

## CDK12 wt/CycK

cyclin dependent kinase 12

Recombinant Human Active Protein Kinase

HGNC Symbol: CDK12

Synonyms: CRK7, CRKR, CrkRS, CRKRS, hCDK12

Product No.: 1483-1484-1

Lot: 001

**Description:** Human CDK12, amino acids Q<sub>696</sub>-S<sub>1082</sub> (as in [NCBI/Protein](#) entry NP\_057591.2), N-terminal GST-HIS<sub>6</sub> fusion protein with a 3C cleavage site and human CycK, amino acids 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, co-expressed in Sf9 insect cells

**Product identity:** CDK12 wt/CycK Lot 001, was confirmed as CDK12/CycK by mass spectroscopy LC-ESI-MS/MS

**Theoretical MW**<sub>GST-CDK12 wt</sub>: 73,066 Da

**Theoretical MW**<sub>CycK</sub>: 63,031 Da

**Expression host:** Sf9 insect cells

**Purification:** GST-Affinity Chromatography

**Activation:** With CAK

**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:** 0.763 µg/µl

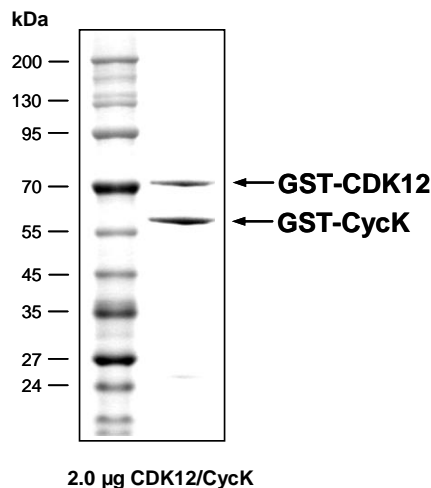
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

**Biochemical Parameters:**

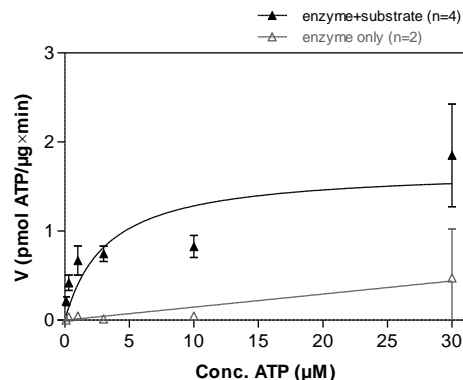
Specific kinase activity (P<sub>i</sub> transfer): 1.7 pmol/µg × min

ATP-K<sub>M</sub>: 3.2 µM

### CDK12 wt/CycK Lot 001: Coomassie stain



### CDK12 wt/CycK 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: RBER-IRStide, 80 µg/ml
  - Kinase: 2 µg/ml
- Filter binding assay
  - MSFC membrane (Millipore)

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# CDK12 wt/CycK

Product No.: 1483-1484-1

GST-CDK12 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	WPLQGWQATF	GGGDHPPKSD	PMG <b>HHHHHG</b>	RDS <b>LEVLFGQ</b>	240
241	<b>PQQPYKKRPK</b>	<b>ICCPRYGERR</b>	<b>QTESDWGKRC</b>	<b>VDKFDIIGII</b>	<b>GEGTYGQVYK</b>	<b>AKDKDTGELV</b>	300
301	<b>ALKKVRLDNE</b>	<b>KEGFPITAIR</b>	<b>EIKILRQLIH</b>	<b>RSVNMKEIV</b>	<b>TDKQDALDFK</b>	<b>KDKGAFYLVF</b>	360
361	<b>EYMDHDLMGL</b>	<b>LESGLVHFSE</b>	<b>DHIKSFMKQL</b>	<b>MEGLE YCHKK</b>	<b>NFLHRDIKCS</b>	<b>NILLNNSGQI</b>	420
421	<b>KLADFGLARL</b>	<b>YNSEESRPYT</b>	<b>NKVITLWYRP</b>	<b>PELLLGEERY</b>	<b>TPAIDVWSCG</b>	<b>CILGELFTKK</b>	480
481	<b>PIFQANLELA</b>	<b>QLELISRLCG</b>	<b>SPCPAVWPDV</b>	<b>IKLPYFNTMK</b>	<b>PKKQYRRRLR</b>	<b>EEFSFIPSA</b>	540
541	<b>LDLLDHMLTL</b>	<b>DPSKRCTAEQ</b>	<b>TLQSDFLKDV</b>	<b>ELSKMAPPDL</b>	<b>PHWQDCHELW</b>	<b>SKKRRRQRQS</b>	600
601	<b>GVVVEEPPPS</b>	<b>KTSRKETTSG</b>	<b>TSTEPVKNS</b>				660

1-218: GST **Red**: HIS6-tag **Green**: 3C cleavage site **blue**: CDK12 fragment

CDK12 wt <sup>1</sup> Amino Acid Sequence							
1	MPNSERHGGK	KDGSGGASGT	LQPSSGGGSS	NSRERHRLVS	KHKRHKSKHS	KDMGLVTPEA	60
61	ASLGTVIKPL	VEYDDISSDS	DTFSDDMAFK	LDRRENDERR	GSDRSDDLHK	HRHHQHRRSR	120
121	DLLKAKQTEK	EKSQEVSSKS	GSMKDRI SGS	SKRSNEETDD	YGKAQVAKSS	SKESRSSKLH	180
181	KEKTRKEREL	KSGHKDRSKS	HRKRETPKSY	KTVDSPKRRS	RSPHRKWSDS	SKQDDSPSGA	240
241	SYGQDYDLSP	SRSHTSSNYD	SYKKS PGGTS	RRQSVSPPYK	EPSAYQSSTR	SPSPYSRRQR	300
301	SVSPYSRRRS	SSYERSGSYS	GRSPSPYGRR	RSSSPFLSKR	SLRSRPLPSR	KSMKSRSRSP	360
361	AYSRHSSSHS	KKKRSSSRSR	HSSISPVRLP	LNSSLGAELS	RKKKERAAAA	AAAKMDGKES	420
421	KGSPVFLPRK	ENSSVEAKDS	GLESKKLPRS	VKLEKSAPDT	ELVNVTHLNT	EVKNSSDTGK	480
481	VKLDENSEKH	LVKDLKAQGT	RDSKPIALKE	EIVTPKETET	SEKETPPPLP	TIASPPPLP	540
541	TTTPPPQTPP	LPPLPPIPAL	PQQPPLPPSQ	PAFSQVPASS	TSTLPPSTHS	KTSAVSSQAN	600
601	SQPPVQVSVK	TQVSVTAAIP	HLKTSTLPP	PLPPLLPGDD	DMDSPKETLP	SKPVKKEKEQ	660
661	RTRHLLTDLP	LPPELPGGDL	SPPDSPEPKA	ITPPQ <b>OPYK</b>	<b>RPKICCPRYG</b>	<b>ERRQTESDWG</b>	720
721	<b>KRCVDFDII</b>	<b>GIIGEGTYGQ</b>	<b>VYKAKKDTG</b>	<b>ELVALKKVRL</b>	<b>DNEKEGFPI</b>	<b>AIREIKILRQ</b>	780
781	<b>LIHRSVNMK</b>	<b>EIVTDKQDAL</b>	<b>DFKKDKGAFY</b>	<b>LVFEYMDHDL</b>	<b>MGLLESGLVH</b>	<b>FSEDHIKSEF</b>	840
841	<b>QQLMEGLE YC</b>	<b>HKKNFLHRDI</b>	<b>KCSNILLNNS</b>	<b>GQIKLADFGL</b>	<b>ARLYNSEESR</b>	<b>PYTNKVITLW</b>	900
901	<b>YRPELLLGE</b>	<b>ERYTPAIDVW</b>	<b>SCGCILGELF</b>	<b>TKKPIFQANL</b>	<b>ELAQLELISR</b>	<b>LCGSPCPAVW</b>	960
961	<b>PDVIKLPYFN</b>	<b>TMKPKKQYRR</b>	<b>RLREEFSFIP</b>	<b>SAALDLLDHM</b>	<b>LTLDP SKRCT</b>	<b>AEQTLQSDFL</b>	1020
1021	<b>KDVELSKMAP</b>	<b>PDLPHWQDCH</b>	<b>ELWSKRRRQ</b>	<b>RQSGVVVEEP</b>	<b>PPSKTSRKET</b>	<b>TSGTSTEPVK</b>	1080
1081	<b>NSSPAPPQPA</b>	<b>PGKVESGAGD</b>	<b>AIGLADITQQ</b>	<b>LNQSELAVLL</b>	<b>NLLQSQTDL S</b>	<b>IPQMAQLLNI</b>	1140
1141	<b>HSNPEMQQL</b>	<b>EALNQSISAL</b>	<b>TEATSQQQDS</b>	<b>ETMAPEESLK</b>	<b>EAPSAPVILP</b>	<b>SAEQTTLEAS</b>	1200
1201	<b>STPADMQNIL</b>	<b>AVLLS QLMKT</b>	<b>QEPAGSLEEN</b>	<b>NSDKNSGPQG</b>	<b>PRRTPTMPQE</b>	<b>EAAACPPHIL</b>	1260
1261	<b>PPEKRPPEPP</b>	<b>GPPPPPPPPP</b>	<b>LVEGDLSSAP</b>	<b>QELNPAVTAA</b>	<b>LLQLLSQPEA</b>	<b>EPPGHL PHEH</b>	1320
1321	<b>QALRPMEYST</b>	<b>RPRPNRTYGN</b>	<b>TDGPETGFSA</b>	<b>IDTDERN SGP</b>	<b>ALTESLVQTL</b>	<b>VKNRTFSGSL</b>	1380
1381	<b>SHLGE SSSYQ</b>	<b>GTGSVQFPD</b>	<b>QDLRFARVPL</b>	<b>ALHPVVGQPF</b>	<b>LKAEGSSNSV</b>	<b>VHAETKLQNY</b>	1440
1441	<b>GELGPGTTGA</b>	<b>SSSAGLHWG</b>	<b>GPTQSSAYGK</b>	<b>LYRGPTRVPP</b>	<b>RGGRGRGVPY</b>		1500

**blue**: CDK12 sequence expressed in recombinant protein

<sup>1</sup>[NCBI/Protein](#) accession number NP\_057591.2



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

1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLIERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPPEML	KMFKDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHG	RDSLEVLFG	240
241	MKENKENS	PSVTSANLDH	TKPCWYWDKK	DLAHTPSQLE	GLDPATEARY	RREGARFID	300
301	VGTRLGLHYD	TLATGIIYFH	RFYMFHSFKQ	FPRYVTGACC	LFLAGKVEET	PKKCKDIKT	360
361	ARSLNDVQF	QQFGDDPKEE	VMVLERILLQ	TIKFDLQVEH	PYQFLLYAK	QLKGDKNKIQ	420
421	KLVQMAWTFV	NDSLCTTSL	QWEPEIIAVA	VMYLAGRLCK	FEIQEWTSKP	MYRRWWEQFV	480
481	QDVPVDVLED	ICHQILDLYS	QGKQMPHHT	PHLQPPSL	QPTPQVPQVQ	QSQPSQSE	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	LAHTPSQLE	LDPATEARYR	REGARFIDV	60
61	GTRLGLHYDT	LATGIIYFHR	FYMFHSFKQF	PRYVTGACCL	FLAGKVEETP	KKCKDIKTA	120
121	RSLNDVQFG	QFGDDPKEEV	MVLERILLQT	IKFDLQVEHP	YQFLLYAKQ	LKGDKNKIQK	180
181	LVQMAWTFVN	DSLCTTSLQ	WEPEIIAVAV	MYLAGRLCKF	EIQEWTSKPM	YRRWWEQFVQ	240
241	DVPVDVLEDI	CHQILDLYSQ	GKQMPHHTP	HQLQPPSLQ	PTPQVPQVQ	SQPSQSSEPS	300
301	QPQQKDPQQP	AQQQQPAQQP	KKPSPQSSP	RQVKRAVVVS	PKEENKAAEP	PPPPIPKIET	360
361	THPPLPPAHP	PPDRKPPLAA	ALGEAEPGP	VDATDLPKVQ	IPPPAHPAPV	HQPPPLPHRP	420
421	PPPPSSYMT	GMSTTSSYMS	GEGYQSLQSM	MKTEGPSYGA	LPPAYGPPAH	LPYHPHYVPP	480
481	NPPPPVPPP	PASFPPPAIP	PPTPGYPPP	PTYNPNFPPP	PPRLPPTHAV	PPHPPGLGL	540
541	PPASYPPPAV	PPGQPPVPP	PIPPGMPPV	GGLGRAAWMR			600

blue: CycK sequence expressed in recombinant protein

<sup>2</sup>[NCBI/Protein](#) accession number NP\_001092872.1  
[HGNC](#) identifier CycK: CCNK

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