

## ProQinase™ 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 M<sub>1</sub>-L<sub>780</sub> (as in NCBI/Protein entry NP\_001273057.1), N-terminal GST-HIS<sub>6</sub> 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**<sub>Fusion Protein</sub>: 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

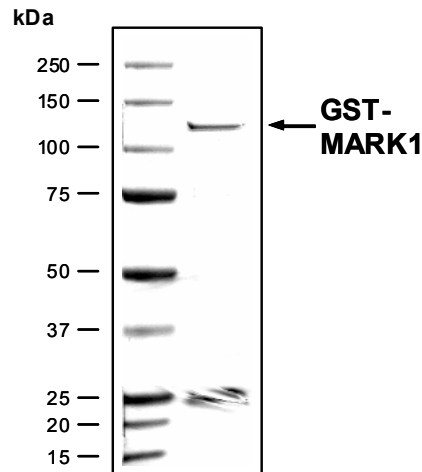
For complete recovery, mix well and spin before use. Product must not be stored in diluted solutions, aliquots below 10µl are not advisable. Avoid repeated freeze-thaw cycles!

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

### Biochemical Parameters:

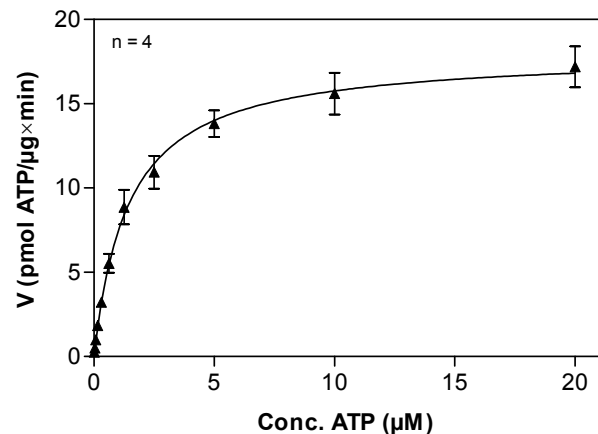
Specific kinase activity (P<sub>i</sub> transfer): 18 pmol/µg×min  
ATP-K<sub>M</sub>: 1.44 µM

### MARK1 Lot 001: Coomassie stain



2.0 µg GST-MARK1

### MARK1 Lot 001: Determination of V<sub>max</sub> and K<sub>M</sub> value for ATP



### Determination of K<sub>M</sub> value & Specific activity:

- Assay conditions:
  - 60 mM HEPES-NaOH, pH 7.5
  - 3 mM MgCl<sub>2</sub>
  - 3 mM MnCl<sub>2</sub>
  - 3 µM Na-orthovanadate
  - 1.2 mM DTT
  - 50 µg / ml PEG<sub>20,000</sub>
  - ATP (variable)
  - Substrate: CHKtide Peptide, KKKVSRSGLYRSPSPENLNRP, 5 µg / ml
  - MARK1: 4.0 µg / ml
- Filter binding assay
  - MSFC membrane (Millipore)

Recombinant Proteins

## ProQinase™ MARK1

Product No.: 0432-0000-1

MARK1 Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQ SMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP EML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI P QID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHHG	RRRASVAAGI	240
241	LVPRGS PGLD	GIYARGIQAS	MSARTPLPTV	NERDTENHTS	VDGYTEPHIQ	PTKSSSRQNI	300
301	PRCRNSITSA	TDEQPHIGNY	RLQKTIGKGN	FAKVKLARHV	LTGREVAVKI	IDKTQLNPTS	360
361	LQKLFREVRI	MKILNHPNIV	KLFEVIETEK	TLYLVM EYAS	GGEVFDYLVA	HGRMKEKEAR	420
421	AKFRQIVSAV	QYCHQKYIVH	RDLKAENLLL	DGDMNIKIAD	FGFSNEFTVG	NKLDTF CGSP	480
481	PYAAP E L F Q G	KKYDGP EVDV	WSLGVILYTL	VSGSLPFDGQ	NLKE LRERVL	RGKYRIPFYM	540
541	STDCENLLKK	LLVLNPIKRG	SLEQIMKDRW	MNVGHEEEEL	KPYTEPDPDF	NDTKRIDIMV	600
601	TMGFARDEIN	DALINQKYDE	VMATYILLGR	KPPEFEGGES	LSSGNLCQRS	RPSSDLNNST	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	TQRVPAASPS	AHSISTATPD	RTRFPRGSSS	RSTFHGEQLR	ERRSVAYNGP	PASPSHETGA	900
901	FAHARRGTST	GIISKITSKF	VRRSTSGEPK	ERDKKEGKDS	KPRSLRFTWS	MKTTSSMDPN	960
961	DMMREIRKVL	DANNC DYE Q K	ERFLLCVHVG	DARQDSL V Q W	EMEVCKLPRL	SLNGVRFKRI	1020
1021	SGT S I A F K N I	ASKIANELKL					1080

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

MARK1 wt <sup>1</sup> 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	AAPELFQGGK	YDGP EVDVWS	LGVILYTLVS	GSLPFDGQNL	240
241	KELRERVLRG	KYRIPFYMST	DCENLLKLL	VLNPIKRGSL	EQIMKDRWMN	VGHEEEELKP	300
301	YTEPDPDFND	TKRIDIMVTM	GFARDEINDA	LINQKYDEV M	ATYILLGRKP	PEFEGGESLS	360
361	SGNLCQRSRP	SSDLNNSTLQ	SPAHLKVQRS	ISANQKQRRF	SDHAGPSIPP	AVSYTKRPQA	420
421	NSVESEQEE	WDKDVARKLG	STTVGSKSEM	TASPLVGP ER	KKSSTIPSNN	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	NNC DYE Q K E R	FLLFCVH GDA	RQDSL V Q W E M	720
721	EVCKLPRLSL	NGVRFKRISG	TSIAFKNIAS	KIANELML			780

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

<sup>1</sup>NCBI/Protein accession number NP\_001273057.1  
M757K variation: see <http://www.uniprot.org/uniprot/Q9P0L2>, sequence BAA96001