

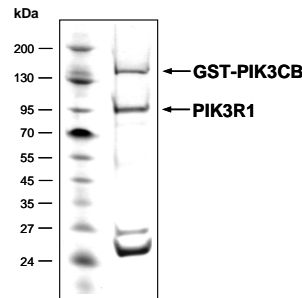
**Protein concentration:** 0.103 µg/µl

(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

#### Biochemical Parameters:

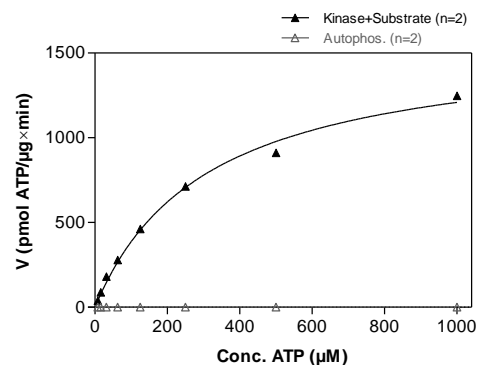
Specific kinase activity (P<sub>i</sub> transfer): 1584 pmol/µg x min  
 ATP-K<sub>M</sub>: 310 µM

#### PIK3CB wt/PIK3R1 Lot 005: Coomassie stain



4 µg GST-PIK3CB/PIK3R1

#### PIK3CB wt/PIK3R1 Lot 005: Determination of V<sub>max</sub> and K<sub>M</sub> value for ATP



- Assay conditions:
  - 60 mM HEPES-NaOH, pH 7.5
  - 3 mM MgCl<sub>2</sub>/MnCl<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-Glycerol-3-(Phosphoinositol-4,5-Bisphosphate))
  - PS: 1-Palmitoyl-2-Oleoyl-sn-Glycerol-3-Phospho-L-Serine
  - Kinase: 1 µg/ml
- Assay technology: ADP-Glo (Promega)

Recombinant Proteins

Sequence information

GST-PIK3CB Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDKVLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPPEM	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPIQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHGG	RDSLEVLFGG	240
241	PLAMVMCFSF	IMPPAMADIL	DIWAVDSQIA	SDGSIPVDFL	LPTGIYIQLE	VPREATISYI	300
301	KQMLWKQVHN	YPMFNLLMDI	DSYMFACVNO	TAVYEELEDE	TRRLCDVRPF	LPVLKLVTRS	360
361	CDPGEKLDK	IGVLIGKGLH	EFDLKDPEV	NEFRKMRKF	SEEKILSLVG	LSWMDWLKQT	420
421	YPPEHEPSIP	ENLEDKLYGG	KLIVAVHFEN	CQDVFSFQVS	PNNMPIKVNE	LAIQKRLTIH	480
481	GKEDEVSPYD	YVLQVSGRVE	YVFGDHPLIQ	FQYIRNCVMN	RALPHFILVE	CCKIKKMYEQ	540
541	EMIAIEAAIN	RNSSNLPLPL	PPKKTRIISH	VWENNNPFQI	VLVKGKNLNT	EETVKVHVRA	600
600	GLFHGTELLC	KTIVSSEVSG	KNDHIWNEPL	EFDINICDLP	RMARLCFAVY	AVLDKVKTKK	660
661	STKTINPSKY	QTIRKAGKVH	YPVAVVNTMV	FDFKGQLRTG	DIILHSWSSF	PDELEEMLNP	720
721	MGTVQTNPYT	ENATALHVKF	PENKKQPYYY	PPFDKIIIEKA	AEIASSDSAN	VSSRGGKFFL	780
781	PVLKEILDRD	PLSQLCENEM	DLIWTLRQDC	REIFPQSLPK	LLLSIKWNKL	EDVAQLQALL	840
841	QIWPKLPPRE	ALELLDFNYA	DQYVREYAVG	CLRQMSDEEL	SQYLLQLVQV	LKYEPFLDCA	900
901	LSRFLLERAL	GNRRIGQFLF	WHLRSEVHIP	AVSVQFGVIL	EAYCRGVSUGH	MKVLKQVEA	960
961	LNKLKTLNSL	IKLNAVKLNK	AKGKEAMHTC	LKQSAAREAL	SDLQSPNLPC	VILSELYVEK	1020
1021	CKYMDSKMKP	LWLVYNNKVF	GEDSVGVIFK	NGDDLQDML	TLQMLRLMDL	LWKEAGLDR	1080
1081	MLPYGCLATG	DRSGLIEVVS	TSETIADIQL	NSSNVAASAA	FNKDALLNWL	KEYNSGDDLD	1140
1141	RAIEEFTLSC	AGYCVASYVL	GIGDRHSDNI	MVKKTGQLFH	IDFGHILFVH	KSKFKIKRER	1200
1201	VPFILTYDFI	HSLIQGKGTGN	TEKFRFRQCI	CEDAYLILRR	HGNLFITLFA	LMLTAGLPEL	1260
1261	TSVKDIQYLK	DSLALGKSEE	EALKQFKQKF	DEALRESWTT	KVNWMAHTVR	KDYRS	1320

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: PIK3CB

PIK3CB wt <sup>1</sup> Amino Acid Sequence							
1	MCFSFIMPPA	MADILDIWAV	DSQIASDGS	PVDFLLPTGI	YIQLEVPREA	TISYIKQMLW	60
61	KQVHNYPMFN	LLMDIDSYMF	ACVNQTAVYE	ELEDETRRLC	DVRPFLPVLK	LVTRSCDPGE	120
121	KLDSKIGVLI	GKGLHEFDSL	KDPEVNEFRR	KMRKFSEEKI	LSLVGLSWMD	WLKQTYPPEH	180
181	EPSIPENLED	KLYGGKLIVA	VHFENCQDVF	SFQVSPNMP	IKVNELAIQK	RLTIHGKED	240
241	VSPYDYVLQV	SGRVEYVFGD	HPLIQFQYIR	NCVMNRALPH	FILVECKIK	KMYEQEMIAI	300
301	EAAINRNSSN	LPLPLPPKKT	RIISHVWENN	NPFQIVLVKG	NKLNTEETVK	VHVRAGLFHG	360
361	TELLCKTIVS	SEVSGKNDHI	WNEPLEFDIN	ICDLPRMRL	CFAVYAVLKD	VTKKSTKI	420
421	NPSKYQTIRK	AGKVHYPVAW	VNTMVFDFRG	QLRTGDIILH	SWSSFPDELE	EMLNPMGTVQ	480
481	TNPYTENATA	LHVKFPENKK	QPYYPFFDK	IEKAAEIAS	SDSANVSSRG	GKKFLPVLKE	540
541	ILDRDPLSQL	CENEMDLIWT	LRQDCREIFP	QSLPKLLLSI	KWNKLEDVAQ	LQALLQIWPK	600
601	LPPREALLEL	DFNYPDQYVR	EYAVGCLRQM	SDEELSQYLL	QLVQVLKYE	FLDCALSRLF	660
661	LERALGNRRI	GQFLFWHLRS	EVHIPAVSVQ	FGVILEAYCR	GSVGHMKVLS	KQVEALNKLK	720
721	TLNSLIKINA	VKLNRAKQKE	AMHTCLKQSA	YREALSDLQS	PLNPCVILSE	LYVECKYMD	780
781	SKMKPLWLVY	NNKVFGEDSV	GVIFKNGDDL	RQDMLTLQML	RLMDLLWKEA	GLDLRMLPYG	840
841	CLATGDRSGL	IEVVSTSETI	ADIQLNSSNV	AAAAAFNKDA	LLNWLKEYNS	GDDLDRATIEE	900
901	FTLSCAGYCV	ASYVLGIGDR	HSDNIMVKK	GQLFHIDFGH	ILGNFKSKFG	IKRERVFPIL	960
961	TYDFIHVIQQ	GKTGNTTEKFG	RFRQCCEDAY	LILRRHGNLF	ITLFAFMLTA	GLPELTSVKD	1020
1021	IQYLKDSLAL	GKSEEEALKQ	FKQKFDALR	ESWTTKVNWM	AHTVRKDYRS		1080

blue: PIK3CB sequence expressed in recombinant protein

<sup>1</sup>[NCBI/Protein](https://www.ncbi.nlm.nih.gov/protein/NP_006210.1) accession number NP\_006210.1

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

1	MEEQKLISEE	DL	PMVMSAEG	YQYRALYDYK	KEREEDIDLH	LGDILTVMKG	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	YWLTLOYLK	HFFKLSQTSS	KNLLNARVLS	EIFSPMLFRF	SAASSDNTE	300	
301	LIKVIEILIS	TEWNERQPAP	ALPPKPPKPT	TVANNGMNN	MSLQDAEWY	GDISREEVNE	360	
361	KLRDADGTF	LVRDASTKMH	GDYTLTLRKG	GNNKLIKIFH	RDGKYGFSDP	LTFSSVVELI	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	QKGVRRQKLN	EWLGNENTED	OYSLVEDDED	LPHHDEKTNW	VGSSNRNKAE	NLLRGKRDGT	660	
661	FLVRESSKQG	CYACSVVDG	EVKHCVINKT	ATGYGFAEPY	NLYSSLKELV	LHYQHTSLVQ	720	
721	HNDSLNVTLA	YPVYAQQRR					780	

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

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

1	MSAEGYQYRA	LYDYKKERE	DIDLHLGDIL	TVNKGSLVAL	GFSGDQEARP	EEIGWLNGYN	60
61	ETTGERGDFP	GTIVEYIGRK	KISPPTPKPR	PPRPLPVAPG	SSKTEADVEQ	QALTLPLDLAE	120
121	QFAPPDIAPP	LLIKLVEAIE	KKGLECSTLY	RTQSSSNLAE	LRQLLCDTTP	SVDLEMIDVH	180
181	VLADAFKRYL	LDLPNPVIPA	AVYSEMISLA	PEVQSSEFYI	QLLKKLIRSP	SIPHQYWLTL	240
241	QYLLKHFFKL	SQTSSKNLLN	ARVLSEIFSP	MLFRFSAASS	DNTENLIKVI	EILISTEWNE	300
301	RQPAPALPPK	PPKPTTVANN	GMNNMSLQD	AEWYWGDISR	EEVNEKLRDT	ADGTFVLVRDA	360
361	STKMHGDYTL	TLRKGNNKL	IKIFHRDGKY	GFSDDLTFSS	VVELINHYRN	ESLAQYNPKL	420
421	DVKLLYPVSK	YQQDQVVKED	NIEAVGKKLH	EYNTQFQEK	REYDRLYEY	TRTSQEIQMK	480
481	RTAIEAFNET	IKIFEEQCQT	QERYKEYIE	KFKREGNEKE	IQRIMHNYDK	LKSRISEIID	540
541	SRRLEEDLK	KQAAEYREID	KRMNSIKPDL	IQLRKTDRDY	LMWLTQKGV	QKKNLNEWLGN	600
601	ENTEDQYSLV	EDDEDLPHHD	EKTWNVGSSN	RNKAENLLRG	KRDGTFVRE	SSKQGCYACS	660
661	VVDGEVVKHC	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

HGNC identifier: PIK3R1