

ProQinase™ CDK13/CycK cyclin dependent kinase 13

Recombinant Human Active Protein Kinase

HGNC Symbol: CDK13

Synonyms: CDC2L, CDC2L5, CHED

Product No.: 1530-1484-1

Lot: 009

Description: Human CDK13, internal fragment amino acids P₆₅₆-G₁₀₅₀ (as in [NCBI/Protein](#) entry NP_003709.3), N-terminal GST-HIS₆ fusion protein with a 3C cleavage site and human CycK, M₁-S₃₀₀ (as in [NCBI/Protein](#) entry NP_001092872.1), N-terminally fused to GST-HIS₆ 3C cleavage site, coexpressed in Sf9 insect cells

Product identity: CDK13/CycK Lot 009, was confirmed as CDK13/CycK by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{GST-CDK13}: 73,831 Da

Theoretical MW_{GST-CycK}: 63,031 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, 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: 0.388 µg/µl

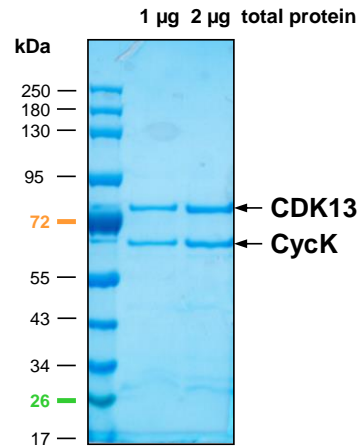
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

Specific kinase activity (P_i transfer): 0.3 pmol/µg x min

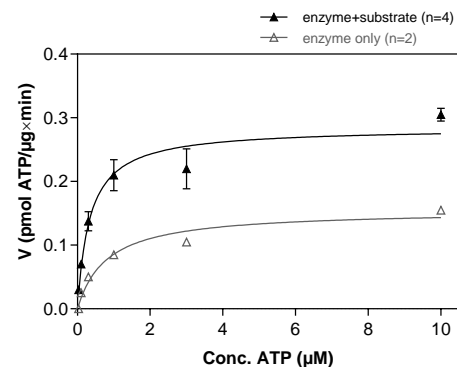
ATP-K_M: 0.34 µM

CDK13/CycK Lot 009: Coomassie stain



CDK13/CycK Lot 009:

Determination of V_{max} and K_M value for ATP



- Assay conditions:
60 mM HEPES-NaOH, pH 7.5
3 mM MgCl₂
3 mM MnCl₂
3 µM Na-orthovanadate
1.2 mM DTT
50 µg/ml PEG_{20,000}
ATP (variable)
Substrate: SUPT5H 20 µg/ml
Kinase: 4 µg/ml
- Filter binding assay
MSFC membrane (Millipore)

Recombinant Proteins

Sequence information

GST-CDK13 Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLIERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSM	IIRYIADKH	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP	KMFKDRLCH	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPIQ	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHGG	RDSLEVLFGG	240
241	PPGGDDLK	PEEKKTATQL	HSKRRPKICG	PRYGETKEKD	IDWGKRCVDK	FDIIGIIGEG	300
301	TYGQVYKAR	KDTGEMVALK	KVRLDNEKEG	FPITAIREIK	ILRQLTHQSI	INMKEIVTDK	360
361	EDALDFKKDK	GAFYLVFEYM	DHDLMLGLES	GLVHFNENHI	KSFMRQLMEG	LDYCHKKNFL	420
421	HRDIKSNIL	LNNRGQIKLA	DFGLARLYSS	EESRPYTNKV	ITLWYRPPPEL	LLGEERYTPA	480
481	IDVWSCGCIL	GELFTKKPIF	QANQELAQLE	LISRICGSPC	PAVWPDVIKL	PYFNTMKPKK	540
541	QYRRKLREEF	VFIPAAALDL	FDYMLALDPS	KRCTAEQALQ	CEFLRDVEPS	KMPPPDLPLW	600
601	QDCHELWSKK	RRRQKQMGMT	DDVSTIKAPR	KDLSLG			660

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: CDK13 fragment

CDK13 wt ¹ Amino Acid Sequence							
1	MPSSSDTALG	GGGGLSWAEK	KLEERRKRRR	FLSPQQPPLL	LPLLQPQLLQ	PPPPPPPLLF	60
61	LAAPGTAAAA	AAAAAASSSC	FSPGPPLEVK	RLARGKRRAG	GRQKRRRGPR	AGQEAEKRRV	120
121	FSLPQPQD	GGGASSGGGV	TPLVEYEDVS	SQSEQLLLG	GASAATAATA	AGGTGGSGGS	180
181	PASSSGTQRR	GEGSERRPRR	DRRSSSGRSK	ERHREHRRRD	GQRGGSEASK	SRSRHSHSGE	240
241	ERAEVAKSGS	SSSSGGRRKS	ASATSSSSSS	RKDRDSKAHR	SRTKSSKEPP	SAYKEPPKAY	300
301	REDKTEPKAY	RRRRSLSPLG	GRDDSPVSHR	ASQSLRSRKS	PSPAGGGSSP	YSRRLRPSPS	360
361	PYSRRRSPSY	SRHSSYERGG	DVSPSPYSSS	SWRRSRSPYS	PVLRRSGKSR	SRSPYSSRHS	420
421	RSRSRHRLSR	SRSRHSSISP	STLTLKSSLA	AELNKNKKAR	AAEAARAAEA	AKAAEATKAA	480
481	EAAAKAAS	NTSTPTKGNT	ETSASASQTN	HVKDVKKIKI	EHAPSPSSGG	TLKNDKAKTK	540
541	PPLQVTKVEN	NLIVDKATKK	AVIVGESKES	AATKEESVSL	KEKTKPLTPS	IGAKEKEQHV	600
601	ALVTSTLPL	PLPPMLPEDK	EADSLRGNIS	VKAVKKEVEK	KLRCLLADLP	LPPPELPGGDD	660
661	LKSPPEEKT	ATQLHSKRRP	KICGPRYGET	KEKDIDWGKR	CVDKFDIIGI	IGEGTYGQVY	720
721	KARDKDTGEM	VALKKVRLDN	EKEGFPITAI	REIKILRQLT	HQSIINMKEI	VTDKEDALDF	780
781	KKDKGAFYLV	FEYMDHDLMG	LLESGLVHFN	ENHIKSFMRQ	LMEGLDYCHK	KNFLHRDIK	840
841	SNILLNRRGQ	IKLADFGLAR	LYSSEESRPY	TNKVITLWYR	PPELLLGEER	YTPAIDVWSC	900
901	GCILGELFTK	KPIFQANQEL	AQLELISRIC	GSPCPAVWPD	VIKLPYFNTM	KPKKQYRRKL	960
961	REEFVFIPAA	ALDLFDYMLA	LDPSKRCTAE	QALQCEFLRD	VEPSKMPPPD	LPLWQDCHEL	1020
1021	WSKRRRRQKQ	MGMTDDVSTI	KAPRKDLSLG	LDDSRNTTPQ	GVLPSQLKS	QGSSNVAPVK	1080
1081	TGPGQHLNHS	ELAILLNLLQ	SKTSVNMADE	VQVLNIKVNS	ETQQQLNKIN	LPAGILATGE	1140
1141	KQTDPTPQQ	ESSKPLGGIQ	PSSQTIQPKV	ETDAAQAAVQ	SAFAVLLTQL	IKAQQSKQKD	1200
1201	VLEERENG	GHEASLQLRP	PPEPSTPVSG	QDDLIQHQM	RILELTPEPD	RPRILPPDQR	1260
1261	PPEPPEPPV	TEEDLDYRTE	NQHVPTTSSS	LTDPHAGVKA	ALLQLLAHQH	PQDDPKREGG	1320
1321	IDYQAGDTYV	STSDYKDNFG	SSSFSSAPYV	SNDGLGSSSA	PPLERRSFIG	NSDIQSLDNY	1380
1381	STASSHSGGP	PQPSAFSESE	PSSVAGYGDI	YLNAGPMLFS	GDKDHRFEYS	HGPIAVLANS	1440
1441	SDPSTGPEST	HPLPAKMHN	NYGGNLQENP	SGPSLMHGQT	WTSPAQGPY	SQGYRGHIST	1500
1501	STGRGRGRGL	PY					1560

blue: CDK13 sequence expressed in recombinant protein

¹[NCBI/Protein](https://www.ncbi.nlm.nih.gov/Protein) accession number NP_003709.3

GST-CycK 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	KMFKDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI PQID	KYLKSSKYIA	WPLQG WQATF	GGGDHPPKSD	PMG HHHHHG	RDS LEVLFQG	240
241	PMKENKENS	PSVTSANLDH	TKPCWYWDK	DLAHTPSQLE	GLDPATEARY	RREGARFI	300
301	VGTRLGLHYD	TLATGIIYFH	RFYMFHSFKQ	FPRYVTGACC	LFLAGKVEET	PKKCKDIKT	360
361	ARSLNDVQF	GQFGDDPKEE	VMVLERILLQ	TIKFDLQVEH	PYQFLLKYAK	QLKGDKNKIQ	420
421	KLVQMAWTFV	NDSLCTTSL	QWEPEIIAVA	VMYLAGRLCK	FEIQEWTSKP	MYRRWWEQFV	480
481	QDVPVDVLED	ICHQILDLYS	QGKQMPHHT	PHLQQPPSL	QPTPQVPQVQ	QSQPSQSSEP	540
541	S						600

1-218: GST **Red:** HIS6-tag **Green:** 3C cleavage site **blue:** CycK fragment

CycK wt² Amino Acid Sequence

1	MKENKENS	SVTSANLDHT	KPCWYWDK	LAHTPSQLE	LDPATEARYR	REGARFI	60
61	GTRLGLHYD	LATGIIYFHR	FYMFHSFKQ	PRYVTGACCL	FLAGKVEETP	KKCKDIKTA	120
121	RSLNDVQFG	QFGDDPKEEV	MVLERILLQT	IKFDLQVEHP	YQFLLKYAKQ	LKGDKNKIQK	180
181	LVQMAWTFVN	DSLCTTSLQ	WEPEIIAVAV	MYLAGRLCKE	EIQEWTSKPM	YRRWWEQFVQ	240
241	DVPVDVLEDI	CHQILDLYSQ	GKQMPHHTP	HQLQPPSLQ	PTPQVPQVQ	SQPSQSSEPS	300
301	QFQKDPQQP	AQQQPAQQP	KKPSPQSSP	RQVKRAVVVS	PKEENKAAEP	PPPKIPKIET	360
361	THPPLPPAHP	PPDRKPPLAA	ALGEAEPGP	VDATDLPKVQ	IPPPAHPAPV	HQPPPLPHRP	420
421	PPPPSSYMT	GMSTTSSYMS	GEGYQSLQSM	MKTEGPSYGA	LPPAYGPPAH	LPYHPHVYPP	480
481	NPPPPVPPP	PASFPFPAIP	PPTPGYPPP	PTYNPNFPPP	PPRLPPTHAV	PPHPPGLGL	540
541	PPASYPPPAV	PPGGQPPVPP	PIPPGMPPV	GGLGRAAWMR			600

blue: CycK sequence expressed in recombinant protein

¹[NCBI/Protein](#) accession number NP_001092872.1

[HGNC](#) identifier CycK: CCNK