

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: 005

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 mass spectrometry LC-ESI-MS/MS

Theoretical MW _{GST-CDK7} :	68934	Da
Theoretical MW _{HIS-CycH} :	42400	Da
Theoretical MW _{HIS-MAT1} :	40579	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

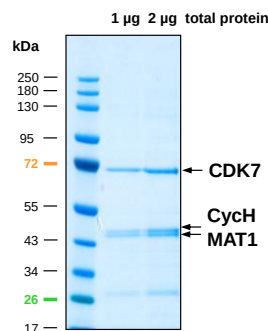
For complete recovery, mix well and spin before use. Product must not be stored in diluted solutions, aliquots below 10 µl are not advisable. Avoid repeated freeze-thaw cycles!

Protein concentration: 0.255 µg/µl
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

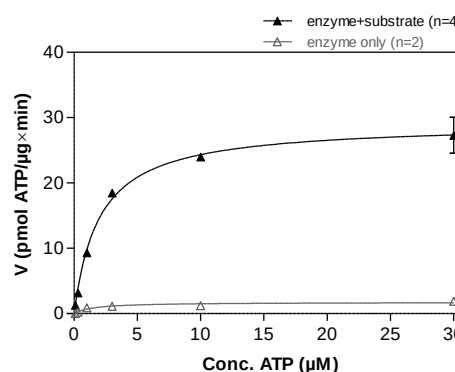
Biochemical Parameters:

Specific kinase activity (P_i transfer): 29 pmol/µg*min
ATP-K_M: 2 µM

CDK7/CycH/MAT1 Lot005:
Coomassie stain



CDK7/CycH/MAT1 Lot005:
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 40 µg/ml
 - Kinase: 1 µg/ml

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

Sequence information

GST-CDK7 Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLIERDEGDK	WRNKKFELGL	EFNLPYYID	60
61	GDVKLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSR	YSKDFETLKV	120
121	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPIQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHHG	RRRASVAAGI	240
241	LVPRGSPGLD	GIYARGIQAS	MALDVKSRAK	RYEKLDLFLGE	GQFATVYKAR	DKNTNQIVAI	300
301	KKIKLGHRSE	AKDGINRTAL	REIKLLQELS	HPNIIGLLDA	FGHKSNI	SLV FDFMETDLEV	360
361	IIKDNSLVLT	PSHIKAYMLM	TLQGLEYLHQ	HWILHRDLKP	NNLLDENG	V LKLADFG	420
421	SFGSPNRAYT	HQVVTRWYRA	PELLFGARMY	GVGVDMWAVG	CILAE	LLRV PFLPGDS	480
481	QLTRIFETLG	TPTEEQWPDM	CSLPDYVTFK	SFPGIPLHHI	FSAAGD	LLD LIQGLFL	540
541	CARITATQAL	KMKYFSNRPG	PTPGCQLPRP	NCPVETLKEQ	SNPALAIK	RK RTEALEQ	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	KKIKLGHRSE	AKDGINRTAL	60
61	REIKLLQELS	HPNIIGLLDA	FGHKSNI	SLV FDFMETDLEV	IIKDNSLVLT	PSHIKAYMLM	120
121	TLQGLEYLHQ	HWILHRDLKP	NNLLDENG	V LKLADFG	LAK SFGSPN	RAYT HQVVTR	180
181	PELLFGARMY	GVGVDMWAVG	CILAE	LLRV PFLPGDS	DL DQLTRIF	ETLG TPTEE	240
241	CSLPDYVTFK	SFPGIPLHHI	FSAAGD	LLD LIQGLFL	FNP CARITAT	QAL KMKYFS	300
301	PTPGCQLPRP	NCPVETLKEQ	SNPALAIK	RK RTEALEQ	GGL 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 VFLEPHE	MT LCKYYEK	RLL EFCSVFK	120
121	PRSVVG	TACM YFKRFY	LNS VMEYHP	RIIM LTCAFL	ACKV DEFNV	SSPQF VGNL	180
181	QEKALEQILE	YELLIIQQLN	FHLIVHNPYR	PFEGFLIDLK	TRYPIL	ENPE ILRKTAD	240
241	NRIALTDAYL	LYTPSQIALT	AILSSASRAG	ITMESYLS	ES LMLKEN	RTCL SQLLD	300
301	RNLVKKYEPP	RSEEVAVLKQ	KLERCHSAEL	ALNVITK	KRK GYEDDDY	VSK KSKHEEE	360
361	DDDLVESL						420

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

CycH wt ² Amino Acid Sequence							
1	MYHNSSQKRH	WTFSS	EEQLA RLRADAN	RKF RCKAVANG	KV LPNDPV	FLEP HEEMTL	60
61	EKRLL	EFCSV FK	PAMPRSVV	GTACMYFK	RF YLNN	SVMEYH PRIIM	120
121	SSPQFVGNLR	ESPLGQEKAL	EQILEYELL	IQQLNFHLIV	HNPYRPF	EGF LIDLK	180
181	LENPEILRKT	ADDLFLNR	IAL TDAYLLY	TPS QIALTAIL	SS ASRAGIT	MES YLSES	240
241	NRTCLS	QLLD IMKSMR	NLVK KYEPPR	SEEV AVLKQK	LERC HSAELAL	NVI TKKRK	300
301	DYVSKKSKHE	EEEWTD	DDLV ESL				360

blue: CycH sequence expressed in recombinant protein

²[NCBI/Protein](#) accession number NP_001230.1

[HGNC](#) identifier CycH: CCNH

MAT1 Recombinant Fusion Protein Amino Acid Sequence

1	MSPIDPMGHH	HHHHGRRRAS	VAAGILVPRG	SPGLDGIYAR	GIQAS	MDDQG	CPRCKTTKYR	60
61	NPSLKLMVNV	CGHTLCESC	V DLLFVRGAGN	CPEC	GTPLRK	SNFRVQLFED	PTVDKEVEIR	120
121	KKVLKIYNKR	EEDFPSLREY	NDFLEEV	EII VFNL	TNNVDL	DNTKKKMEIY	QKENKDVIQK	180
181	NKCLKLTREQE	ELEEAL	EVER QENE	QRRLEFI	QKEEQ	LQQIL KRKNKQAF	LD ELESSDLPVA	240
241	LLLAQH	KDRS TQLEM	QLEKP KPV	KPVTFST	GIKMGQHISL	APIHKLEEAL	YEYQPLQIET	300
301	YGP	HVPELEM	LGRLGYLNHV	RAAS	PQDLG	GYTSSLACHR	ALQDAFSGLF	WQPS 360

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

MAT1 wt³ Amino Acid Sequence

1	MDDQGCPRCK	TTYRNP	SLK	LMVNV	CGHTL	CESC	VDLLFV	RGAGNC	PECG	TPLRKS	NFRV	60
61	QLFEDPTVDK	EVEIRK	KVLK	IYNK	REEDFP	SLREY	NDFLE	EVEEIV	FNLT	NNVDLD	NTKK	120
121	KMEIYQKENK	DVIQKN	KLKL	TREQ	EELEEA	LEVERQ	ENEQ	RRLFI	QKEEQ	LQQIL	KRKNK	180
181	QAFLELESS	DLPVALLA	Q	HKDR	STQLEM	QLEK	PKPVKP	VTFST	GIKMG	QHISL	APIHK	240
241	LEEALYEQP	LQIETY	GPHV	PELEML	GRLG	YLNHV	RAASP	QDLAG	GYTSS	LACHRAL	QDA	300
301	FSGLF	WQPS										360

blue: MAT1 sequence expressed in recombinant protein

³[NCBI/Protein](#) accession number NP_002422.1

[HGNC](#) identifier MAT1: MNAT1