

## *Division of Signal Transduction Therapy*

### **Standard Operating Procedure**

#### **Preparation of active DAPK3 [1 – 404]**

**Enzyme description:-** DAPK3 [1 – 404]

**Clone number:-** DU 32285

**Source:-** Recombinant

**Expression system:-** *E.coli*

**Tag:-** N-terminal GST

**Purification method:-** GSH Sepharose

**Calculated molecular mass:-**

Monoisotopic 79, 310.01 daltons

Average Mass 79, 359.87 daltons

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 6.16

**Purity:-** 85 %

**Activation protocol:-** 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, 0.2 mM PMSF, 1 mM Benzamidine

**Storage temperature:-** -70 °C

**Assay buffer:-**

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

**Substrate:-**

KKLNRTL<sup>S</sup>FAEPG Final concentration: 300  $\mu$ M

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### **Clone Data Sheet**

#### **DAPK3 [1 – 404]**

**Protein** DAPK3 [1 - 404]

**Clone number** DU 32285

**Species** Human

**Accession number** NM\_001348.1

**Tags** N-terminal GST

**Bacterially expressed protein** MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKK  
FELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERA  
EISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFED  
RLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFK  
KRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPKSDLEVL  
FQGPLGSMSTFRQEDVEDHYEMGEELGSGQFAIVRKCRQKGTGKEY  
AAKFIKKRRLLSSRRGVSREEIEREVNILREIRHPNIITLHDIFE  
NKTDVVLILELVSGGELDFLAEKESLDEDEATQFLKQILDGVHY  
LHSKRIAHFDLKPENIMLLDKNVNPRIKLIIDFGIAHKIEAGNEF  
KNIFGTPEFVAPEIVNYEPLGLEADMWSIGVITYILLSGASPFLG  
ETKQETLTNISAVNYDFDEEYFSNTSELAKDFIRLLLVKDPKRRM  
TIAQSLEHSWIKAIRRRNVRGEDSGRKPERRRLKTTRLKEYTIKS  
HSSLPPNNSYADFERFSKVL EEA AAEGLRELQRSRRLCHEDVE  
ALAAIYEEKEAWYREESDSLQDLRRLRQELLKTEALKRQAQEEA  
KGALLGTSGLKRRFSRLENRYEALAKQVASEMRVQDLVRALEQE  
KLGVECGLR

**Native sequence** Amino acids M1 – R404 of human DAPK3.  
Residue M232 of the fusion protein is equivalent to M1 of the  
native enzyme. The GST tag is located at residues 1 - 220.

**Protease cleavage** PreScission (LEVLFQGP) residues 221 - 228

**Cloning sites** *Bam*H1 sites of pGEX-6P-1

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**Nucleotide  
sequence of insert**

ggatccATGTCCACGTTTCAGGCAGGAGGACGTGGAGGACCATTAT  
GAGATGGGGGAGGAGCTGGGCAGCGGCCAGTTTGCATCGTGCGG  
AAGTGCCGGCAGAAGGGCACGGGCAAGGAGTACGCAGCCAAGTTC  
ATCAAGAAGCGCCGCCTGTTCATCCAGCCGGCGTGGGGTGAGCCGG  
GAGGAGATCGAGCGGGAGGTGAACATCCTGCGGGAGATCCGGCAC  
CCAACATCATCACCTGCACGACATCTTCGAGAACAAGACGGAC  
GTGGTCCTCATCCTGGAGCTGGTCTCTGGCGGGGAGCTCTTTGAC  
TTCCTGGCGGAGAAGGAGTTCGCTGACGGAGGACGAGGCCACCCAG  
TTCCTCAAGCAGATCCTGGACGGCGTTCACTACCTGCACTCTAAG  
CGCATCGCACACTTTGACCTGAAGCCGAAAACATCATGCTGCTG  
GACAAGAACGTGCCAACCCACGAATCAAGCTCATCGACTTCGGC  
ATCGCGCACAAGATCGAGGCGGGGAACGAGTTCAAGAACATCTTC  
GGCACCCCGGAGTTTGTGGCCCCAGAGATTGTGAACTATGAGCCG  
CTGGGCCTGGAGGCGGACATGTGGAGCATCGGTGTCATCACCTAT  
ATCCTCCTGAGCGGTGCATCCCCGTTCTGGGCGAGACCAAGCAG  
GAGACGCTCACCAACATCTCAGCCGTGAACTACGACTTCGACGAG  
GAGTACTTCAGCAACACCAGCGAGCTGGCCAAGGACTTCATTCGC  
CGGCTGCTCGTCAAAGATCCAAGCGGAGAATGACCATTGCCAG  
AGCCTGGAACATTCCTGGATTAAGGCGATCCGGCGGCGGAACGTG  
CGTGGTGAGGACAGCGGCCGCAAGCCCGAGCGGCGGCCTGAAG  
ACCACGCTCTGAAGGAGTACACCATCAAGTCGCACTCCAGCTTG  
CCGCCAACAACAGCTACGCCGACTTCGAGCGCTTCTCCAAGGTG  
CTGGAGGAGGCGGCGGCCGCGAGGAGGCTGCGCGAGCTGCAG  
CGCAGCCGGCGGCTCTGCCACGAGGACGTGGAGGCGCTGGCCGCC  
ATCTACGAGGAGAAGGAGGCCTGGTACCGCGAGGAGAGCGACAGC  
CTGGGCCAGGACCTGCGGAGGCTACGGCAGGAGCTGCTCAAGACC  
GAGGCGCTCAAGCGGCAGGCGCAGGAGGAGGCCAAGGGCGCGCTG  
CTGGGGACCAGCGGCCTCAAGCGCCGCTTCAGCCGCTGGAGAAC  
CGCTACGAGGCGCTGGCCAAGCAAGTAGCCTCCGAGATGCGCTTC  
GTGCAGGACCTCGTGCGGCCCTGGAGCAGGAGAAGCTGCAGGGC  
GTGGAGTGCGGGCTGCGCtagggatcc