

ProQinase™ CDK1/CycE2

cyclin dependent kinase 1

Recombinant Human Active Protein Kinase

HGNC Symbol: CDK1

Synonyms: CDC2

Product No.: 0134-2123-1

Lot: 001

Description: Human CDK1, full length, amino acids M₁-M₂₉₇ (as in [NCBI/Protein](#) entry NP_000177.1), N-terminal GST-HIS₆ fusion protein with a Thrombin cleavage site, and human CycE2, full length, amino acids M1-H404 (as in [NCBI/Protein](#) entry NP_477097.1), N-terminal GST-HIS₆ fusion protein with a 3C cleavage site expressed in Sf9 insect cells

Product identity: CDK1/CycE2 Lot 001, has been verified by mass spectrometry LC-ESI-MS/MS

Theoretical MW _{GST-CDK1} :	63882	Da
Theoretical MW _{GST-CycE2} :	74847	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

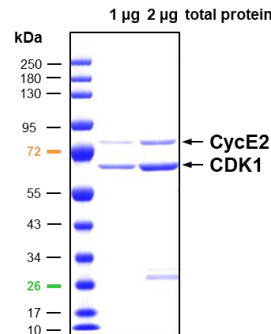
For complete recovery, mix well and spin before use. Product must not be stored in diluted solutions, aliquots below 10 µl are not advisable. Avoid repeated freeze-thaw cycles!

Protein concentration: 0.473 µg/µl
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

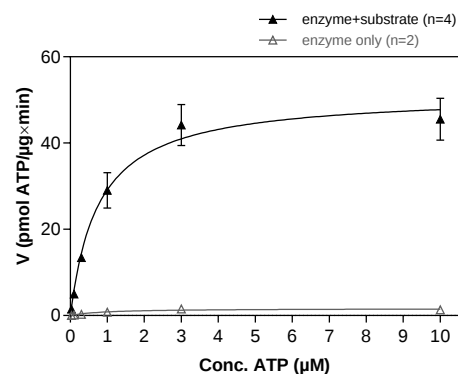
Biochemical Parameters:

Specific kinase activity (P_i transfer): 51 pmol/µg*min
ATP-K_M: 0.8 µM

CDK1/CycE2 Lot 001:
Coomassie stain



CDK1/CycE2 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 80 µg/ml
 - Kinase: 0.5 µg/ml

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

Sequence information

GST-CDK1 Recombinant Fusion Protein Amino Acid Sequence

1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLIERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPOID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHHG	RRRASVAAGI	240
241	LVPRGSPGLD	GICSIEEFTM	EDYTKIEKIG	EGTYGVVYKG	RHKTGTQVVA	MKKIRLESGE	300
301	EGVPSTAIRES	ISLLKELRHP	NIVSLQDVLM	QDSRLYLIFE	FLSMDLKKYL	DSIPPGQYMD	360
361	SSLVKSILYQ	ILQGVFCHS	RRVLHRDLKP	QNLLIDDKGT	IKLADFGGLAR	AFGIPIRVYT	420
421	HEVVTLLWYRS	PEVLLGSARY	STPVDIWSIG	TIFAELATKK	PLFHGDSEID	QLFRIFRALG	480
481	TPNNEVWPEV	ESLQDYKNTF	PKWKPGSLAS	HVKNLDENGL	DLLSKMLIYD	PAKRISGKMA	540
541	LNHPYFNDLD	NQIKKM					600

1-218: GST Red: HIS6-tag Pink: Thrombin cleavage site blue: CDK1

CDK1 wt¹ Amino Acid Sequence

1	MEDYTKIEKI	GEGTYGVVYK	GRHKTGTQVV	AMKKIRLESE	EEGVPSTAIR	EISLLKELRH	60
61	PNIVSLQDVL	MQDSRLYLIF	EFLSMDLKKY	LDSIPPGQYM	DSSLVKSILY	QILQGVFCH	120
121	SRRVLHRDLK	PQNLLIDDKG	TIKLADFGGLA	RAFGIPIRVY	THEVVTLLWYR	SPEVLLGSAR	180
181	YSTPVDIWSI	GTIFAELATK	KPLFHGDSEI	DQLFRIFRAL	GTPNNEVWPE	VESLQDYKNT	240
241	FPKWKPGSLA	SHVKNLDENG	LDLLSKMLIY	DPAKRISGKM	ALNHPYFNDL	DNQIKKM	300

blue: CDK1 sequence expressed in recombinant protein

¹[NCBI/Protein](#) accession number NP_001777.1

GST-CycE2 Recombinant Fusion Protein Amino Acid Sequence

1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLIERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPOID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHHG	RDSLEVLFCG	240
241	PMSSRRSSRLQ	AKQPPQPSQT	ESPQEAQIIQ	AKKRKTQDV	KKRREEVTKK	HQYEIRNCWP	300
301	PVLSGGISPC	IIETPHKEI	GTSDFSRFTN	YRFKNLFINP	SPLPDLSWG	SKEVWLNMLK	360
361	KESRYVHDKH	FEVLHSDLEP	QMSILLDWL	LEVCEVYTLH	RETFYLAQDF	FDRFMLTQKD	420
421	INKNMLQLIG	ITSLFIASKL	EIYAPKLQE	FAYVTDGACS	EEDILRMELI	ILKALKWELC	480
481	PVTIISWNLN	FLQVDALKDA	PKVLLPQYSQ	ETFIQIAQLL	DLCLALDSL	EFQYRILTAA	540
541	ALCHFTSIEV	VKKASGLEWD	SISECDWMV	PFVNVVKSTS	PVKLKTFFKI	PMEDRHNIQT	600
601	HTNYLAMLEE	VNYINTFRKG	QQLSPVCNGG	IMTPPKSTEK	PPGKH		660

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: CycE2

CycE2 wt² Amino Acid Sequence

1	MSRRSSRLQA	KQPPQPSQTE	SPQEAQIIQA	KKRKTQDVK	KRREEVTKKH	QYEIRNCWPP	60
61	VLSGGISPCI	IIETPHKEIG	TSDFSRTNY	RFKNLFINPS	PLPDLSWGCS	KEVWLNMLKK	120
121	ESRYVHDKHF	EVLHSDLEPQ	MRSILLDWLL	EVCEVYTLHR	ETFYLAQDF	DRFMLTQKDI	180
181	NKNMLQLIGI	TSLFIASKLE	EIYAPKLQEF	AYVTDGACSE	EDILRMELII	LKALKWELCP	240
241	VTIISWNLNF	LQVDALKDAP	KVLLPQYSQE	TFIQIAQLLD	LCILALDSLE	FQYRILTAAA	300
301	LCHFTSIEVV	KKASGLEWDS	ISECDWMV	FVNVVKSTSP	VKLKTFKKIP	MEDRHNIQTH	360
361	TNYLAMLEEV	NYINTFRKGG	QLSPVCNGGI	MTPPKSTEK	PGKH		420

blue: CycE2 sequence expressed in recombinant protein

²[NCBI/Protein](#) accession number NP_477097.1

[HGNC](#) identifier CycE2: CCNE2