

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of PINK1 126 – end P. humanus

<u>Enzyme description:-</u>	GST-PINK1 126-end
<u>Clone number:-</u>	DU34798
<u>Source:-</u>	Pediculus humanus recombinant
<u>Tag:-</u>	N-terminal GST-
<u>Purification method:-</u>	GSH-agarose
<u>Expression system:-</u>	<i>E.coli</i>
<u>Calculated molecular mass:-</u>	
Monoisotopic	78328
Average Mass	78377
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	6.92
<u>Purity:-</u>	> 80%
<u>Enzyme storage buffer:-</u>	
50 mM HEPES pH 7.5, 10% glycerol, 75mM NaCl, 1mM DTT	
<u>Storage temperature:-</u>	-80°C
<u>Assay:-</u>	

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Clone Data Sheet

Protein name PINK1 126 – end (P.h.)

<u>Protein</u>	GST-PINK1 126-end
<u>Synonyms</u>	
<u>Clone Number</u>	DU34798
<u>Species</u>	Pediculus humanus (body louse)
<u>Accession Number</u>	E0W1I1
<u>Tags</u>	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKF ELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERA EI SMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLC HKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIE AIPQIDKYLKSSKYIAWPLOGWQATFGGGDHPPKSDLEVLFGQPLG SGICWEIREAVSKGKWNDSESENVEQLQAANLDELDLGEPIAKGCN AVVYSAKLKNVQSNKLAHQ LAVKMMFNVDVESNSTAILKAMYRETV PAMSYFFNQNLFNIE NISDFKIRLPPHPNIVRMYSVFADRI PDLC NKQLYPEALPPRINPEGSGRNMSLFLVMKRYDCTLKEYLRDKTPNM RSSILLLSQLLEAVAHMNIHNISHRDLKSDNILVDLSEGDAYPTIV ITDFGCCCLCDKQNGLVIPYRSEDQDKGGNRALMAPEIANAKPGTFS WLNYKKS DLWAVGAIAYEIFNIDNPFYDKTMKLLSKSYKEEDLP EL PDTIPFIIRNLVSNMLSRSTNKRLDCDVAATVAQLYLWAPSSWLKE NYTLPNSNEIIQWLLCLSSKVL CERDITARNKTNTMS ESVS KAQYK GRRSLPEYELIASFLRRVRLHLVRKGLKWIQELHIYN
Native sequence	in bold
Protease cleavage	Prescission Protease site underlined
Cloning sites	BamHI / NotI

DNA sequence of insert

ggatccGGCATTTGCTGGGAAATCCGCGAAGCAGTTAGCAAGGGTAAA
TGGAACGATTCAGAATCGGAAAATGTCGAACAGCTGCAAGCAGCTAAT
CTGGATGAACTGGACCTGGGCGAACCGATTGCAAAAGGTTGTAACGCT
GTGGTTTATTCTGCGAAACTGAAAAACGTGCAGAGTAATAAACTGGCG
CACCAACTGGCCGTGAAAATGATGTTCAACTACGATGTTGAAAGCAAT
TCTACCGCAATTCTGAAAGCTATGTATCGTGAAACGGTTCGGCGATG
TCTTACTTTTTCAACCAGAACCTGTTTAACATCGAAAACATCAGTGAT
TTCAAAATTGCGCTGCCGCCGCATCCGAATATCGTTCGTATGTATAGC
GTCTTTGCCGATCGCATTCGGGACCTGCAGTGCAACAAACAACGTAC
CCGGAAGCACTGCCGCCGCGTATCAACCCGGAAGGCTCTGGTCGCAAT
ATGAGTCTGTTCTTGGTCATGAAACGTTATGATTGTACCCTGAAAGAA
TACCTGCGTGACAAAACGCCGAACATGCGCAGCTCTATTCTGCTGCTG
TCCCAGCTGCTGGAAGCAGTTGCTCATATGAACATTCACAATATCTCC
CATCGCGATCTGAAATCAGACAATATCCTGGTCGATCTGAGCGAAGGC
GACGCCTATCCGACCATTGTGATCACGGATTTTGGCTGCTGTCTGTGC
GACAAACAGAACGGTCTGGTGATTCCGTACCGTAGCGAAGATCAAGAC
AAAGGCGGTAACCGTGCCCTGATGGCACCGGAAATCGCGAATGCCAAA
CCGGGCACCTTCTCGTGGCTGAACTATAAAAAATCTGATCTGTGGGCG
GTTGGTGCAATCGCTTACGAAATCTTCAACATCGATAACCCGTTCTAC
GACAAAACCATGAAACTGCTGAGTAAATCCTATAAAGAAGAAGATCTG
CCGGAAGTCCCGGACACGATCCCGTTTATTATCCGCAACCTGGTGTCT
AATATGCTGTCACGTTTCGACCAATAAACGCCTGGATTGTGATGTTGCC
GCAACCGTGGCACAGCTGTATCTGTGGGCACCGAGTTCCTGGCTGAAA
GAAACTACACCCTGCCGAACAGTAATGAAATTATCCAATGGCTGCTG
TGCCTGTCATCGAAAGTGCTGTGTGAACGTGATATTACGGCTCGCAAC
AAAACCAATACGATGAGCGAAAGCGTGAGTAAAGCGCAGTATAAAGGT
CGTCGCTCCCTGCCGGAATACGAACTGATCGCGTCATTCTGCGTCGC
GTCCGTCTGCATCTGGTCCGTAAAGGTCTGAAATGGATTCAAGAACTG
CACATCTACAATAAgcgccgc