

PIK3CB E1051K/PIK3R1

phosphoinositide-3-kinase, catalytic, beta polypeptide/
phosphoinositide-3-kinase, regulatory subunit 1 (alpha)

Recombinant Human Active Lipid Kinase

HGNC Symbol: PIK3CB

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

Synonyms PIK3R1: GRB1, p85, p85-ALPHA, PtdIns-3-kinase regulatory subunit p85-alpha

Lipid Kinase Family: PI3K Class I

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

Product No.: 1532-1165-1

Lot: 003

Description: Human PIK3CB, full length, amino acids M₁-S₁₀₇₀ (as in NCBI/Protein entry NP_006210.1) with a E1051K mutation, N-terminal GST-HIS₆ fusion protein with a 3C cleavage site and PIK3R1 full length, amino acids M₁-R₇₂₄ (as in NCBI/Protein entry NP_852664.1), N-terminal fused to a MYC-tag, expressed in Sf9 insect cells

Product identity: PIK3CB E1051K/PIK3R1 Lot 003, was confirmed as PIK3CB/PIK3R1 by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{GST-PIK3CB E1051K}: 151,266 Da

Theoretical MW_{PIK3R1}: 85,371 Da

Expression: Baculovirus infected Sf9 cells

Purification: GST-Affinity Chromatography

Storage buffer: 50 mM HEPES pH 7.5, 100 mM NaCl, 5 mM DTT, 15 mM reduced glutathione, 20% glycerol

Storage temperature: -80°C

Avoid repeated freeze-thaw cycles!

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: 0.098 µg/µl

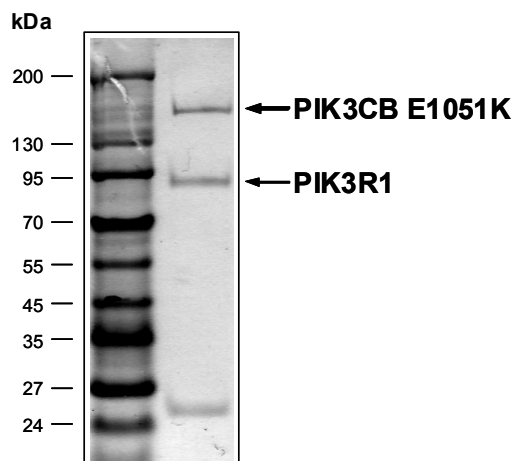
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

Specific kinase activity (P_i transfer): 849 pmol/µg×min

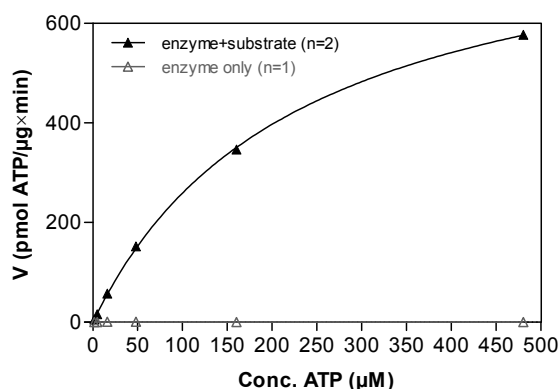
ATP-K_M: 228 µM

PIK3CB E1051K/PIK3R1 Lot 003: Coomassie stain



2 µg PIK3CB E1051K/PIK3R1

PIK3CB E1051K/PIK3R1 Lot 003: Determination of V_{max} and K_M value for ATP ADP-Glo™ Kinase Assay / Promega



Determination of K_M value & Specific activity:

• Assay conditions:

60 mM HEPES-NaOH, pH 7.5

3 mM MnCl₂

3 µM Na-orthovanadate

1.2 mM DTT

50 µg / ml PEG_{20,000}

ATP (variable)

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]

PIK3CB E1051K/PIK3R1: 2.0 µg / ml

For further information on ADP-Glo™ kinase activity detection please visit



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PIK3CB E1051K/PIK3R1

Product No.: 1532-1165-1

PIK3CB E1051K Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQ SMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP EML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI PQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMG HHHHHH G	RDS LEVL FQG	240
241	PLAMV MCF SF	IMPPAMADIL	DIWAVDSQIA	SDGSIPVDFL	LPTGIYIQLE	VPREATISYI	300
301	KQMLWKQVHN	YPMFNLLMDI	DSYMFACVNO	TAVYEELEDE	TRRLCDVRPF	LPVLKLVTRS	360
361	CDPGEKLD SK	IGVLIGKGLH	EFDSLKDPEV	NEFRRKMRKF	SEEKILSLVG	LSWMDWLKQT	420
421	YPPEHEPSIP	ENLEDKLYGG	KLIVAVHFEN	QDVFSFQVS	PNMNPIK VNE	LAIQKRLTIH	480
481	GKEDEVSPYD	YVLQVSGRVE	YVFGDHPLIQ	FQYIRNCVMN	RALPHFILVE	CKIKKMYEQ	540
541	EMIAIEAAIN	RNSSNLPLPL	PKKTRIISH	VWENNNPFOI	VLVKGKLNLT	EETVKVHVRA	600
601	GLFHGT ELLC	KTIVSSEVSG	KNDHIWNEPL	EFDINICDLP	RMARLCFAVY	AVLDKVKTKK	660
661	STKTINELSKY	QTIRKAGKVH	YPVAWNTMV	FDFKQLRTG	DIILHSWSSF	DELEEMLNP	720
721	MGTVQTNPYT	ENATALHVKF	PENKQPYYY	PPFDKIEKA	AEIASSDSAN	VSSRGGK KFL	780
781	PVLKEILDRD	PLSQLCENEM	DLIWTLRQDC	REIFPQSLPK	LLLSIKWNKL	EDVAQLQALL	840
841	QIWPKLPPRE	ALELLDFNYP	DQYVREYAVG	CLRQMSDEEL	SQYLLQLVQV	LKYEPFLDCA	900
901	LSRFL LERAL	GNRRIGQFLF	WHLRSEVHIP	AVSVQFGVIL	EAYCRGSVGH	MKVL SKQVEA	960
961	LNKLT LNSL	IKLNAVKLN R	AKGKEAMHTC	LKQSA YREAL	SDLQSP LNPC	VILSELYVEK	1020
1021	CKYMD SKMKP	LWLVYNNKVF	GEDSVGVIFK	NGDDL RQDML	TLQMLRLMDL	LWKEAGDLR	1080
1081	MLPYGCLATG	DRSGLIEVVS	TSETIADIQL	NSSNVA AAAAA	FNKDALLNWL	KEYNSGDDLD	1140
1141	RAIEEFTLSC	AGYCVASYVL	GIGDRHSDNI	MVKKTGQLFH	IDFGHILGNF	KSKFGIKRER	1200
1201	VPFILTYDFI	HVIQQKGTGN	TEKFRFRQC	CEDAYLILRR	HGNLFITLFA	LMLTAGLPEL	1260
1261	TSVKDIQYLK	DSLALGKSEE	EALKQFKQKF	DEALR KSWTT	KVNWMAHTVR	KDYRS	1320

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue:PIK3CB boxed:E1051K

PIK3CB wt ¹ amino acid sequence							
1	MCF SFIMPPA	MADILDIWAV	DSQIASD GSI	PVDFLLPTGI	YIQLEVPREA	TISYIKQMLW	60
61	KQVHNYP MFN	LLMDIDSYMF	ACVNQTAVYE	ELEDETRRLC	DVRPFLPVLK	LVTRSCDPGE	120
121	KLDSKIGVLI	GKGLHEFDSL	KDPEVNEFR R	KMRKFSEEKI	LSLVGLSWMD	WLKQTY PPEH	180
181	EPSIPENLED	KLYGGKLIVA	VHFENCQDVF	SFQVSPNMNP	IKVNELAIQK	RLTIHGKEDE	240
241	VSPYDYVLQV	SGRVEYVFGD	HPLIQFQYIR	NCVMNRALPH	FILVECKIK	KMYEQEMIAI	300
301	EAAINRNSSN	LPLPLPPKKT	RIISHVWENN	NPFQIVLVKG	NKLNTEETVK	VHVRAGLFHG	360
361	TELLCKTIVS	SEVSGKNDHI	WNEPLEFDIN	ICDLPRMARI	CFAVYAVL DK	VKTKKSTKTI	420
421	NPSKYQTIRK	AGKVHYPVAW	VNTMVDFDKG	QLRTGDIILH	SWSSFPDELE	EMLNPMGTVQ	480
481	TNPYTENATA	LHVKFPENKK	QPYYP PFDK	IEKAAEIAS	SDSANVSSRG	GKKFLPVLKE	540
541	ILDRDPLSQL	CENEMDLIWT	LRQDCREIFP	QSLPKLLLSI	KWNKLEDVAQ	LQALLQIWPK	600
601	LPPREALELL	DFNYPDQYVR	EYAVGCLRQM	SDEELSQYLL	QLVQVLKYEP	FLDCALSRFL	660
661	LERALGNRRI	GQFLFWHLRS	EVHIPAVSVQ	FGVILEAYCR	GSVGHMKVLS	KQVEALNKLK	720
721	TLNSLIKLNA	VKLNRAK GKE	AMHTCLKQSA	YREALSDLQS	PLNPCVILSE	LYVECKYMD	780
781	SKMKPLWL VY	NNKVF GEDSV	GVIFKNGDDL	RQDMLTLQML	RLMDLLWKEA	GLDLRMLPYG	840
841	CLATGDRSGL	IEVSTSETI	ADIQLNSSNV	AAAAAFNKDA	LLNWLKEYNS	GDDLDR AIEE	900
901	FTLSCAGYCV	ASYVLGIGDR	HSDNIMVKKT	GQLFHIDFGH	ILGNFKSKFG	IKRERV PFIL	960
961	TYDFIHVIQQ	GKTGNTK EFG	RFRQCCE DAY	LILRRHGNLF	ITL FALMLTA	GLPELTSVKD	1020
1021	IQYLKDSLAL	GKSEEEAL KQ	FKQKFDEALR	ESWTTKVNWM	AHTVRKDYRS		1080

blue: PIK3CB sequence expressed in fusion protein Red: variant in fusion protein

¹NCBI/Protein accession number NP_006210.1

PIK3R1 Recombinant Fusion Protein Amino Acid Sequence						
1	M EEQKLISEE DLPMVMSAEG YQYRALYDYK KEREEDIDLH LGDILTVNKG SLVALGFS	60				
61	QEARPEEIGW LNGYNETTGE RGDFPGTYVE YIGRKKISPP TPKRPPRPL PVAPGSSKTE	120				
121	ADVEQQALTL PDLAEQFAPP DIAPPLLIK VEAIEKKGLE CSTLYRTQSS SNLAE LRQLL	180				
181	DCDTPSV DLE MIDVHVLADA FKRYLLDLPN PVIPAAVYSE MISLAPEVQS SEEYIQLLKK	240				
241	LIRSPSIPHQ YWLTLYLLK HFFKLSQTSS KNLLNARVLS EIFSPMLFRF SAASSDNTEN	300				
301	LIKVIEILIS TEWNERQPAP ALPPKPPKPT TVANNGMNNN MSLQDAEWYW GDISREEVNE	360				
361	KLRDTADGTF LVRDASTKMH GDYTLTLRKG GNNKLIKIFH RDGKYGFSDP LTFSSVVELI	420				
421	NHYRNESLAQ YNPKLDVKLL YPVSKYQQDQ VVKEDNIEAV GKKLH K YNTQ FQEKSR	480				
481	LYEYTRTSQ EIQMRTAIE AFNETIKIFE EQCQTQERYS KEYIEKFKRE GNEKEIQRIM	540				
541	HNYDKLSRI SEIIDSRRRL EEDLKKQAAE YREIDKRMNS IKPDLIQLRK TRDQYLMWLT	600				
601	QKGV RQKLN EWLGNENTED QYSLVEDDED LPHHDEKTWN VGSSNRNKA E NLLRGRDGT	660				
661	FLVRESSKQG CYACSVVDG EVKHCVINKT ATGYGFAEPY NLYSSLKELV LHYQHTSLVQ	720				
721	HNDSLNVTLA YPVYAQQRR	780				

Red: MYC-tag blue: PIK3R1 **K**: E451K variation

PIK3R1 wt ² amino acid sequence						
1	MSAEGYQYRA LYDYKKEREE DIDLHLGDIL TVNKGSLVAL GFS	60				
61	QEARPEEIGW LNGYNETTGE RGDFPGTYVE YIGRKKISPP TPKRPPRPL PVAPGSSKTE	120				
121	ADVEQQALTL PDLAEQFAPP DIAPPLLIK VEAIEKKGLE CSTLYRTQSS SNLAE LRQLL	180				
181	DCDTPSV DLE MIDVHVLADA FKRYLLDLPN PVIPAAVYSE MISLAPEVQS SEEYIQLLKK	240				
241	LIRSPSIPHQ YWLTLYLLK HFFKLSQTSS KNLLNARVLS EIFSPMLFRF SAASSDNTEN	300				
301	LIKVIEILIS TEWNERQPAP ALPPKPPKPT TVANNGMNNN MSLQDAEWYW GDISREEVNE	360				
361	KLRDTADGTF LVRDASTKMH GDYTLTLRKG GNNKLIKIFH RDGKYGFSDP LTFSSVVELI	420				
421	NHYRNESLAQ YNPKLDVKLL YPVSKYQQDQ VVKEDNIEAV GKKLH E YNTQFQEK	480				
481	LYEYTRTSQ EIQMRTAIE AFNETIKIFE EQCQTQERYS KEYIEKFKRE GNEKEIQRIM	540				
541	HNYDKLSRI SEIIDSRRRL EEDLKKQAAE YREIDKRMNS IKPDLIQLRK TRDQYLMWLT	600				
601	QKGV RQKLN EWLGNENTED QYSLVEDDED LPHHDEKTWN VGSSNRNKA E NLLRGRDGT	660				
661	FLVRESSKQG CYACSVVDG EVKHCVINKT ATGYGFAEPY NLYSSLKELV LHYQHTSLVQ	720				
721	HNDSLNVTLA YPVYAQQRR	780				

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

²NCBI/Protein accession number NP_852664.1
E451K: SNP variation see NCBI/dbSNP:rs17852841