

ProQinase™ MAP4K3 1-380

mitogen-activated protein kinase kinase kinase 3

Recombinant Human Active Protein Kinase

HGNC Symbol: MAP4K3

Synonyms: GLK, MAPKKKK3

Product No.: 2051-0000-1

Lot: 003

Description: Human MAP4K3, N-terminal fragment, amino acids M₁-G₃₈₀ (as in [NCBI/Protein](#) entry NP_003609.2), N-terminal GST-HIS₆ fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

Product identity: MAP4K3 LOT003, has been verified by mass spectrometry LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 71847 Da

Expression host: Sf9 insect cells

Purification: Immobilized Metal 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, 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: 0.568 µg/µl

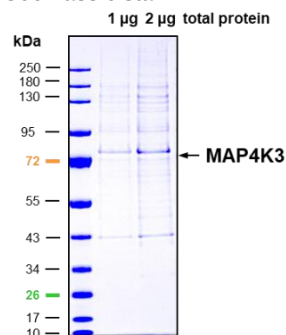
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

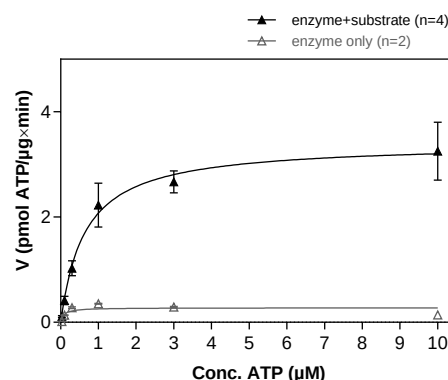
Specific kinase activity (P_i transfer): 3.4 pmol/µg*min

ATP-K_M: 0.6 µM

MAP4K3 1-380 LOT003:
Coomassie stain



MAP4K3 1-380 LOT003:
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: CDCA8 80 µg/ml
 - Kinase: 1 µg/ml

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

Sequence information

GST-MAP4K3 1-380 Recombinant Fusion Protein Amino Acid Sequence

1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLIERDEGDK	WRNKKFELGL	EFNPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPEML	KMFKDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPIQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHHG	RDSLEVLFGQ	240
241	PLAMVMNPGF	DLRRNPQED	FELIQRIGSG	TYGDVYKARN	VNTGELAAIK	VIKLEPGEDF	300
301	AVVQOEIIMM	KDCKHPNIVA	YFGSYLRDRK	LWICMEFCGG	GSLQDIYHVT	GPLSELQIAY	360
361	VSRETLOGLY	YLHSGKGMHR	DIKANILLT	DNGHVKLADF	GVSAQITATI	AKRKSFIGTP	420
421	YWMAPEVAAV	ERKGGYNQLC	DLWAVGITAI	ELAELOPPMF	DLHPMRALFL	MTKSNFQPPK	480
481	LKDKMKWSNS	FHHFVKMALT	KNPKKRPTAE	KLLQHPFVTQ	HLTRSLAIEL	LDKVNNDPHS	540
541	TYHDFDDDDP	EPLVAVPHRI	HSTSRNVREE	KTRSEITFGQ	VKFDPPLRKE	TEPHHELPDS	600
601	DGFLDSSEEI	YYTARSNLDL	QLEYG				660

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: MAP4K3 fragment

MAP4K3 wt¹ Amino Acid Sequence

1	MNPGFDLSRR	NPQEDFELIQ	RIGSGTYGDV	YKARNVNTGE	LAAIKVIKLE	PGEDFAVVQQ	60
61	EIIMMKDCKH	PNIVAYFGSY	LRRDKLWICM	EFCGGGSLQD	IYHVTGPLESE	LQIAYVSRET	120
121	LQGLYYLHSH	GKMHRDIKGA	NILLTDNGHV	KLADFGVSAQ	ITATIAKRKS	FIGTPYWMAP	180
181	EVAEVERKGG	YNQLCDLWAV	GITAIELAEI	QPPMFDLHPM	RALFLMTKSN	FQPPKLKDKM	240
241	KWSNSFHHFV	KMALTKNPKK	RPTAEKLLQH	PFVTQHLTRS	LAIELLDKVN	NPDHSTYHDF	300
301	DDDDPEPLVA	VPHRIHSTR	NVREEKTRSE	ITFGQVKFDP	PLRKETEPHH	ELPDSGFLD	360
361	SSEEIYYTAR	SNLDLQLEYG	QGHQGGYFLG	ANKSLLKSVE	EELHQRGHVA	HLEDDEGDDD	420
421	ESKHSTLKAK	IPPLPPPKPK	SIFIPQEMHS	TEDENQGTIK	RCPMSGSPAK	PSQVPPRPPP	480
481	PRLPPHKPVA	LGNGMSSFQI	NGERDGSICQ	QQNEHRGTNL	SRKEKKDVPK	PISNGLPPTP	540
541	KVHMGACFSK	VFNGCPLKIH	CASSWINPDT	RDQYLIFGAE	EGIYTLNLNE	LHETSMEQLF	600
600	PRRCTWLYVM	NNCLLSISGK	ASQLYSHNLP	GLFDYARQMQ	KLPVAIPAHK	LPDRILPRKF	660
661	SVSAKIPETK	WCQKCCVVRN	PYTGHKYLKG	ALQTSIVLLE	WVEPMQKFML	IKHIDFPIPC	720
721	PLRMFEMLVV	PEQEYPLVCV	GVSRGRDFNQ	VVRFETVNP	STSSWFTESD	TPQTNVTHVT	780
781	QLERDTILVC	LDCCIKIVNL	QGRKLSSRKL	SSELTDFDFQI	ESIVCLQDSV	LAFWKHGMQG	840
841	RSFRSNEVTQ	EISDSTRIFR	LLGSDRVVVL	ESRPTDNPTA	NSNLYILAGH	ENSY	900

blue: MAP4K3 sequence expressed in recombinant protein

¹[NCBI/Protein](#) accession number NP_003609.2