

## *MRCPPU Reagents and Services*

### **Standard Operating Procedure**

#### **Preparation of active NEK9 [1 - 979]**

<b><u>Enzyme description:-</u></b>	NEK9 [1 - 979]
<b><u>Clone number:-</u></b>	DU 71945
<b><u>Source:-</u></b>	Recombinant
<b><u>Expression system:-</u></b>	Baculovirus expression vector system
<b><u>Tag:-</u></b>	N-terminal GST
<b><u>Purification method:-</u></b>	GSH Agarose

#### **Calculated molecular mass:-**

Monoisotopic      133,906.85 daltons  
Average Mass      133,992.63 daltons  
[cysteines reduced, methionines have not been oxidised]

<b><u>Theoretical pI:-</u></b>	5.55
<b><u>Purity:-</u></b>	>80 %
<b><u>Activation protocol:-</u></b>	Constitutively active

#### **Enzyme storage buffer:-**

50 mM Tris-HCl pH 7.5, 270 mM sucrose, 150 mM NaCl, 0.1 mM EGTA, 0.5 mM TCEP

<b><u>Storage temperature:-</u></b>	-70 °C
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#### **Assay Buffer:-**

50 mM Tris-HCl pH 7.5, 0.1mM EGTA, 10 mM DTT, 5 mM MnCl

#### **Substrate:-**

Myelin Basic Protein      Final concentration: 1 mg/ml

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## Clone Data Sheet

NEK9 [1 - 979]

**Protein** NEK9 [1 - 979]

**Clone number** DU 71945

**Species** Human

**Accession number** NM\_033116.6

**Tags** N-terminal GST

**Baculovirus  
expressed protein**

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNK  
KFELGLEFPNLPYYIDGDVKLTSMAIIRYIADKHNMLGGCPKE  
RAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKM  
FEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKL  
VCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPKSD  
LEVLFGQPLGSM SVLGEYERHCDSINSDFGSESGGCGDSSPGPS  
ASQGPRAGGAAEQEELHYIPIRVLGRGAFGEATLYRRTEDDSL  
VVWKEVDLTRLSEKERRDALNEIVILALLQHDNI IAYNHFMND  
TLLIELEYCNGGNLYDKILRQKDKLFEEEMVVWYLFQIVSAVS  
CIHKAGILHRDIKTLNIFLTKANLIKLG DYGLAKKLNSEYSMAE  
TLVGT PYYMSPELCQGVKYNFKSDI WAVGCVIFELLTLKRTFDA  
TNPLNLCVKIVQGIRAMEVDSSQYSLELIQM VHSCLDQDPEQRP  
TADELLDRPLLRRRREMEKVTLLNAPT KRPRSSTVTEAPIAV  
VTSRTSEVYVWGGGKSTPQKLDVIKSGCSARQVCAGNTHFAVVT  
VEKELYTWVNMQGGTKLHGQLGHGDKASYRQPKHVEKLQGKAIR  
QVSCGDDFTVCVTDEGQLYAFGSDYYGCMGVDKVAGPEVLEPMQ  
LNFFLSNPVEQVSCGDNHVVVLTNRNKEVYSWGCGEYGRGLDSE  
EDYYTPQKVDVPKALII VAVQCGCDGTFLLTQSGKVLACGLNEF  
NKLGLNQCM SGIINHEAYHEVPYTTTSFTLAKQLSFYKIRTIAPG  
KHTAAIDERGRLLTFGCNKCGQLGVGN YKKRLGINLLGGPLGG  
KQVIRVSCGDEFTIAATDDNHIFAWGN GNGRLAMTPTERPHGS  
DICTSWPRPIFGSLHHVPDLS CRGWHTILIVEKVLNSKTIRSNS  
SGLSIGTVFQSSSPGGGGGGGGEEEDSQQESETPDPSGGFRGT  
MEADRGMEGLISPTTEAMGNSNGASS SCPGWLRKELENAEFIPMP  
DSPSPLSAAFSESEKDTLPYEELQGLKVASEAPLEHKPQVEASS  
PRLNPAVTCAGKGTPLTPACACSS LQVEVERLQGLVLKCLAEQ  
QKLQQENLQIF TQLQKLNKKLEGGQQVGMHSGTQT TAKEEMEMD  
PKPDLSDSWCLLGT DSCRPSL

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<b><u>Native sequence</u></b>	Amino acids M1 – L979 (end residue) of human NEK9. Residue M232 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 - 220.
<b><u>Protease cleavage</u></b>	PreScission ( <u>LEVLFQGP</u> ) residues 221 - 228
<b><u>Cloning sites</u></b>	<i>Bam</i> H1 and <i>Not</i> 1 sites of pFastBac Dual.

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**Nucleotide  
sequence of insert**

ATGTCGGTGCTGGGCGAGTACGAGCGACACTGCGATTCCATCAAC  
TCGGACTTTGGGAGCGAGTCCGGGGGTTGCGGGGACTCGAGTCCG  
GGCCTAGCGCCAGTCAGGGGCCGCGAGCCGGCGGGCGCGGGCG  
GAGCAGGAGGAACTGCACTACATCCCCATCCGCGTCTCTGGGCCG  
GGCGCCTTCGGGGAAGCCACGCTGTACCGCCGCACCGAGGATGAC  
TCACTGGTTGTGTGGAAGGAAGTCGATTTGACCCGGCTGTCTGAG  
AAGGAACGTCGTGATGCCTTGAATGAGATAGTTATTCTGGCACTG  
CTGCAGCACGACAACATTATTGCCTACTACAATCACTTCATGGAC  
AATACCACGCTGCTGATTGAGCTGGAATATTGTAATGGAGGGAAC  
CTGTATGACAAAATCCTTCGTCAGAAGGACAAGTTGTTTTGAGGAA  
GAGATGGTGGTGTGGTACCTATTTTCAGATTGTTTCAGCAGTGAGC  
TGCATCCATAAAGCTGGAATCCTTCATAGAGATATAAAGACATTA  
AATATTTTTCTGACCAAGGCAAACCTGATAAACTTGAGATTAT  
GGCCTAGCAAAGAACTTAATTCTGAGTATTCCATGGCTGAGACG  
CTTGTGGGAACCCCATATTACATGTCTCCAGAGCTCTGTCAAGGA  
GTAAAGTACAATTTCAAGTCTGATATCTGGGCAGTTGGCTGCGTC  
ATTTTTGAACTGCTTACCTTAAAGAGGACGTTTGATGCTACAAAC  
CCACTTAACCTGTGTGTGAAGATCGTGCAAGGAATTCGGGCCATG  
GAAGTTGACTCTAGCCAGTACTCTTTGGAATTGATCCAAATGGTT  
CATTCGTGCCTTGACCAGGATCCTGAGCAGAGACCTACTGCAGAT  
GAACTTCTAGATCGCCCTCTTCTCAGGAAACGCAGGAGAGAGATG  
GAGGAAAAGTCACTCTGCTTAATGCACCTACAAAGAGACCAAGG  
TCAAGCACTGTGACTGAAGCACCCATTGCTGTAGTAACATCACGA  
ACCAGTGAAGTCTATGTTTGGGGTGGTGGAAAATCCACCCCCCAG  
AAACTGGATGTTATCAAGAGTGGCTGTAGTGCCCGGCAGGTCTGT  
GCAGGGAATACCCACTTTGCTGTGGTCACAGTGGAGAAGGAACTG  
TACACTTGGGTGAACATGCAAGGAGGCACTAACTCCATGGTCAG  
CTGGGCCATGGAGACAAAGCCTCCTATCGACAGCCAAAGCATGTG  
GAAAAGTTGCAAGGCAAAGCTATCCGTCAGGTGTCATGTGGTGAT  
GATTTCACTGTCTGTGTGACTGATGAGGGTCAGCTCTATGCCTTC  
GGATCAGATTATTATGGCTGCATGGGGGTGGACAAAGTTGCTGGC  
CCTGAAGTGCTAGAACCATGCAGCTGAACTTCTTCTCAGCAAT  
CCAGTGGAGCAGGTCTCCTGTGGAGATAATCATGTGGTGGTTCTG  
ACACGAAACAAGGAAGTCTATTCTTGGGGCTGTGGCGAATATGGA  
CGACTGGGTTTGGATTGAGAAGAGGATTATTATACACCACAAAAG  
GTGGATGTTCCCAAGGCCTTGATTATTGTTGCAGTTCAATGTGGC  
TGTGATGGGACATTTCTGTTGACCCAGTCAGGCAAAGTGTGGCC  
TGTGGACTCAATGAATTCAATAAGCTGGGTCTGAATCAGTGCATG  
TCGGGAATTATCAACCATGAAGCATAACCATGAAGTTCCCTACACA  
ACGTCCTTTACCTTGGCCAAACAGTTGTCCTTTTATAAGATCCGT  
ACCATTGCCCCAGGCAAGACTCACACAGCTGCTATTGATGAGCGA  
GGCCGGCTGCTGACCTTTGGCTGCAACAAGTGTGGGCAGCTGGGC  
GTTGGGAACTACAAGAAGCGTCTGGGAATCAACCTGTTGGGGGA  
CCCCTTGGTGGGAAGCAAGTGATCAGGGTCTCCTGCGGTGATGAG  
TTTACCATTGCTGCCACTGATGATAATCACATTTTTGCCTGGGGC  
AATGGTGGTAATGGCCGCCTGGCAATGACCCCCACAGAGAGACCA  
CATGGCTCTGATATCTGTACCTCATGGCCTCGGCCTATTTTTGGA

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TCTCTGCATCATGTCCCGGACCTGTCTTGCCGTGGATGGCATAACC  
ATTCTCATCGTTGAGAAAGTATTGAATTCTAAGACCATCCGTTCC  
AATAGCAGTGGCTTATCCATTGGAAGTGTGTTTCAGAGCTCTAGC  
CCGGGAGGAGGCGGCGGGGGCGGCGGTGGTGAAGAAGAGGACAGT  
CAGCAGGAATCTGAAACTCCTGACCCAAGTGGAGGCTCCGAGGA  
ACAATGGAAGCAGACCGAGGAATGGAAGGTTTAAATCAGTCCCACA  
GAGGCCATGGGGAACAGTAATGGGGCCAGCAGCTCCTGTCCTGGC  
TGGCTTCGAAAGGAGCTGGAAAATGCAGAATTTATCCCCATGCCT  
GACAGCCCATCTCCTCTCAGTGCAGCGTTTTTCAGAATCTGAGAAA  
GATACCCCTGCCCTATGAAGAGCTGCAAGGACTCAAAGTGGCCTCT  
GAAGCTCCTTTGGAACACAAACCCCAAGTAGAAGCCTCGTACCT  
CGGCTGAATCCTGCAGTAACCTGTGCTGGGAAGGGAACACCACTG  
ACTCCTCCTGCGTGTGCGTGCAGCTCTCTGCAGGTGGAGGTTGAG  
AGATTGCAGGGTCTGGTGTAAAGTGTCTGGCTGAACAACAGAAG  
CTACAGCAAGAAAACCTCCAGATTTTTTACCCAAGTGCAGAAGTTG  
ACAAGAAATTAGAAGGAGGGCAGCAGGTGGGGATGCATTCCAAA  
GGAAGTCTCAGACAGCAAAGGAAGAGATGGAAATGGATCCAAAGCCT  
GACTTAGATTTCAGATTCCTGGTGCCTCCTGGGAACAGACTCCTGT  
AGACCCAGCCTCtag