

ProQinase™ CDK17/CycY

cyclin dependent kinase 17

Recombinant Human Active Protein Kinase

HGNC Symbol: CDK17

Synonyms: PCTK2, PCTAIRE2

Product No.: 1526-1116-1

Lot: 001

Description: Human CDK17, full length, amino acids M1-F523 (as in [NCBI/Protein](#) entry NP_002586.2), N-terminal GST-HIS₆ fusion protein with a 3C cleavage site and human CycY, full length, amino acids M1-S341 (as in [NCBI/Protein](#) entry NP_659449.3) N-terminal HIS₆ fusion protein with a TEV cleavage site, co-expressed in Sf9 insect cells

Product identity: CDK17/CycY Lot 001, has been verified by mass spectrometry LC-ESI-MS/MS

Theoretical MW_{GST-CDK17}: 87672 Da

Theoretical MW_{HIS-CycY}: 41697 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 10 µl are not advisable. Avoid repeated freeze-thaw cycles!

Protein concentration: 0.21 µg/µl

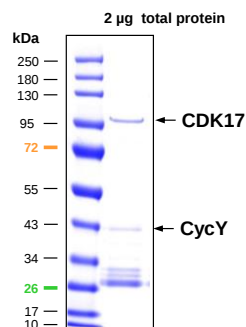
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

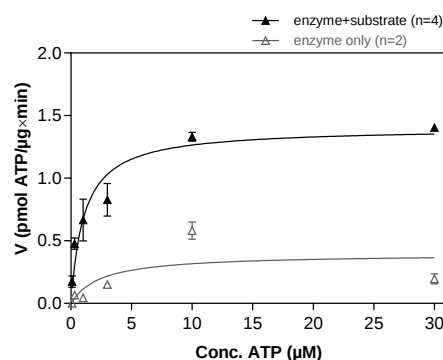
Specific kinase activity (P_i transfer): 1.4 pmol/µg*min

ATP-K_M: 1.1 µM

CDK17/CycY Lot 001: Coomassie stain



CDK17/CycY Lot 001: 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: CDCA8 40 µg/ml
- Kinase: 2 µg/ml

Assay technology:
Radiometric filter binding assay
MSFC membrane (96 well plate, Millipore)

Sequence information

GST-CDK17 Recombinant Fusion Protein Amino Acid Sequence

1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLIERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPEML	KMFKDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPIQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHGG	RDSLEVLFGG	240
241	PMKKFKRRLS	LTLRGSQTID	ESLSELAEQM	TIEENSSKDN	EPIVKNGRPP	TSHSMHSFLH	300
301	QYTGSFKKPP	LRRPHSVIGG	SLGSFMAMPR	NGSRLDIVHE	NLKMGSDES	DQASGTSSDE	360
361	VQSPTGVCLR	NRIHRRISME	DLNKRLSLPA	DIRIPDGYLE	KLQINSPPFD	QPMRRSRRA	420
421	SLSEIGFGKM	ETIYIKLEKL	EGTYATVYKG	RSKLTENLVA	LKEIRLEHEE	GAPCTAIREV	480
481	SLLKDLKHAN	IVTLHDIVHT	DKSLTLVFEY	LDKDLKQYMD	DCGNIMSMHN	VKLFLYQILR	540
541	GLAYCHRRKV	LHRDLKPQNL	LINEKGELKL	ADFGLARAKS	VPTKYSNEV	VTWYRPPDV	600
601	LLGSSEYSTQ	IDMWGVGCI	FEMASGRPLF	PGSTVEDELH	LIFRLLGTPS	QETWPGISSN	660
661	EEFKYNFPPK	YKQPLINHA	PRLDSEGIEL	ITKFLQYESK	KRVSAEEAMK	HVYFRSLGPR	720
721	IHALPESVSI	FSLKEIQLQK	DPGFRNSSYP	ETGHGKNRRQ	SMLF		780

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: CDK17

CDK17 wt¹ Amino Acid Sequence

1	MKKFKRRLSL	TLRGSQTIDE	SLSELAEQMT	IEENSSKDNE	PIVKNGRPPT	SHSMHSFLHQ	60
61	YTGSFKKPPL	RRPHSVIGGS	LGSFMAMPRN	GSRLDIVHEN	LKMGSDES	QASGTSSDEV	120
121	QSPTGVCLRN	RIHRRISMED	LNKRLSLPAD	IRIPDGYLEK	LQINSPPFDQ	PMSRRSRRAS	180
181	LSEIGFGKME	TYIKLEKLGE	GTYATVYKGR	SKLTENLVAL	KEIRLEHEEG	APCTAIREVS	240
241	LLKDLKHANI	VTLHDIVHTD	KSLTLVFEYL	DKDLKQYMD	CGNIMSMHNV	KLFLYQILRG	300
301	LAYCHRRKVL	HRDLKPQNLL	INEKGELKLA	DFGLARAKSV	PTKYSNEVV	TLWYRPPDVL	360
361	LGSSEYSTQI	DMWGVGCIFF	EMASGRPLFP	GSTVEDELHL	IFRLLGTPSQ	ETWPGISSNE	420
421	EEFKYNFPPK	KQPLINHAP	RLDSEGIELI	TKFLQYESK	RVSAAEAMKH	VYFRSLGPRI	480
481	HALPESVSIF	SLKEIQLQKD	PGFRNSSYPE	TGHGKNRRQS	MLF		540

blue: CDK17 sequence expressed in recombinant protein

¹[NCBI/Protein](#) accession number NP_002586.2

HIS-CycY Recombinant Fusion Protein Amino Acid Sequence

1	MSHHHHH	AMT	ENLYFQG	AMV	MGNTTSCCVS	SSPKLRNAH	SRLESYRPDT	DLSREDTGCN	60
61	LQHISDRENI	DDLNMEFNPS	DHPRASTIFL	SKSQTDVREK	RKSLFINHHP	PGQIARKYSS			120
121	CSTIFLDDST	VSQPNLKYTI	KCVLAIIYH	IKNRDPDGRM	LLDIFDENLH	PLSKSEVPPD			180
181	YDKHNPEQKQ	IYRFVRTLFS	AAQLTAECAI	VTLVYLERLL	TYAEIDICPA	NWKRIVLGAI			240
241	LLASKVWDDQ	AVWNVDCYQI	LKDITVEDMN	ELERQFLELL	QFNINVPSSV	YAKYYFDLRS			300
301	LAEANNSLFP	LEPLSRERAH	KLEAISRLCE	DKYKDLRRA	RKRSASADNL	TLPRWSPAI			360
361	S								420

Red: HIS6-tag Green: TEV cleavage site blue: CycY

CycY wt² Amino Acid Sequence

1	MGNTTSCCVS	SSPKLRNAH	SRLESYRPDT	DLSREDTGCN	LQHISDRENI	DDLNMEFNPS	60
61	DHPRASTIFL	SKSQTDVREK	RKSLFINHHP	PGQIARKYSS	CSTIFLDDST	VSQPNLKYTI	120
121	KCVLAIIYH	IKNRDPDGRM	LLDIFDENLH	PLSKSEVPPD	YDKHNPEQKQ	IYRFVRTLFS	180
181	AAQLTAECAI	VTLVYLERLL	TYAEIDICPA	NWKRIVLGAI	LLASKVWDDQ	AVWNVDCYQI	240
241	LKDITVEDMN	ELERQFLELL	QFNINVPSSV	YAKYYFDLRS	LAEANNSLFP	LEPLSRERAH	300
301	KLEAISRLCE	DKYKDLRRA	RKRSASADNL	TLPRWSPAI	S		360

blue: CycY sequence expressed in recombinant protein

²[NCBI/Protein](#) accession number NP_659449.3[HGNC](#) identifier CycY: CCNY