

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of active MINK1 [1 - 320]

<u>Enzyme description:-</u>	MINK1 [1 - 320]
<u>Clone number:-</u>	DU 19081
<u>Source:-</u>	Recombinant
<u>Expression system:-</u>	Baculovirus expression vector system
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH Sepharose
<u>Expression level:-</u>	3 mg/L

Calculated molecular mass:-

Monoisotopic	63, 174.33 daltons
Average Mass	63, 214.95 daltons

[cysteines reduced, methionines have not been oxidised]

<u>Theoretical pI:-</u>	6.25
<u>Purity:-</u>	>80 %
<u>Activation protocol:-</u>	Constitutively active

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF

<u>Storage temperature:-</u>	-70 °C
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<u>Assay:-</u>	Standard filter binding assay
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Assay buffer:-

50 mM Tris-HCl pH 7.5, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol, 10 mM magnesium acetate

Substrate:-

MBP	Final concentration: 0.3 mg/ml
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<u>Specific activity range:-</u>	To be determined
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Clone Data Sheet

MINK1 [1 - 320]

<u>Protein</u>	MINK1 [1 - 320]
<u>Clone number</u>	DU 19081
<u>Species</u>	Human
<u>Accession number</u>	NM_015716
<u>Tags</u>	N-terminal GST
<u>Baculovirus expressed protein</u>	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAETSMLEGA VLDIRYGVSR IAYS KDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFGQPLGSMGDPAPARSLDDID LSALRDPAGIFELVEVVGNGTYGQVYKGRHVKTGQLAAIKVMDVTEDEE EEIKQEIINMLKKYSHRNIATYYGAFIKKSPPGNDDQLWLVMEFCGAGS VTDLVKNTKGNALKEDCIAYICREILRGLAHLHAHKVIHRDIKGQNVLL TENAEVKLVDFGVSAQLDRTVGRNRTFIGTPYWMAPEVIACDENPDATY DYRSDIWSLGITAIEMAEGAPPLCDMHPMRALFLIPRNP PRLKSKKWS KKFIDFIDTCLIKTYLSRPTEQLLKFPFIRDQPTERQVRIQLKDHIDR SRKKRGEKEETE
<u>Native sequence</u>	Amino acids M1 – E320 (end W1295) of human MINK1. Residue M232 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.
<u>Protease cleavage</u>	PreScission (<u>LEVLFQGP</u>) residues 221 - 228
<u>Cloning sites</u>	<i>Bam</i> H1 and <i>Not</i> I site of pFastBac GST

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Nucleotide

Sequence of insert

ggatccATGGGCGACCCAGCCCCGCCCCGAGCCTGGACGACATCGACC
TGTCCGCCCTGCGGGACCCCTGCTGGGATCTTTGAGCTTGTGGAGGTGGT
CGGCAATGGAACCTACGGACAGGTGTACAAGGGTCGGCATGTCAAGACG
GGGCAGCTGGCTGCCATCAAGGTCATGGATGTCACGGAGGACGAGGAGG
AAGAGATCAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACCACCG
CAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCCCGGGA
AACGATGACCAGCTCTGGCTGGTGATGGAGTTCTGTGGTGCTGGTTCAG
TGACTGACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTG
TATCGCCTATATCTGCAGGGAGATCCTCAGGGGTCTGGCCCATCTCCAT
GCCCACAAGGTGATCCATCGAGACATCAAGGGGCAGAATGTGCTGCTGA
CAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTGAGTGCTCAGCT
GGACCGCACCGTGGGCAGACGGAACACTTTTCATTGGGACTCCCTACTGG
ATGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATG
ATTACAGGAGTGATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGC
AGAGGGAGCCCCCCTCTGTGTGACATGCACCCCATGCGAGCCCTCTTC
CTCATTCCTCGGAACCCTCCGCCCAGGCTCAAGTCCAAGAAGTGGTCTA
AGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTACCTGAG
CCGCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAG
CCCACGGAGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGAT
CCCGGAAGAAGCGGGGTGAGAAAGAGGAGACAGAAtgagcggccgc