

## ProQinase™ CDC42BPB

CDC42 binding protein kinase beta

Recombinant Human Active Protein Kinase

HGNC Symbol: CDC42BPB

Synonyms: MRCKB, DMPK-like

Product No.: 0382-0000-1

Lot: 001

**Description:** Human CDC42BPB, N-terminal fragment, amino acids M<sub>1</sub>-H<sub>472</sub> (as in [NCBI/Protein](#) entry NP\_006026.2), N-terminal GST-HIS<sub>6</sub> fusion protein with a Thrombin cleavage site, expressed in Sf9 insect cells

**Product identity:** CDC42BPB Lot 001, was confirmed as CDC42BPB by mass spectroscopy LC-ESI-MS/MS

**Theoretical MW<sub>Fusion Protein</sub>:** 84,444 Da

**Expression host:** Sf9 insect cells

**Purification:** GST-Affinity Chromatography

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

**Storage buffer:** 50 mM TRIS-HCl pH 8.0, 100 mM NaCl, 5 mM DTT, 4 mM reduced glutathione, 20 % glycerol

**Storage temperature:** -80°C

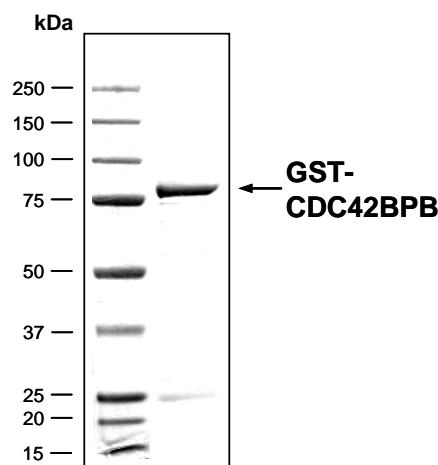
For complete recovery, mix well and spin before use. Product must not be stored in diluted solutions, aliquots below 10µl are not advisable. Avoid repeated freeze-thaw cycles!

**Protein concentration:** 0.205 µg/µl  
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

### Biochemical Parameters:

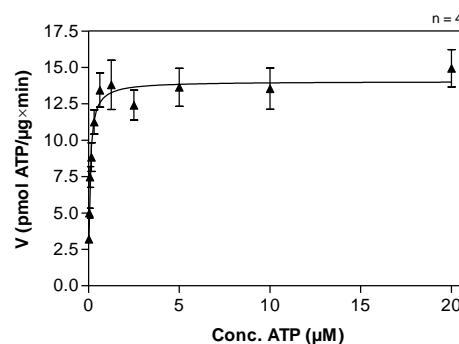
Specific kinase activity (P<sub>i</sub> transfer): 14 pmol/µg × min  
ATP-K<sub>M</sub>: 0.1 µM

### CDC42BPB Lot 001: Coomassie stain



2.0 µg GST-CDC42BPB

### CDC42BPB Lot 001: 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>  
3 mM MnCl<sub>2</sub>  
3 µM Na-orthovanadate  
1.2 mM DTT  
50 µg/ml PEG<sub>20,000</sub>  
ATP (variable)  
Substrate: INSRRTide 20 µg/ml  
Kinase: 1 µg/ml
- Filter binding assay  
MSPH membrane (Millipore)

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GST-CDC42BPB 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	RRRASVAAGI	240
241	LVPRGSPGLD	GIYARGIQAS	MSAKVRLKKL	EQLLLDGPWR	NESALSVETL	LDVLVCLYTE	300
301	CSHSALRRDK	YVAEFLEWAK	PFTQLVKEMQ	LHREDFEI IK	VIGRGAFGEV	AVVKMKNTER	360
361	IYAMKILNKW	EMLKRAETAC	FREERDVLVN	GDCQWITALH	YAFQDENHLY	LVMDYYVGGD	420
421	LLTLLSKFED	KLPEDMARFY	IGEMVLAIDS	IHQHLYVHRD	IKPDNVLLDV	NGHIRLADFG	480
481	SCLKMND DGT	VQSSVAVGTP	DYISPEILQA	MEDGMGKYGP	ECDWWSLGVC	MYEMLYGETP	540
541	FYAESLVETY	GKIMNHEERF	QFP SHVTDVS	EEAKDLIQRL	ICSRERRLQ	NGIEDFKKHA	600
601	FFEGLN WENI	RNLEAPYIPD	VSSP SDT SNF	DVDDDLRNT	EILPPGSH TG	FSGLHLPFIG	660
661	FTFTTESCF S	DRGSLK SIMQ	SNTLTKDEDV	QRDL EHS LQM	EAYERRIRRL	EQEKLELSRK	720
721	LQESTQT VQS	LH					780

1-218: GST Red: HIS6-tag Pink: Thrombin cleavage site blue: CDC442BPB fragment

CDC42BPB wt <sup>1</sup> Amino Acid Sequence							
1	MSAKVRLKKL	EQLLLDGPWR	NESALSVETL	LDVLVCLYTE	CSHSALRRDK	YVAEFLEWAK	60
61	PFTQLVKEMQ	LHREDFEI IK	VIGRGAFGEV	AVVKMKNTER	IYAMKILNKW	EMLKRAETAC	120
121	FREERDVLVN	GDCQWITALH	YAFQDENHLY	LVMDYYVGGD	LLTLLSKFED	KLPEDMARFY	180
181	IGEMVLAIDS	IHQHLYVHRD	IKPDNVLLDV	NGHIRLADFG	SCLKMND DGT	VQSSVAVGTP	240
241	DYISPEILQA	MEDGMGKYGP	ECDWWSLGVC	MYEMLYGETP	FYAESLVETY	GKIMNHEERF	300
301	QFP SHVTDVS	EEAKDLIQRL	ICSRERRLQ	NGIEDFKKHA	FFEGLN WENI	RNLEAPYIPD	360
361	VSSP SDT SNF	DVDDDLRNT	EILPPGSH TG	FSGLHLPFIG	FTFTTESCF S	DRGSLK SIMQ	420
421	SNTLTKDEDV	QRDL EHS LQM	EAYERRIRRL	EQEKLELSRK	LQESTQT VQS	LHGSSRALSN	480
481	SNRDKEIKKL	NEEIERLKNK	IADSNRLERQ	LEDTVLRQE	REDSTQRLRG	LEKQHRVVRQ	540
541	EKEELHKQLV	EASERLKSQA	KELKDAHQQR	KLALQEFSEL	NERMAELRAQ	KQKVSRLRD	600
601	KEEEME VATQ	KVDAMRQEMR	RAEKLRKELE	AQLDDAVAEA	SKERKLREHS	ENFCKQMESE	660
661	LEALKVKQGG	RGAGATLEHQ	QEISKIKSEL	EKKVLFYEEE	LVRREASHVL	EVKNVKKVEVH	720
721	DSESHQLALQ	KEILMLKDKL	EKSKRERHNE	MEEAVGTIKD	KYERERAMLF	DENKKLTAEN	780
781	EKLCSFVDKL	TAQNRQLEDE	LQDLAAKKES	VAHWEAQIAE	IIQWVSDEKD	ARGYLQALAS	840
841	KMTEELEALR	SSSLGSRTLD	PLWKVRRSQK	LDMSARLELQ	SALEAEIRAK	QLVQEE LRKV	900
901	KDANLTLESK	LKDSEAKNRE	LLEEMEILKK	KMEEKFRADT	GLKLPDFQDS	IFEYFNTAPL	960
961	AHDLTFR TSS	ASEQETQAPK	PEASPSMSVA	ASEQQEDMAR	PPQRPSAVPL	PTTQALALAG	1020
1021	PKPKAHQFSI	KSFSSPTQCS	HCTSLMVGLI	RQGYACEVCS	FACHVSCKD G	APQVCPI PPE	1080
1081	QSKRPLGVDV	QRGIGTAYKG	HVKVPKPTGV	KKGWQRAYAV	VCECKLFLYD	LPEGKSTQPG	1140
1141	VIASQVLDLR	DDEF SVSSVL	ASDVIHATR	DIPCIFRVTA	SLLGAPSKTS	SLLILTENEN	1200
1201	EKRK WVGILE	GLQSILHKNR	LRNQVVHVPL	EAYDSSLPLI	KAILTAAIVD	ADRIAVGLEE	1260
1261	GLYVIEVTRD	VIVRAADCKK	VHQIELAPRE	KIVILLCGRN	HHVHLYPWSS	LDGAEGSFDI	1320
1321	KLPETKGCQL	MATATLKRNS	GTCLFVAVKR	LILCYEIQRT	KPFHRKFNEI	VAPGVSQCLA	1380
1381	VLRDRLCVGY	PSGFCLLSIQ	GDGQPLNLVN	PNDPSLAFLS	QQSFDALCAV	ELESEEYLLC	1440
1441	FSHMGLYVDP	QGRRARAQEL	MWPAAPVACS	CSPTHVTVYS	EYGVDFVDVR	TMEWVQTIGL	1500
1501	RRIRPLNSEG	TLNLLNCEPP	RLIYFKSKFS	GAVLNVPTS	DNSKKQMLRT	RSKRRFVFKV	1560
1561	PEEERLQQR	EMLRDPELRS	KMISNPTNFN	HVAHMGPGDG	MQVLM DPLS	AVPPSQEERP	1620
1621	GPAPTNLARQ	PPSRNKPYIS	WPSSGGSEPS	VTVPLRSMDS	PDQDFDKEPD	SDSTKHSTPS	1680
1681	NSSNPSGPPS	PNSPHRSQLP	LEGLEQPACD	T			1740

blue: CDC42BPB sequence expressed in recombinant protein

<sup>1</sup>NCBI/Protein accession number NP\_006026.2