

MARK1

MAP/microtubule affinity-regulating kinase 1

Recombinant Human Active Protein Kinase

HGNC Symbol: MARK1

Synonyms: MARK, KIAA1477

Product No.: 0432-0000-1

Lot: 001

Description: Human MARK1, full length, amino acids M₁-L₇₈₀ (as in NCBI/Protein entry NP_001273057.1), N-terminal GST-HIS₆ fusion protein with a Thrombin cleavage site, expressed in Sf9 insect cells

Product identity: MARK1 Lot 001, was confirmed as MARK1 by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 117,352 Da

Expression: Baculovirus infected Sf9 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, 4 mM reduced glutathione, 20% glycerol

Storage temperature: -80°C

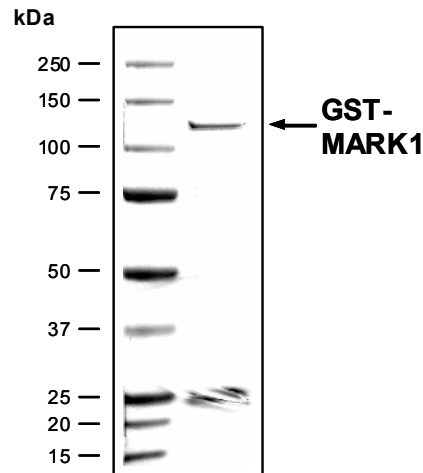
For complete recovery, mix well and spin before use. Product must not be stored in diluted solutions, aliquots below 10µl are not advisable. Avoid repeated freeze-thaw cycles!

Protein concentration: 0.111 µg/µl (Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

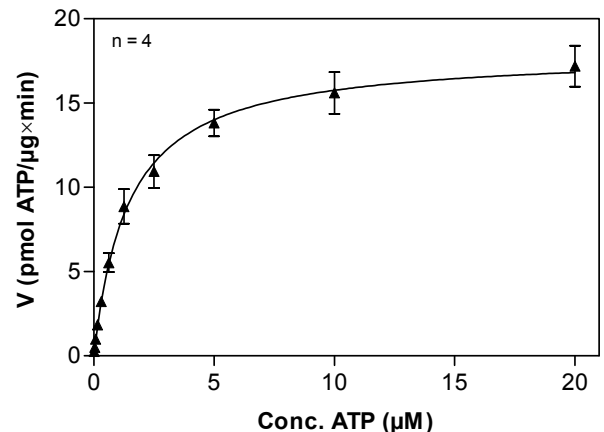
Specific kinase activity (P_i transfer): 18 pmol/µg×min
ATP-K_M: 1.44 µM

**MARK1 Lot 001:
Coomassie stain**



2.0 µg GST-MARK1

**MARK1 Lot 001:
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: CHKtide Peptide, KKKVSRSGLYRSPSPENLNRRP, 5 µg / ml
 - MARK1: 4.0 µg / ml
- Filter binding assay
 - MSFC membrane (Millipore)

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MARK1

Product No.: 0432-0000-1

MARK1 Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMG HHHHHH HG	RRRASVAAGI	240
241	LVPRGS PGLD	GIYARGIQAS	MSARTPLPTV	NERDTENHTS	VDGYTEPHIQ	PTKSSSRQNI	300
301	PRCRNSITSA	TDEQPHIGNY	RLQKTIGKGN	FAKVKLARHV	LTGREVAVKI	IDKTQLNPTS	360
361	LQKLFREVRI	MKILNHPNIV	KLFEVIETEK	TYLYVMEYAS	GGEVFDYLV	HGRMKEKEAR	420
421	AKFRQIVSAV	OYCHQKYIVH	RDLKAENLLL	DGDMNIKIAD	FGFSNEFTVG	NKLDTFCGSP	480
481	PYAAPQLFQ	KKYDGPVVDV	WSLGVILYTL	VSGSLPFDGQ	NLKELRERVL	RGKYRIPFYM	540
541	STDCENLLKK	LLVLNPIKRG	SLEQIMKDRW	MNVGHEEEEL	KPYTEPDFDF	NDTKRIDIMV	600
601	TMGFARDEIN	DALINQKYDE	VMATYILLGR	KPPEFEGGES	LSSGNLCQRS	RPSSDLNNS	660
661	LQSPAHLKVQ	RSISANQKQR	RFSDHAGPSI	PPAVSYTKRP	QANSVESEQK	EEWDKDVARK	720
721	LGSTTVGSKS	EMTASPLVGP	ERKKSSTIPS	NNVYSGGSMA	RRNTYVCERT	TDRYVALQNG	780
781	KDSSLTEMSV	SSISSAGSSV	ASAVPSARPR	HQKSMSTSGH	PIKVTLPTIK	DGSEAYRPGT	840
841	TQVPAASPS	AHSISTATPD	RTRFPRGSSS	RSTFHGEQLR	ERRSVAYNGP	PASPSHETGA	900
901	FAHARRGTST	GIISKITSKF	VRRSTSGEPK	ERDKKEGKDS	KPRSLRFTWS	MKTTSSMDPN	960
961	DMREIRKVL	DANNCDEYQK	ERFLLFCVHG	DARQDSLQVW	EMEVCKLPRL	SLNGVRFKRI	1020
1021	SGTSTIAFKNI	ASKIANELKL					1080

1-218: GST **Red:** HIS6-tag **Pink:** Thrombin cleavage site **blue:** MARK1 **boxed:** variation from RefSeq

MARK1 wt ¹ Amino Acid Sequence							
1	MSARTPLPTV	NERDTENHTS	VDGYTEPHIQ	PTKSSSRQNI	PRCRNSITSA	TDEQPHIGNY	60
61	RLQKTIGKGN	FAKVKLARHV	LTGREVAVKI	IDKTQLNPTS	LQKLFREVRI	MKILNHPNIG	120
121	EVFDYLVAHG	RMKEKEARAK	FRQIVSAVQY	CHQKYIVHRD	LKAENLLLDG	DMNIKIADFG	180
181	FSNEFTVGNK	LDTFCGSPPY	AAPELQFGKK	YDGPVVDVWS	LGVILYTLVS	GSLPFDGQNL	240
241	KELRERVLRG	KYRIPFYMST	DCENLLKLL	VLNPIKRGSL	EQIMKDRWMN	VGHEEEELKP	300
301	YTEPDFDFND	TKRIDIMVTM	GFARDEINDA	LINQKYDEVM	ATYILLGRKP	PEFEGGESLS	360
361	SGNLCQRSRP	SSDLNNSLQ	SPAHLKVQRS	ISANQKQRRF	SDHAGPSIPP	AVSYTKRPQA	420
421	NSVESEQKEE	WDKDVARKLG	STTVGSKSEM	TASPLVGP	PERKKSSTIPSN	VYSGGSMARR	480
481	NTYVCERTTD	RYVALQNGKD	SSLTEMSVSS	ISSAGSSVAS	AVPSARPRHQ	KSMSTSGHPI	540
541	KVTLPTIKDG	SEAYRPGTTQ	RVPAASPSAH	SISTATPDRT	RFPRGSSSRS	TFHGEQLRER	600
601	RSVAYNGPPA	SPSHETGAFA	HARRGTSTGI	ISKITSKFVR	RSTSGEPKER	DKEEGKDSKP	660
661	RSLRFTWSMK	TTSSMDPNDM	MREIRKVLDA	NNCDEYQKER	FLLFCVHGDA	RQDSLQVWEM	720
721	EVCKLPRLSL	NGVRFKRISG	TSIAFKNIAS	KIANELML			780

blue: MARK1 sequence expressed in fusionprotein **Red:** variant in fusionprotein

¹NCBI/Protein accession number NP_001273057.1
M757K variation: see <http://www.uniprot.org/uniprot/Q9P0L2>, sequence BAA96001

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