

ProQinase™ 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:

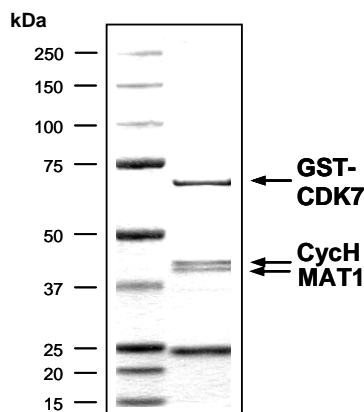
Specific kinase activity (P_i transfer): 22 pmol/µg × min

ATP-K_M: 4.1 µM

Additional assay technology:

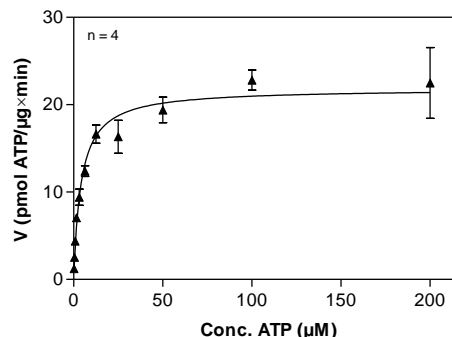
CDK7/CycH/MAT1 Lot 002 was also successfully tested by Reaction Biology for the use with the ADP-Glo™ Kinase assay from Promega ADP-Glo assay conditions may vary from radiometric assay conditions, please inquire for assay details

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)

ProQinase™ 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 EML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI PQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMG HHHHHG	RRRASVAAGI	240
241	LVPRG SPGLD	GIYARGIQAS	MALDVKSRAK	RYEKLDLFLGE	GQFATVYKAR	DKNTNQIVAI	300
301	KKIKLGRSE	AKDGINRTAL	REIKLLQELS	HPNIIGLLDA	FGHKSNI SLV	PDFMETDLEV	360
361	IIKDNSLVLT	PSHIKAYMLM	TLQGLEYLHQ	HWILHRDLKP	NNLLDENG V	LKLADFGLAK	420
421	SFGSPNRAYT	HQVVTRWYRA	PELLFGARMY	GVGVD MWAVG	CILAE LLLRV	PFLPGDS DLD	480
481	QLTRIFETLG	TPTEE QWPDM	CSLPDYVTFK	SFPGIPLHHI	FSAAGD DLD	LIQGLFLFNP	540
541	CARITATQAL	KMKYFSNRPG	PTPGCQLPRP	NCPVETLKEQ	SNPALAIK RK	RTEALEQGL	600
601	PKKLIF						660

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

CDK7 wt ¹ Amino Acid Sequence							
1	MALDVKSRAK	RYEKLDLFLGE	GQFATVYKAR	DKNTNQIVAI	KKIKLGRSE	AKDGINRTAL	60
61	REIKLLQELS	HPNIIGLLDA	FGHKSNI SLV	PDFMETDLEV	IIKDNSLVLT	PSHIKAYMLM	120
121	TLQGLEYLHQ	HWILHRDLKP	NNLLDENG V	LKLADFGLAK	SFGSPNRAYT	HQVVTRWYRA	180
181	PELLFGARMY	GVGVD MWAVG	CILAE LLLRV	PFLPGDS DLD	QLTRIFETLG	TPTEE QWPDM	240
241	CSLPDYVTFK	SFPGIPLHHI	FSAAGD DLD	LIQGLFLFNP	CARITATQAL	KMKYFSNRPG	300
301	PTPGCQLPRP	NCPVETLKEQ	SNPALAIK RK	RTEALEQGL	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	MSPIDPMG HH	HHHH GRRRAS	VAAGI LVPRG	SPGLDGIYAR	GIQAS MYHNS	SQKRHWTFSS	60
61	EEQLARLRAD	ANRKFRC KAV	ANGKVL PNDP	VFLEPHEEMT	LCKYYEKRL L	EFCSVFKPAM	120
121	PRSVVGTACM	YFKRFYLNNS	VMEYHPRIIM	LTC AFLACKV	DEFNVSSPQF	VGNLRESPLG	180
181	QEKALEQILE	YELLIQQLN	FHLIVHNPYR	PFEGFLIDLK	TRYPIL ENPE	ILRKTADDFL	240
241	NRIALTDAYL	LYTPSQIALT	AILSSASRAG	ITMESYLSES	LMLKENRTCL	SQLLDIMKSM	300
301	RNLVKKYEP	RSEEVAVLKQ	KLERCHSAEL	ALNVITKRRK	GYEDDDYVSK	KSKHEEEEW T	360
361	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	HEEMTLCKYY	60
61	EKRLLEFC SV	FKPAMP RSVV	GTACMYFKRF	YLNNSVMEYH	PRIIMLTCAF	LACKVDEFNV	120
121	SSPQFVGNLR	ESPLGQEKAL	EQILEYELL	IQQLNFHLIV	HNPYRPFEGE	LIDLKTRYPI	180
181	LENPEILRKT	ADDFLNRIAL	TDAYLLYTPS	QIALTAILSS	ASRAGITMES	YLSSESLMLKE	240
241	NRTCLSQLLD	IMKSMRNLVK	KYEP RSEEV	AVLKQKLERC	HSAELALNVI	TKKRKGYEDD	300
301	DYVSKKSKHE	EEEW TDDDLV	ESL				360

blue: CycH sequence expressed in recombinant protein

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

MAT1 Recombinant Fusion Protein Amino Acid Sequence

1	MSPIDPMGHH HHHHGRRRAS VAAGILVPRG SPGLDGIYAR GIQASMDDQG CPRCKTTKYR	60
61	NPSLKLMVNV CGHTLCEVCV DLLFVRGAGN CPECGTPLRK SNFRVQLFED PTVDKVEVEIR	120
121	KKVLKIYNKR EEDFPSLREY NDFLEEVVEI VFNLTNVNDL DNTKKKMEIY QKENKDVIQK	180
181	NKIKLTREQE ELEEALVEVER QENEQRRLFI QKEEQLOQIL KRKNKQAFD ELESSDLPVA	240
241	LLLAQHKDRS TQLEMQLEKP KPVKPVTFST GIKMGQHISL APIHKLEAL YEYQPLQIET	300
301	YGPHVPELEM LGRLGYLNHV RAASQDLG GYTSSLACHR ALQDAFSGLF WQPS	360

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

MAT1 wt¹ Amino Acid Sequence

1	MDDQGCPRCK TTKYRNPSLK LMVNVCGHTL CESCVDLLFV RGAGNCPECG TPLRKSNFRV	60
61	QLFEDPTVDK EVEIRKKVLK IYNKREDFP SLREYDFLE EVEEIVFNLN NVDDLNTKK	120
121	KMEIYQKENK DVIQKNKLLK TREQEELEEA LEVERQENEQ RRLFIQKEEQ LQQILKRKNK	180
181	QAFDLEESS DLPVALLLAQ HKDRSTQLEM QLEKPKPVKP VTFSTGIKMG QHISLAPIHK	240
241	LEEALYEQP LQIETYGPHV PELEMLGRLG YLNHVRAASP QDLAGGYTSS LACHRALQDA	300
301	FSGLFWQPS	360

blue: MAT1 sequence expressed in recombinant protein

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