

ProQinase™ CDK18/CycY

cyclin dependent kinase 18

Recombinant Human Active Protein Kinase

HGNC Symbol: CDK18

Synonyms: PCTAIRE, PCTAIRE3, PCTK3

Product No.: 1546-1619-1

Lot: 008

Description: Human CDK18, amino acids M₁-F₄₇₄ (as in [NCBI/Protein](#) entry NP_997667.1) and human CyclinY, amino acids M₁-S₃₄₁ (as in [NCBI/Protein](#) entry NP_659449.3), both N-terminal GST-HIS₆ fusion proteins with a 3C cleavage site, coexpressed in Sf9 insect cells.

Product identity: CDK18/CycY Lot 008, was confirmed as CDK18/CycY by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{CDK18} : 82,514 Da

Theoretical MW_{CycY} : 67,841 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: 0.335 µg/µl

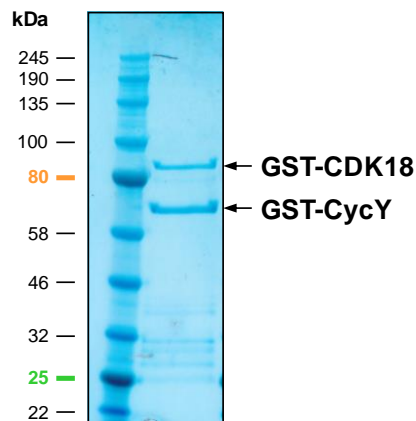
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

Specific kinase activity (P_i transfer): 30 pmol/µg × min

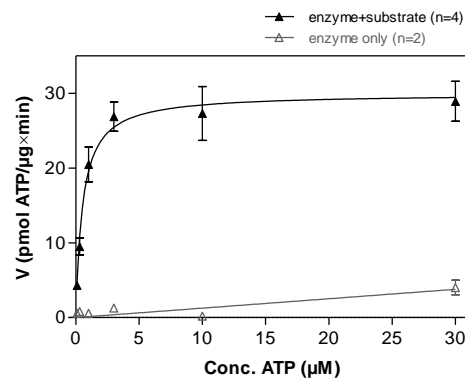
ATP-K_M: 0.53 µM

CDK18/CycY Lot 008:
Coomassie stain



1 µg GST-CDK18/CycY

CDK18/CycY Lot 008:
Determination of V_{max} and K_M value for ATP



Determination of K_M value & Specific activity:

- 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-NTRK3tide 4 µg/ml
 - Kinase: 0.5 µg/ml
- Filter binding assay
MSFC membrane (Millipore)

Additional assay technology:

CDK18/CycY Lot 008 was also successfully tested by Reaction Biology for the use with the ADP-Glo™ Kinase assay from Promega ADP-Glo assay conditions may vary from radiometric assay conditions, please inquire for assay details

ProQinase™ CDK18/CycY

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GST-CDK18 Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQ SMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP EML	KMFKDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI P QID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHG	RDSLEVLFGQ	240
241	PMIMNMKNF	KRRFSLSVPR	TETIEESLAE	FTEQFNQLHN	RRNENLQLGP	LGRDPPQEC	300
301	TFSPD S GEE	PGQLSPGVQF	QRRQNRRFS	MEDVSKRLSL	PMDIRLPQEF	LQKLQMESPD	360
361	LPKPLSRMSR	RASLSDIGFG	KLETYVKLDK	LGEGTYATVF	KGRSKLTENL	VALKEIRLEH	420
421	EEGAPCTAIR	EVSLLNKLNK	ANIVTLHDLI	HTDRSLTLVF	EYLDSDLKQY	LDHCGNLM SM	480
481	HNVKIFMFQL	LRGLAYCHHR	KILHRDLKPQ	NLLINER GEL	KLADFLARA	KSVPTKTYSN	540
541	EVVTLWYRPP	DVLLGSTEYS	TPIDMWGVC	IHYEMATGRP	LFPGSTVKEE	LHLIFRLLGT	600
601	PTEETWPGVT	AFSEFR TYSF	PCYLPQPLIN	HAPRLDTDGI	HLLSLLLYE	SKSRMSAEAA	660
661	LSHSYFRSLG	ERVHQLEDTA	SIFSLKEIQL	QKDPGYRGLA	FQQPGRGKNR	RQSIF	720

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: CDK18

CDK18 wt ¹ Amino Acid Sequence							
1	MIMNMKNFK	RRFSLSVPR	ETIEESLAEF	TEQFNQLHNR	RNENLQLGPL	GRDPPQECST	60
61	FSPTDSGEEP	QQLSPGVQFQ	RRQNRRFSM	EDVSKRLSLP	MDIRLPQEF	QKLQMESPD	120
121	PKPLSRMSR	ASLSDIGFGK	LETYVKLDKL	GEGTYATVFK	GRSKLTENLV	ALKEIRLEHE	180
181	EGAPCTAIR	VSLLNKLNKHA	NIVTLHDLIH	HTDRSLTLVF	YLDSDLKQYL	DHCGNLM SMH	240
241	NVKIFMFQLL	RGLAYCHHRK	ILHRDLKPQN	LLINER GELK	LADFLARAK	SVPTKTYSNE	300
301	VVTLWYRPPD	VLLGSTEYST	PIDMWGVC	IHYEMATGRPL	FPGSTVKEEL	HLIFRLLGTP	360
361	TEETWPGVTA	FSEFR TYSFP	CYLPQPLINH	APRLDTDGIH	LLSLLLYES	KSRMSAEAA	420
421	SHSYFRSLGE	RVHQLEDTAS	IFSLKEIQLQ	KDPGYRGLAF	QQPGRGKNRR	QSIF	480

blue: CDK18 sequence expressed in recombinant protein

¹NCBI/Protein accession number NP_997667.1

GST-CycY Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQ SMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP EML	KMFKDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI P QID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHG	RDSLEVLFGQ	240
241	PLAMVMGNTT	SCCVSSPKL	RRNAHSRLES	YRPD T DLSRE	DTGCNLQHIS	DRENIDDLNM	300
301	EFNPSDHPRA	STIFLSKSQT	DVREKRKSLF	INHHPPGQIA	RKYSSCSTIF	LDDSTVSQPN	360
361	LKYTIKCV AL	AIYYHIKNRD	PDGRMLLDIF	DENLHPLSKS	EVPPDYDKHN	PEQKQIYRFV	420
421	RTLFSAAQLT	AECAIVTLVY	LERLLTYAEI	DICPANWKRI	VLGAILLASK	VWDDQAVWNV	480
481	DYQCILKDI T	VEDMNELE RQ	FLELLQFNIN	VPSSVYAKYY	FDLRSLAEAN	NLSFPLEPLS	540
541	RERAKLEAT	SRMCEKDYKD	LRRSARKRSA	SADNLTLP RW	SPAIIS		600

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

CycY wt ² Amino Acid Sequence							
1	MGNTTSCCVS	SSPKLRRNAH	SRLESYRPDT	DLSREDTGCN	LQHISDRENI	DDLNMEFNPS	60
61	DHPRASTIFL	SKSQTDVREK	RKSLFINHHP	PGQIARKYSS	CSTIFLDDST	VSQPNLKYTI	120
121	KCVALAIYYH	IKNRDPDGRM	LLDIFDENLH	PLSKSEVPPD	YDKHNPEQKQ	IYRFVRLTFS	180
181	AAQLTAECAI	VTLYLERLL	TYAEIDICPA	NWKRIVLGAI	LLASKVWDDQ	AVWNVDYQCI	240
241	LKDITVEDMN	ELERQFLELL	QFNINVPSSV	YAKYFDLRS	LAEANLSFP	LEPLSRERAH	300
301	KLEAISRLCE	DKYKDLR RSA	RKRSASADNL	TLPRWSPAIIS			360

blue: CycY sequence expressed in recombinant protein

²NCBI/Protein accession number NP_659449.3
HGNC identifier CycY: CCNY

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