

CDK14/CycY Kinase

cyclin dependent kinase 14

Recombinant Human Active Protein Kinase

HGNC Symbol: CDK14

Synonyms: PFTK1, PFTAIRE1

Product No.: 1572-1116-1

Lot: 001

Description: Human CDK14, full length, amino acids M₁-H₄₆₉ (as in [NCBI/Protein](#) entry NP_001274064.1), human CycY, full length, amino acids M₁-S₃₄₁ (as in [NCBI/Protein](#) entry NP_659449.3), both N-terminal GST-HIS₆ fusion proteins with a 3C cleavage site, co-expressed in Sf9 insect cells

Product identity: CDK14/CycY Lot 001, was confirmed as CDK14/CycY by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{GST-CDK14}: 81,146 Da

Theoretical MW_{GST-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: 0.704 µg/µl

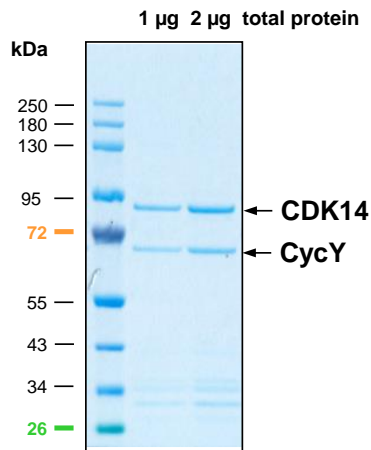
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

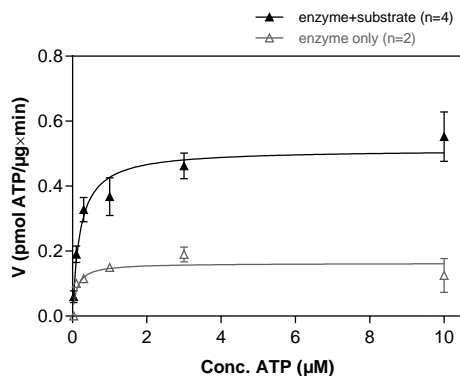
Specific kinase activity (P_i transfer): 0.51 pmol/µg x min

ATP-K_M: 0.2 µM

CDK14/CycY Lot 001: Coomassie stain



CDK14/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-IRStide 80 µg/ml
- Kinase: 4 µg/ml

- Filter binding assay
- MSFC membrane

Recombinant Proteins

CDK14/CycY

Product No.: 1572-1116-1

Recombinant Proteins

GST-CDK14 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	KMFKDR LCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI PQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMG HHHHHG	RDS LEVLFGQ	240
241	PMCDLIEPQ	AEKIGKMKL	RRTLSEFSR	IALKKDDTTF	DEICVTKMST	RNCQGMDSVI	300
301	KPLDTIPEDK	KVRVQRTQST	FDPFEKPA	NQVKRVHSE	NCINFKTSSTG	KESPKVRRHS	360
361	SPSSPTSPKF	GKADSYEKLE	KLGE GSYATV	YK GSKVNGK	LVALKVIRLQ	EEEGTPFTAI	420
421	REASLLKGLK	HANIVLLHDI	IHTKETLTLV	FEYVHTDLCQ	YMDKHPGGLH	PDNVKFLFLQ	480
481	LLRGLSYIHQ	RYILHRDLKP	QNLLISDTGE	LKLADFGLAR	AKSVPSHTYS	NEVVT LWYRP	540
541	PDVLLGST EY	STCLDMWGVG	CIFVEMIQGV	AAFPGMKDIQ	DQLERIFLVL	GTPNEDTWPG	600
601	VHSLPHFKPE	RFTLYSSKNL	RQAWNKLSYV	NHAEDLASKL	LQCS PKNRLS	AQAALSHEYF	660
661	SDLPPRLWEL	TDMSSIFTVP	NVRLQPEAGE	SMRAF GKNS	YGKSLSNSKH		720

1-218: GST **Red:** HIS6-tag **Green:** 3C cleavage site **blue:** CDK14

CDK14 wt¹ Amino Acid Sequence

1	MCDLIEPQPA	EKIGKMKLR	RRTLSEFSRI	ALKKDDTTFD	EICVTKMSTR	NCQGMDSVIK	60
61	PLDTIPEDKK	VRVQRTQSTF	DPFEKPA	NQVKRVHSE	NCINFKTSSTGK	ESPKVRRHSS	120
121	PSSPTSPKFG	KADSYEKLEK	LGE GSYATVY	KGKSKVNGKL	VALKVIRLQEQ	EEGTPFTAIR	180
181	EASLLKGLKH	HANIVLLHDI	IHTKETLTLVF	EYVHTDLCQY	MDKHPGGLHP	DNVKFLFLQL	240
241	LRGLSYIHQR	YILHRDLKPQ	NLLISDTGEL	KLADFGLARA	KSVPSHTYSN	EVVTLWYRPP	300
301	DVLLGSTEYS	TCLDMWGVGC	IFVEMIQGVA	AFPGMKDIQD	QLERIFLVLG	TPNEDTWPGV	360
361	HSLPHFKPER	FTLYSSKNLR	QAWNKLSYVN	HAEDLASKLL	QCS PKNRLSA	QAALSHEYFS	420
421	DLPPRLWELT	DMSSIFTVPN	VRLQPEAGES	MRAF GKNSY	GKSLSNSKH		480

blue: CDK14 sequence expressed in recombinant protein

¹[NCBI/Protein](#) accession number NP_001274064.1
A100B: SNP variation see [NCBI/dbSNP](#) ID: rs0000000

GST-CycY 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	KMFKDR LCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI PQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMG HHHHHG	RDS LEVLFGQ	240
241	PLAMVMGNTT	SCCVSSPKL	RRNAHSRLES	YRPD TDL SRE	DTGCNLQHIS	DRENIDDLNM	300
301	EFNPSDH PRA	STIFLSKSQT	DVREKRKSLF	INHHPPGQIA	RKYSSCSTIF	LDDSTV SQPN	360
361	LKYTIKVAL	AIYYHIKNRD	PDGRMLLDIF	DENLHPLSKS	EVPPDYDKHN	PEQKQIYRFV	420
421	RTLFSAAQLT	AECAIVTLVY	LERLLTYAEI	DICPANWKRI	VLGAILLASK	VWDDQAVWNV	480
481	DYQILK DIT	VEDMNELE RQ	FLELLQFNIN	VPSSVYAKYY	FDLRSLAEAN	NLSFPLEPLS	540
541	RERAHKLEAI	SRLCEDKYKD	LRRSARKRSA	SADNLTLP RW	SPAIIS		600

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

CycY wt² Amino Acid Sequence

1	MGNTTSCCVS	SSPKLRRNAH	SRLESYRPDT	DLSREDTGCN	LQHISDRENI	DDLNMEFNPS	60
61	DHPRASTIFL	SKSQTDVREK	RKSLFINHHP	PGQIARKYSS	CSTIFLDDST	VSQPNLKYTI	120
121	KCV ALAIYYH	IKNRDPDGRM	LLDIFDENLH	PLSKSEVPPD	YDKHNPEQKQ	IYRFVRTLFS	180
181	AAQLTAECAI	VTLVYLERLL	TYAEIDICPA	NWKRIVLGAI	LLASKVWDDQ	AVWNV DYCQI	240
241	LKDITVEDMN	ELERQFLELL	QFNINVPSSV	YAKYYFDLRS	LAEANNSLFF	LEPLSRERAH	300
301	KLEAISRLCE	DKYKDLRRSA	RKRSASADNL	TLPRWSPAIIS			360

blue: CycY sequence expressed in recombinant protein

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

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