

CDK7/CycH/MAT1

cyclin dependent kinase 7

Recombinant Human Active Protein Kinase

HGNC Symbol: CDK7

Synonyms: CAK1; CDKN7; STK1

Product No.: 0366-0360-4

Lot: 002

Description: Human CDK7, amino acids M₁-F₃₄₆ (as in [NCBI/Protein](#) entry NP_001790.1), N-terminal GST-HIS₆ fusion protein with a Thrombin cleavage site, human CycH, amino acids M₁-L₃₂₃ (as in [NCBI/Protein](#) entry NP_001230.1), N-terminally fused to HIS₆-Thrombin cleavage site and human MAT1, amino acids M₁-S₃₀₆ (as in [NCBI/Protein](#) entry NP_002422.1), N-terminally fused to HIS₆-Thrombin cleavage site, coexpressed in Sf9 insect cells

Product identity: CDK7/CycH/MAT1 Lot 002 was confirmed as CDK7/CycH/MAT1 by specific Western Blotting

Theoretical MW_{GST-CDK7}: 68,934 Da

Theoretical MW_{CycH}: 42,400 Da

Theoretical MW_{MAT1}: 40,579 Da

Expression host: Sf9 insect cells

Purification: GST-Affinity Chromatography

Activation: This kinase was not activated by special procedures

Storage buffer: 50 mM TRIS-HCl pH 8.0, 100 mM NaCl, 5 mM DTT, 4 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: 0.139 µg/µl

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

Biochemical Parameters:

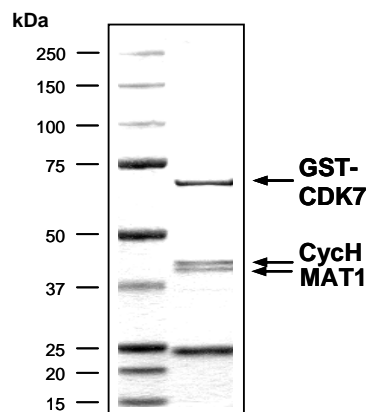
Specific kinase activity (P_i transfer): 22 pmol/µg × min

ATP-K_M: 4.1 µM

Additional assay technology:

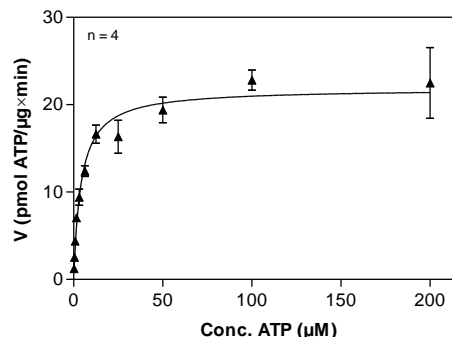
CDK7/CycH/MAT1 Lot 002 was also successfully tested by ProQinase for the use with the ADP-Glo™ Kinase assay from Promega ADP-Glo assay conditions may vary from radiometric assay conditions, please inquire for assay details

CDK7/CycH/MAT1 Lot 002:
Coomassie stain



2.0 µg CDK7/CycH/MAT1

CDK7/CycH/MAT1 Lot 002:
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: RB-CTF, 200 µg/ml
 - CDK7/CycH/MAT1: 4 µg/ml
- Filter binding assay
- MSFC membrane (Millipore)

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CDK7/CycH/MAT1

Product No.: 0366-0360-4

GST-CDK7 Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI	PQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHH	240
241	RRRASVAAGI						
241	LVPRG	PGLD	GIYARGIQAS	MALDVKSRAK	RYEKLDLGE	GQFATVYKAR	300
301	DKNTNQIVAI						
301	KKIKLHRSE	AKDGINRTAL	REIKLLQELS	HPNIIGLLDA	FGHKSNI	SLV	360
361	FDFMETDLEV						
361	IIKDNSL	VLT	PSHIKAYMLM	TLQGLEYLHQ	HWILHRDLK	NNLLDENG	420
421	V						
421	SFGSPN	RAYT	HQVVTRWYRA	PELLFGARMY	GVGVD	MWAVG	480
481	CILAE	LLLRV	PFLPGDSDLD	QLTRIFETLG	TPTEE	QWPD	540
541	CARITATQAL	KMKYFSNRPG	PTPGCQLPRP	NCPVETLKEQ	SNPALAIK	RK	600
601	RTEALEQGL						
601	PKKLIF						660

1-218: GST Red: HIS6-tag Pink: Thrombin cleavage site blue: CDK7

CDK7 wt ¹ Amino Acid Sequence							
1	MALDVKSRAK	RYEKLDLGE	GQFATVYKAR	DKNTNQIVAI	KKIKLHRSE	AKDGINRTAL	60
61	REIKLLQELS	HPNIIGLLDA	FGHKSNI	SLV	FDFMETDLEV	IIKDNSL	120
121	VLT	PSHIKAYMLM	TLQGLEYLHQ	HWILHRDLK	NNLLDENG	V	180
181	SFGSPN	RAYT	HQVVTRWYRA	PELLFGARMY	GVGVD	MWAVG	240
241	CILAE	LLLRV	PFLPGDSDLD	QLTRIFETLG	TPTEE	QWPD	300
301	CARITATQAL	KMKYFSNRPG	PTPGCQLPRP	NCPVETLKEQ	SNPALAIK	RK	360
301	RTEALEQGL						
301	PKKLIF						360

blue: CDK7 sequence expressed in recombinant protein

¹[NCBI/Protein](#) accession number NP_001790.1

CycH Recombinant Fusion Protein Amino Acid Sequence							
1	MSPIDPMGHH	HHHHGRRRAS	VAAGILVPRG	SPGLDGIYAR	GIQASMYHNS	SQKRHWTFSS	60
61	EEQLARLRAD	ANRKFRC	KAV	ANGKVL	PNDP	VFLEPHEEMT	120
121	LCKYYEKRL	L	EFCSVFKPAM	PRSVVGTACM	YFKRFYLN	S	180
181	VMEYHPRIIM	LTCAFLACKV	DEFNVSSPQF	VGNLRESPLG	QEKALEQILE	YELLIQQLN	240
241	FHLIVHNPYR	PFEGFLIDLK	TRYPILNPE	ILRKTADDFL	NRIALTDAYL	LYTPSQIALT	300
301	AILSSASRAG	ITMESYLSES	LMLKENRTCL	SQLLDIMKSM	RNLVKKYEP	RSEEVAVLKQ	360
361	KLERCHSAEL	ALNVITKKRK	GYEDDDYVSK	KSKHEEEW	DDDLVESL		420

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

CycH wt ¹ Amino Acid Sequence							
1	MYHNSSQKRH	WTFSS	EEQLA	RLRADANRKF	RCKAVANGKV	LPNDPVFLEP	60
61	HEEMTLCKYY	EKRLLEFCSV	FKPAMPRSVV	GTACMYFKRF	YLNNVMEYH	PRIIMLTCAF	120
121	LACKVDEFNV	SSPQFVGNLR	ESPLGQEKAL	EQILEYELL	IQQLNFHLIV	HNPYRPFEGE	180
181	LIDLKTRYPI	LENPEILRKT	ADDFLNRIAL	TDAYLLYTPS	QIALTAILSS	ASRAGITMES	240
241	YLSESLMLKE	NRTCLSQLLD	IMKSMRNLVK	KYEP	RSEEV	AVLKQKLERC	300
301	HSAELALNVI	TKKRKGYEDD					
301	ESL						360

blue: CycH sequence expressed in recombinant protein

¹[NCBI/Protein](#) accession number NP_001230.1

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MAT1 Recombinant Fusion Protein Amino Acid Sequence

1	MSPIDPMG HH HHHH GRRRAS VAAGIL LVPRG S PGLDGIYAR GIQAS MDDQG CPRCKT TKYR	60
61	NPSL KLMVNV CGHT LCESCV DLLF VRGAGN CPEC GTPLRK SNFR VQLFED PTVD KEVEIR	120
121	KKVL KIYNKR EEDF PSLREY NDFL EEVEEI VFNL TNNVDL DNTK KKMEIY QKEN KDVIQK	180
181	NK KL TREQE ELEE ALEVER QENE QRRFI QKEE QLQQIL KRKN QAFLD ELESS DLPVA	240
241	LL LAQH KDRS TQLE MQLEKP KPVK PVTFST GKMG QHISL APIH KLEEAL YEQP LQIET	300
301	YGPH VPELEM LGRL GYLNHV RAAS PQDLAG GYTSS LACHR ALQD AFSGLF WQPS	360

1-218: GST **Red**: HIS6-tag **Pink**: Thrombin cleavage site **blue**: MAT1

MAT1 wt¹ Amino Acid Sequence

1	MDDQ GCPRCK TTKY RNPSLK LMVN VCGHTL CESC VDLLFV RGAG NCPECG TPLR KS NFRV	60
61	QLFE DPTV DK EVEI RKKVLK IYNK REDFP SLRE YDNFLE EVEE I VFNLT NNVD LDNTKK	120
121	KMEI YQENK DVIQ KNK LKL TREQ EELEEA LEVER QENEQ RRLF IQKEEQ LQQI LKRK KNK	180
181	QAF LDELESS DLPV ALLLAQ HKDR STQLEM QLEK PKPV KP VTFST GIKMG QHIS LAPI HK	240
241	LEE ALYEQP LQI ETYGPHV PELE MLGRLG YLNH VRAASP QDLA GGYTSS LACH RALQDA	300
301	FSGL FWQPS	360

blue: MAT1 sequence expressed in recombinant protein

¹[NCBI/Protein](#) accession number NP_002422.1

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