

## 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:** 008

**Description:** Human CDK13, internal fragment amino acids P<sub>656</sub>-G<sub>1050</sub> (as in [NCBI/Protein](#) entry NP\_003709.3), N-terminal GST-HIS<sub>6</sub> fusion protein with a 3C cleavage site and human CycK, M<sub>1</sub>-S<sub>300</sub> (as in [NCBI/Protein](#) entry NP\_001092872.1), N-terminally fused to GST-HIS<sub>6</sub> 3C cleavage site, coexpressed in Sf9 insect cells

**Product identity:** CDK13/CycK Lot 008, was confirmed as CDK13/CycK by mass spectroscopy LC-ESI-MS/MS

**Theoretical MW<sub>GST-CDK13</sub>:** 73,831 Da

**Theoretical MW<sub>GST-CycK</sub>:** 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

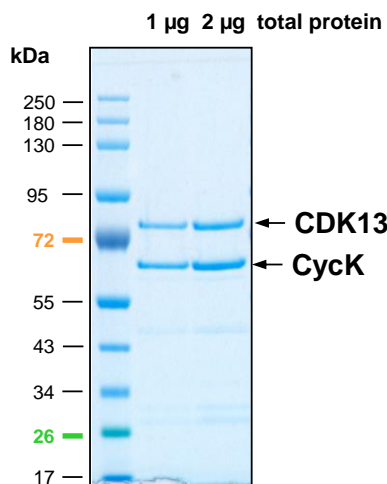
For complete recovery, mix well and spin before use. Product must not be stored in diluted solutions, aliquots below 10µl are not advisable. Avoid repeated freeze-thaw cycles!

**Protein concentration:** 0.438 µg/µl  
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

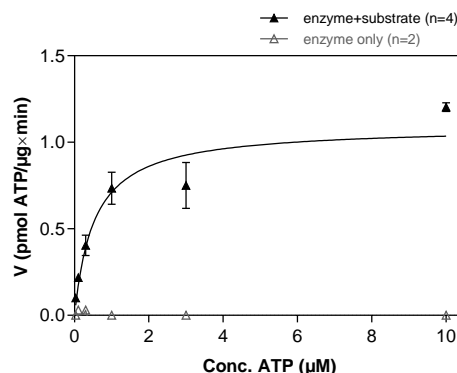
**Biochemical Parameters:**

Specific kinase activity (P<sub>i</sub> transfer): 1.1 pmol/µg x min  
ATP-K<sub>M</sub>: 0.53 µM

### CDK13/CycK Lot 008: Coomassie stain



### CDK13/CycK Lot 008: 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: SUPT5H 754-837 20 µg/ml  
Kinase: 4 µg/ml

- Filter binding assay  
MSFC membrane (Millipore)

# CDK13/CycK

Product No.: 1530-1484-1

GST-CDK13 Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPEML	KMFKDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPOID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHG	RDSLEVLFCG	240
241	PPGGDDLKSKS	PEEKKTATQL	HSKRRPKICG	PRYGETKEKD	IDWGKRCVDK	FDIIGIIGEG	300
301	TYGQVYKARD	KDTGEMVALK	KVRLDNEKEG	FPITAIREIK	ILRQLTHQSI	INMKEIVTDK	360
361	EDALDFKDK	GAFYLVFEYM	DHDLMLGLES	GLVHFNENHI	KSFMRQLMEG	LDYCHKKNFL	420
421	HRDIKCSNIL	LNNRQGIKLA	DFGLARLYSS	EESRPYTNKV	ITLWYRPEPEL	LLGEERYTPA	480
481	IDVWSCGCIL	GELFTTKPIF	QANQELAQL	LISRTICGSPC	PAVWPDVIKL	PYFNTMKPKK	540
541	QYRKLREF	VRFPAALDL	FDYMLADPS	KRCTAEQALQ	CEFLRDVEPS	KMPPPDLPLW	600
601	QDCHELWSKK	RRQKQMGMT	DDVSTIKAPR	KDLSLG			660

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

CDK13 wt <sup>1</sup> Amino Acid Sequence							
1	MPSSSDTALG	GGGGLSWAEK	KLEERRKRRR	FLSPQQPPLL	LPLLQPQLLQ	PPPPPPPLLF	60
61	LAAPGTAATA	AAAAAASSSC	FSPGPPLEVK	RLARGKRRAG	GRQRRRGPR	AGQEAERKRV	120
121	FSLPQPQDQ	GGGASSGGGV	TPLVEYEDVS	SQSEQQLLLG	GASAATAATA	AGGTGGSGGS	180
181	PASSSTQRR	GEGSERRPRR	DRSSSSGRSK	ERHREHRRD	GQRGGSEASK	SRSRHSHSGE	240
241	ERAEVAKSGS	SSSSGGRRKS	ASATSSSSSS	RKDRDSKAHR	SRTKSSKEPP	SAYKEPPKAY	300
301	REDKTEPKAY	RRRRSLSPG	GRDDSPVSHR	ASQSLRSRKS	PSPAGGGSSP	YSRRLRSPSP	360
361	PYSRRRSPSY	SRHSSYERGG	DVSPSPYSSS	SWRRSRSPYS	PVLRRSRGS	SRSPYSSRHS	420
421	RSRHRHLSR	SRSRHSSISP	STLTLKSSLA	AELNKNKKAR	AAEAARAEA	AKAAEATKAA	480
481	EAAAKAAKAS	NTSTPTKGN	ETSASASQTN	HVKDVKKIKI	EHAPSPSSGG	TLKNDKAKTK	540
541	PPLQVTKVEN	NLIVDKATK	AVIVGKESKS	AATKEESVSL	KEKTKPLTPS	IGAKEKEQHV	600
601	ALVTSTLPL	PLPPMLPEDK	EADSLRGNIS	VKAVKKEVEK	KLRCLLADLP	LPPELPGGDD	660
661	LKSPPEEKT	ATQLHSKRRP	KICGPRYGET	KEKDIDWGR	CVDKFDIIGI	IGEGTYQVY	720
721	KARDKDTGEM	VALKKVRLDN	EKEGFPITAI	REIKILRQLT	HQSIINMKEI	VTDKEDALDF	780
781	KKDKGAFYLV	FEYMDHDLMG	LLESGLVHFN	ENHIKSFMRQ	LMEGLDYCHK	KNFLHRDIK	840
841	SNILLNNRQ	IKLADFGLAR	LYSSEESRPY	TNKVITLWYR	PPELLLGEER	YTPAIDVWSC	900
901	GCILGELFTK	KPIFQANQEL	AQLELISRIC	GSPCPAVWPD	VIKLPYFNTM	KPKKQYRRKL	960
961	REEVFVIPA	ALDLFDYMLA	LDPSKRCSTAE	QALQCEFLRD	VEPSKMPPPD	LPLWQDCHEL	1020
1021	WSKRRRQKQ	MGMTDDVSTI	KAPRKDSLGL	LDDSRNTNPQ	GVLPSSQLKS	QGSSNVA PVK	1080
1081	TGPGQHLNHS	ELAILLNLQ	SKTSVNMAF	VQVLNIKVNS	ETQQQLNKIN	LPAGILATGE	1140
1141	KQTDPTPQQ	ESSKPLGGIQ	PSSQTIQPKV	ETDAAQAAVQ	SAFAVLLTQL	IKAQQSKQKD	1200
1201	VLLEERENG	GHEASLQLRP	PPEPSTPVSG	QDDLIQHQM	RILELTPEPD	RPRILPPDQR	1260
1261	PPEPPEPPV	TEEDLDYRTE	NQHVPTTSSS	LTDPHAGVKA	ALLQLLAQHQ	PQDDPKREGG	1320
1321	IDYQAGDTYV	STSDYKDNFG	SSSFSSAPYV	SNDGLGSSSA	PPLERRSFIG	NSDIQSLDNY	1380
1381	STASSHSGGP	PQPSAFSESF	PSSVAGYGDI	YLNAGPMLFS	GDKDHRFEYS	HGPIAVLANS	1440
1441	SDPSTGPEST	HPLPAKMNY	NYGGNLQENP	SGPSLMHGQT	WTSPAQGGPY	SQGYRGHIST	1500
1501	STGRGRGRGL	PY					1560

**blue:** CDK13 sequence expressed in recombinant protein

<sup>1</sup>NCBI/Protein accession number NP\_003709.3

Recombinant Proteins

**GST-CycK Recombinant Fusion Protein Amino Acid Sequence**

1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLIERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPPEM	KMFKDRCLCH	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPOID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHGG	RDSLEVLFGG	240
241	MKENKENS	PSVTSANLDH	TKPCWYWDKK	DLAHTPSQLE	GLDPATEARY	RREGARFIFD	300
301	VGTRLGLHYD	TLATGIIYFH	RFYMFHSFKQ	FPRYVTGACC	LFLAGKVEET	PKCKDIIKT	360
361	ARSLNDVQF	QQFGDDPKEE	VMVLERILLQ	TIKFDLQVEH	PYQFLLYAK	QLKGDKNKIQ	420
421	KLVMAWTFV	NDSLCTTSL	QWEPEIIAVA	VMYLAGRLCK	FEIQWTSKP	MYRRWVEQFV	480
481	QDVPVDVLED	ICHQILDLYS	QGKQMPHHT	BHQLQPPSL	QPTQVPVQVQ	QSQPSQSSSE	540
541	S						600

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

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

1	MKENKENS	SVTSANLDHT	KPCWYWDKKD	LAHTPSQLEG	LDPATEARYR	REGARFIFDV	60
61	GTRLGLHYDT	LATGIIYFHR	FYMFHSFKQF	PRYVTGACCL	FLAGKVEETP	KKCKDIIKTA	120
121	RSLNDVQFG	QFGDDPKEEV	MVLERILLQT	IKFDLQVEHP	YQFLLYAKQ	LKGDKNKIQK	180
181	LVQMAWTFVN	DSLCTTSLQ	WEPEIIAVAV	MYLAGRLCKF	EIQWTSKPM	YRRWVEQFVQ	240
241	DVPVDVLEDI	CHQILDLYS	GKQMPHHTP	HQLQPPSLQ	PTPQVPVQVQ	SQPSQSSSEPS	300
301	QPQQKDPQQP	AQQQQPAQQP	KKPSPQSSP	RQVKRAVVVS	PKEENKAAEP	PPPKIPKIET	360
361	THPPLPPAHP	PPDRKPPLAA	ALGEAEPGP	VDATDLPKVQ	IPPPAHPAPV	HQPPPLPHRP	420
421	PPPPSSSYMT	GMSTTSSYMS	GEGYQSLQSM	MKTEGPSYGA	LPPAYGPPAH	LPYHPHVYPP	480
481	NPPPPVPPP	PASFPPPAIP	PPTPGYPPP	PTYNPNFPPP	PPRLPPTHAV	PPHPPGLGL	540
541	PPASYPPPAV	PPGGQPPVPP	PIPPPGMPPV	GGLGRAAWMR			600

blue: CycK sequence expressed in recombinant protein

<sup>1</sup>[NCBI/Protein](#) accession number NP\_001092872.1

[HGNC](#) identifier CycK: CCKN