

PIK3CB E633K/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 signaling and drug discovery: James R Brown & Kurt R Auger, BMC Evolutionary Biology 11, 4-14 (2011))

Product No.: 1531-1165-1

Lot: 003

Description: Human PIK3CB, full length, amino acids M₁-S₁₀₇₀ (as in NCBI/Protein entry NP_006210.1) with a E633K 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 E633K/PIK3R1 Lot 003, was confirmed as PIK3CB/PIK3R1 by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{GST-PIK3CB E633K}: 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: 0.116 µg/µl

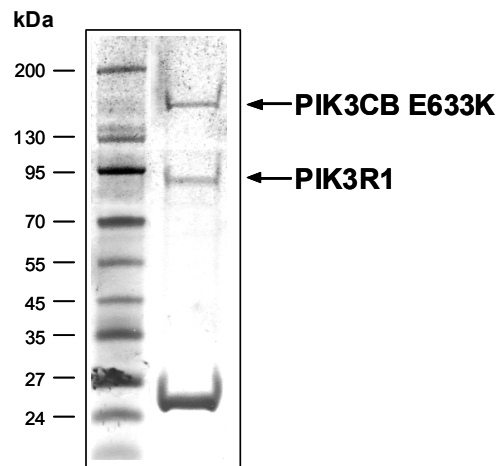
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

Specific kinase activity (P_i transfer): 78 pmol/µg×min

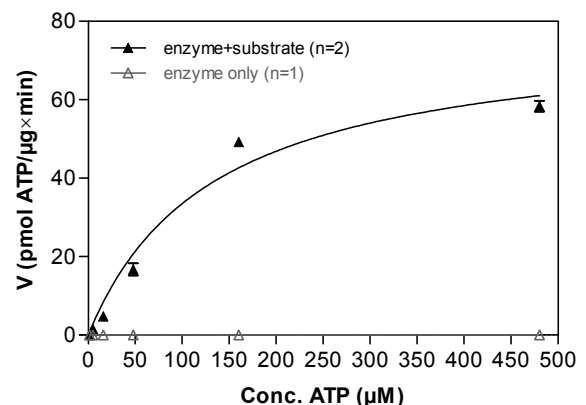
ATP-K_M: 132 µM

PIK3CB E633K/PIK3R1 Lot 003: Coomassie stain



2 µg PIK3CB E633K/PIK3R1

PIK3CB E633K/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 E633K/PIK3R1: 4.0 µg / ml

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

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PIK3CB E633K/PIK3R1

Product No.: 1531-1165-1

PIK3CB E633K 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	PMGHHHHHGG	RDSLEVL FQG	240
241	PLAMVMCFSF	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	CQDVFSFQVS	PNMNPIK VNE	LAIQKRLTIH	480
481	GKEDEVSPYD	YVLQVSGRVE	YVFGDHPLIQ	FQYIRNCVMN	RALPHFILVE	CKIKKMYEQ	540
541	EMIAIEAAIN	RNSSNLPLPL	PPKTRIISH	VWENNNPFOI	VLVKGKLNLT	EETVKVHVRA	600
601	GLFHGT ELLC	KTIVSSEVSG	KNDHIWNEPL	EFDINICDLP	RMARLCFAVY	AVLDKVKTKK	660
661	STKTINELSKY	QTIRKAGKVH	YPVAWVNTMV	FDFKQQLRTG	DIILHSWSSF	PDELEEMLNP	720
721	MGTVQTNPYT	ENATALHVKF	PENKQPYYY	PPFDKIEKA	AEIASSDSAN	VSSRGGK KFL	780
781	PVLKEILDRD	PLSQLCENEM	DLIWTLRQDC	REIFPQSLPK	LLLSIKWNKL	EDVAQLQALL	840
841	QIWPKLPPRE	ALELLDFNYP	DQYVREYAVG	CLRQMSDKEL	SQYLLQLVQV	LKYEPFLDCA	900
901	LSRFL LERAL	GNRRIGQFLF	WHLRSEVHIP	AVSVQFGVIL	EAYCRGSVGH	MKVL SKQVEA	960
961	LNKLT LNSL	IKLNAV KLN R	AKGKEAMHTC	LKQSAYREAL	SDLQSP LNPC	VILSELYVEK	1020
1021	CKYMSDKMKP	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	DEALRESWTT	KVNWMAHTVR	KDYRS	1320

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue:PIK3CB boxed:E633K

PIK3CB wt ¹ amino acid sequence							
1	MCFSFIMPPA	MADILDIWAV	DSQIASD GSI	PVDFLLPTGI	YIQLEVPREA	TISYIKQMLW	60
61	KQVHNYP MFN	LLMDIDSYMF	ACVNQTAVYE	ELEDETRRLC	DVRPFLPVLK	LVTRSCDPGE	120
121	KLDSKIGVLI	GKGLHEFDSL	KDPEVNEFRR	KMRKFSEEKI	LSLVGLSWMD	WLKQTY PPEH	180
181	EPSIPENLED	KLYGGKLIVA	VHFENCQDVF	SFQVSPNMNP	IKVNELAIQK	RLTIHGKED E	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	AGKVHY PVAW	VNTMVDFDKG	QLRTGDIILH	SWSSF PDELE	EMLNPMGTVQ	480
481	TNPYTENATA	LHVKFPENKK	QPYYP PFDK	IIEKAAEIAS	SDSANVSSRG	GKKFLPVLKE	540
541	ILDRDPLSQL	CENEMDLIWT	LRQDCREIFP	QSLPKLLLSI	KWNKLEDVAQ	LQALLQIWP K	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	GVI FKN GDDL	RQDMLTLQML	RLMDLLWKEA	GLDLRMLPYG	840
841	CLATGDRSGL	IEVSTSETI	ADIQLNSSNV	AAAAAFNKDA	LLNWLKEYNS	GDDLDR AIEE	900
901	FTLSCAGYCV	ASYVLGIGDR	HSDNIMVKKT	GQLFHIDFGH	ILGNFKSKFG	IKRERV PFIL	960
961	TYDFIHVIQQ	GKTGNT ECFG	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	DL	PMVMSAEG	YQYRALYDYK	KEREEDIDLH	LGDILTVNKG	SLVALGFS	SDG	60
61	Q	EARPEEIGW	L	NGYNETTGE	RGDFPGTYVE	YIGRKKISPP	TPKPRPPRPL	PVAPGSSKTE		120
121	A	DVEQQALTL	P	LAEQFAPP	DIAPPLLIKL	VEAIEKKGLE	CSTLYRTQSS	SNLAE LRQLL		180
181	D	CDTPSVDLE	M	IDVHVLADA	FKRYLLDLPN	PVIPAAYVSE	MISLAPEVQS	SEEYIQLLKK		240
241	L	IRSPSIPHQ	Y	WLTLOYLK	HFFKLSQTSS	KNLLNARVLS	EIFSPMLFRF	SAASSDNTEN		300
301	L	IKVIEILIS	T	EWNERQPAP	ALPPKPPKPT	TVANNGMNNN	MSLQDAEWYW	GDISREEVNE		360
361	K	LRDTADGTF	L	VRDASTKMH	GDYTLTLRKG	GNNKLIKIFH	RDGKYGFS	DP LTFSSVVELI		420
421	N	HYNESLAQ	Y	NPKLDVKLL	YPVSKYQQDQ	VVKEDNIEAV	GKKLH	EYNTQ FQEK	SREYDR	480
481	L	YEEYTRTSQ	E	IQMKRTAIE	AFNETIKIFE	EQCQTQERYS	KEYIEKFKRE	GNEKEIQRIM		540
541	H	NYDKLSRI	S	EIIDSRRRL	EEDLKKQAAE	YREIDKRMNS	IKPDLIQLRK	TRDQYLMWLT		600
601	Q	KGVRQKLN	E	WLGNENTED	QYSLVEDDED	LPHHDEKTWN	VGSSNRNKAE	NLLRGKRDGT		660
661	F	LVRESSKQG	C	YACSVVDG	EVKHCVINKT	ATGYGFAEPY	NLYSSLKELV	LHYQHTSLVQ		720
721	H	NDSLNVTLA	Y	PVYAQQRR						780

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

PIK3R1 wt ² amino acid sequence															
1	M	SAEGYQYRA	L	YDYKKEREE	DIDLHLGDIL	TVNKGSLVAL	GFS	DGQEARP	EEIGWLN	GYN	60				
61	E	TTGERGDFP	G	TYVEYIGRK	KISPPTPKPR	PPRPLPVAPG	SSKTEADVEQ	QAL	TL	PD	LAE	120			
121	Q	FAPPDIAPP	L	LIKLVEAIE	KKGLECSTLY	RTQSSSNLAE	LRQLLDCDTP	SVD	LEM	ID	VH	180			
181	V	LADAFKRYL	L	DLPNPVIPA	AVYSEMISLA	PEVQSSEEI	YI QLLK	KL	IR	SP	SIPHQY	WLT	240		
241	Q	YLLKHFFKL	S	QTSSKNLLN	ARVLSEIFSP	MLFRFSAASS	DNTENLIKVI	EIL	ISTE	WNE		300			
301	R	QPAPALPPK	P	PKPTTVANN	GMNNNMSLQD	AEWYWGDISR	EEVNEKLRDT	ADG	T	FL	VR	DA	360		
361	S	TMHGDYTL	T	LRKGGNNKL	IKIFHRDGKY	GFS	DPLTFSS	V	VEL	IN	HY	RN	420		
421	D	VKLLYPVSK	Y	QQDQVVKED	NIEAVGKKLH	EYNTQFQEK	S REYDR	L	Y	E	E	Y	480		
481	R	TAIEAFNET	I	KIFEEQCQT	QERYSKEYIE	KFKREGNEKE	IQRIMHNYDK	L	K	S	R	I	SE	540	
541	S	RRLEEDLK	Q	AAEYREID	KRMNSIKPDL	IQLRKTRDQY	LMWLTQK	G	V	R	Q	K	L	NE	600
601	E	NTE	D	QYSLV	EDDEDLPHHD	EKTWNVGSSN	RNKAENLLRG	K	R	D	G	T	F	L	660
661	V	VVDGEVKHC	V	INKTATGYG	FAEPYNLYSS	LKELVLHYQH	TSLVQH	N	D	S	L	N	V	T	720
721	Q	QRR													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

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