

## *Division of Signal Transduction Therapy*

### **Standard Operating Procedure**

#### **Preparation of active HIPK1 [158 – 555]**

**Enzyme description:-** HIPK1 [158 - 555]

**Clone number:-** DU 5523

**Source:-** Recombinant

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

**Tag:-** N-terminal GST

**Purification method:-** GSH Sepharose

**Expression level:-** 2 mg/L

**Calculated molecular mass:-**

Monoisotopic 72,954.03 daltons

Average Mass 73,001.33 daltons

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 6,54

**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, 1 mM benzamidine, 0.2 mM PMSF

**Storage temperature:-** -70 °C

**Assay buffer:-**

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

**Substrate:-**

Myelin basic protein                      Final concentration: 0.3 mg/ml

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**Clone Data Sheet**

**HIPK1 [158 - 555]**

**Protein** HIPK1 [158 - 555]

**Clone number** DU 5523

**Species** Human

**Accession number** NM\_198268

**Tags** N-terminal GST

**Bacterially expressed protein** MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG  
LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA  
VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH  
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS  
KYIAWPLQGWQATFGGGDHPPKSDLEVLFGQPLGSPEFTTTTTVTTKSSS  
SSGEGDYQLVQHEILCSMTNSYEVLEFLGRGTFGQVAKCWKRSTKEIVA  
IKILKNHPSYARQGQIEVSILSRLSSENADEYNFVRSYECFQHKNHHTCL  
VFEMLEONLYDFLKQNKFSPLPLKYIRPILOQVATALMKLKSLGLIHAD  
LKPENIMLVDPVRQPYRVKVIDFGSASHVSKAVCSTYLQSRYYRAPEII  
LGLPFCEAIDMWSLGCVIAELFLGWPLYPGASEYDQIRYISQTQGLPAE  
YLLSAGTKTTRFFNRDPNLGYPLWRLKTPEEHELETGIKSKEARKYIFN  
CLDDMAQVNMSTDLEGTDLAEKADRREYIDLLKMLTIDADKRITPLK  
TLNHQFVTMTHLLDFPHSNHVKSCFQNMETCKRRVHMYDTVSQI

**Native sequence** Amino acids T158 – I555 of human HIPK1.  
[Full length protein ends at residue L1210]

Residue T235 of the fusion protein is equivalent to T158 of the native enzyme. The GST tag is located at residues 1 – 220.

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

**Cloning sites** *Eco*R1 sites of pGEX 6P-1

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**Nucleotide**  
**Sequence of insert**

gaattcACAACCACCACTGTGACCACAAAGAGTAGCAGTTCCAGCGGAG  
AAGGGGATTACCAGCTGGTCCAGCATGAGATCCTTTGCTCTATGACCAA  
TAGCTATGAAGTCTTGGAGTTCCTAGGCCGGGGACATTTGGACAGGTG  
GCTAAGTGCTGGAAGAGGAGCACCAAGGAAATTGTGGCTATTAAAATCT  
TGAAGAACCACCCCTCCTATGCCAGACAAGGACAGATTGAAGTGAGCAT  
CCTTTCCCGCCTAAGCAGTGAAAATGCTGATGAGTATAATTTTGTCCGT  
TCATACGAGTGCTTTCAGCATAAGAATCACACCTGCCTTGTTTTGAAA  
TGTTGGAGCAGAACTTATATGATTTTCTAAAGCAAAACAAATTTAGCCC  
ACTGCCACTCAAGTACATCAGACCAATCTTGCAGCAGGTGGCCACAGCC  
TTGATGAAGCTCAAGAGTCTTGGTCTGATCCACGCTGACCTTAAGCCTG  
AAACATCATGCTGGTTGATCCAGTTCGCCAGCCCTACCGAGTGAAGGT  
CATTGACTTTGGTCTGCTAGTCACGTTTCCAAAGCTGTGTGCTCAACC  
TACTTACAGTCACGTTACTACAGAGCTCCTGAAATTATTCTTGGGTAC  
CATTTTGTGAAGCTATTGATATGTGGTCACTGGGCTGTGTGATAGCTGA  
GCTGTTCTGGGATGGCCTCTTTATCCTGGTGCTTCAGAATATGATCAG  
ATTTCGTTATATTTCAAAACACAAGGCTTGCCAGCTGAATATCTTCTCA  
GTGCCGGAACAAAACAACCAGTTTTTTCAACAGAGATCCTAATTTGGG  
GTACCCACTGTGGAGGCTTAAGACACCTGAAGAACATGAACTGGAGACT  
GGAATAAAATCAAAGAAGCTCGGAAGTACATTTTAAATTGCTTAGATG  
ACATGGCTCAGGTGAATATGTCTACAGACCTGGAGGGAACAGACATGTT  
GGCAGAGAAGGCAGACCGAAGAGAATACATTGATCTGTTAAAGAAAATG  
CTCACAATTGATGCAGATAAGAGAATTACCCCTCTAAAAACTCTTAACC  
ATCAGTTTGTGACAATGACTCACCTTTTGGATTTTCCACATAGCAATCA  
TGTTAAGTCTTGTTTTCAGAACATGGAGATCTGCAAGCGGAGGGTTTAC  
ATGTATGATACAGTGAGTCAGATCtaggaattc