

CDK16/CycY

cyclin dependent kinase 16

Recombinant Human Active Protein Kinase

HGNC Symbol: CDK16

Synonyms: PCTAIRE, PCTGAIRE, PCTK1

Product No.: 1117-1116-1

Lot: 001

Description: Human CDK16, full length, amino acids M₁-F₄₉₆ (as in [NCBI/Protein](#) entry NP_006192.1), N-terminally fused to GST-HIS₆-3C cleavage site and human CycY, full length, amino acids M₁-S₃₄₁ (as in [NCBI/Protein](#) entry NP_659449.3), N-terminally fused to HIS₆-TEV cleavage site, co-expressed in Sf9 insect cells

Product identity: CDK16/CycY Lot 001, was confirmed CDK16/CycY by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{GST-CDK16}: 84,221 Da

Theoretical MW_{HIS-CycY}: 41,697 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: 0.227 µg/µl

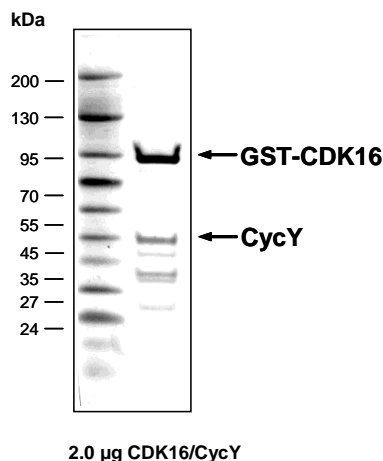
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

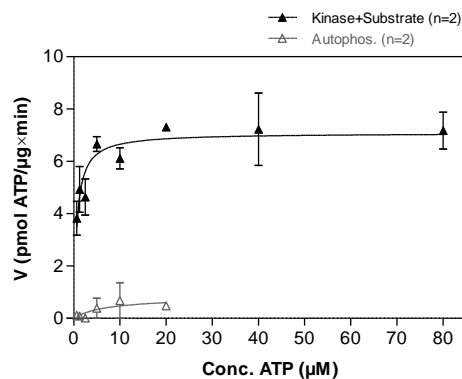
Specific kinase activity (P_i transfer): 7 pmol/µg × min

ATP-K_M: 0.6 µM

CDK16/CycY Lot 001: Coomassie stain



CDK16/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: RBER-GSK3 200 µg/ml
Kinase: 2 µg/ml
- Filter binding assay
MSFC membrane (Millipore)

CDK16/CycY

Product No.: 1117-1116-1

GST-CDK16 Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP EML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI PQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHG	RDSLEVLFGC	240
241	PLAMVMDRMK	KIKRQLSMTL	RGGRGIDKTN	GAPEQIGLDE	SGGGGSDPG	EAPTRAAPGE	300
301	LR SARGPLSS	APEIVHEDLK	MGS DGESDQA	SATSSDEVQS	PVRV MRNHP	PRKISTEDIN	360
361	KRLSLPADIR	LPEGYLEKLT	LNSPIFDKPL	SRRLRRVLSL	EIGFGKLETY	IKLDKLGEGT	420
421	YATVYK GKSK	LTDNLVALKE	IRLEHEEGAP	CTAIREVSL	KDLKHANIVT	LHDIHTEKS	480
481	LTLVFEYLDK	DLKQYLD DCG	NIINMHNVKL	FLFQLLRGLA	YCHRQKVLHR	DLKPQNLLIN	540
541	ERGELKLADF	GLARAKS IPT	KTYSNEVVT	WYRPPDILLG	STDYSTQIDM	WGVGCIFYEM	600
600	ATGRPLFPGS	TVEEQLHFIF	RILGTPTEET	WPGILSNEEF	KTYNYPKYRA	EALLSHAPRL	660
661	DS DGADLLTK	LLQFEGRNRI	SAEDAMKHPF	FLSLGERIHK	LPDTTSIFAL	KEIQLQKEAS	720
721	LRSSMPDSG	RPAFRVVDTE	F				780

1-218: GST **Red**: HIS6-tag **Green**: 3C cleavage site **blue**: CDK16

CDK16 wt ¹ Amino Acid Sequence							
1	MDRMKKIKRQ	LSMTLRGGRG	IDKTINGAPEQ	IGLDESGGGG	GSDPGEAPTR	AAPGELRSAR	60
61	GPLSSAPEIV	HEDLKMGS DG	ESDQASATSS	DEVQSPVVR	MRNHPPRKIS	TEDINKRLSL	120
121	PADIRLPEGY	LEKLTLSPI	FDKPLSRRLR	RVSLSEIGFG	KLETYIKLDK	LGEGTATVY	180
181	KGKSKLTDNL	VALKEIRLEH	EEGAPCTAIR	EVSLKDLKH	ANIVTLHDI	HTEKSLTVF	240
241	EYLDKDLKQY	LDDCGNIINM	HNVKLF LFQL	LRGLAYCHRQ	KVLHRDLKPQ	NLLINER GEL	300
301	KLADFG LARA	KS IPTKTYSN	EVVTLWYRPP	DILLGSTDYS	TQIDMWVGC	IFYEMATGRP	360
361	LFPGSTVEEQ	LHFIFRILGT	PTEETWPGIL	SNEEFKTYNY	PKYRAEALLS	HAPRLDS DGA	420
421	DLLTKLLQFE	GRNRISAEDA	MKHPFFLSLG	ERIKLDPDTT	SIFALKEIQL	OKEASLRSSS	480
481	MPDSGRPAFR	VVDTEF					540

blue: CDK16 sequence expressed in recombinant protein

¹[NCBI/Protein](#) accession number NP_006192.1
A100B: SNP variation see [NCBI/dbSNP](#) ID: rs0000000

HIS-CycY Recombinant Fusion Protein Amino Acid Sequence							
1	MSHHHHAMT	ENLYFQ GAMV	MGNTTSCCVS	SSPKLRNAH	SRLESYRPDT	DLSREDTGCN	60
61	LQHISDRENI	DDLNMEFNPS	DHPRASTIFL	SKSQT DVREK	RKSLFINHHP	PGQIARKYSS	120
121	CSTIFLDDST	VSQPNLKYTI	KCV ALAIYYH	IKNRDPDGRM	LLDIFDENLH	PLSKSEVPPD	180
181	YDKHNPEQKQ	IYRFVRTLFS	AAQLTAECAI	VTLVYLERLL	TYAEIDICPA	NWKRIVLGAI	240
241	LLASKVWDDQ	AVWNVDYCQI	LKDITVEDMN	ELERQFLELL	QFNINVPSSV	YAKYYFDLRS	300
301	LAEANLSFP	LEPLSRERAH	KLEAISRLCE	DKYKDLR RSA	RKRSASADNL	TLPRWSPAI	360
361	S						420

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

CycY wt ² Amino Acid Sequence							
1	MGNTTSCCVS	SSPKLRNAH	SRLESYRPDT	DLSREDTGCN	LQHISDRENI	DDLNMEFNPS	60
61	DHPRASTIFL	SKSQT DVREK	RKSLFINHHP	PGQIARKYSS	CSTIFLDDST	VSQPNLKYTI	120
121	KCV ALAIYYH	IKNRDPDGRM	LLDIFDENLH	PLSKSEVPPD	YDKHNPEQKQ	IYRFVRTLFS	180
181	AAQLTAECAI	VTLVYLERLL	TYAEIDICPA	NWKRIVLGAI	LLASKVWDDQ	AVWNVDYCQI	240
241	LKDITVEDMN	ELERQFLELL	QFNINVPSSV	YAKYYFDLRS	LAEANLSFP	LEPLSRERAH	300
301	KLEAISRLCE	DKYKDLR RSA	RKRSASADNL	TLPRWSPAI	S		360

blue: CycY sequence expressed in recombinant protein

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

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