

Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of active PPM1 beta isoform 1 [2 - 479] (PP2C beta isoform 1)

Enzyme description:- PPM1 beta isoform 1 [2 - 479]

Clone number:- DU 3021

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Expression level:- 5-10 mg/L

Calculated molecular mass:- 79, 658 daltons

Purity:- >80 %

Activation protocol:- Constitutively active

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 2 mM MnCl₂, 0.03 % Brij 35, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol, 50 % glycerol, 1 mM benzamidine and 0.1 mM PMSF

Storage temperature:- -20 °C

Assay:- Standard phosphatase assay

Assay buffer:-

50 mM Tris-HCl pH 7.5, 2 mM MnCl₂, 0.03 % Brij 35, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol

Substrate:-

6 µM ³²P labelled casein (phosphorylated by PKA)

Specific activity range:- To be determined

Division of Signal Transduction Therapy

Clone Data Sheet

PPM1 beta isoform 1 [2 – 479]

<u>Protein</u>	PPM1 beta isoform 1 [2 – 479]
<u>Clone number</u>	DU 3021
<u>Species</u>	Human
<u>Accession number</u>	AAH64381
<u>Tags</u>	N-terminal GST
<u>Bacterially expressed protein</u>	MSPILGYWKIKGLVQPTRLLEKYEEHYERDEGDKWRNKKFEL GLEFPNLPLYIDGVKLTQSMAIIRYIADKHNLGGCPKERAEISMLE GAVLDIYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLN GDHVTHPDFMLYDALDVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKY LKSSKYIAWPLQGWQATFGGGDHPPKS <u>DEVLFQGPL</u> GSPEFGAFLDK PKTEKHNAHGAGNGLRYGLSSMQGWRVEMEDAHTAVVGIPHGLEDSWF FAVYDGHAGSRVANYCSTHLLEHITTNEFDRAAGKSGSAELSVENVK NGIRTGFLLKIDEYMRNFSDLRNGMDRSGSTAVGVMISPKHIYFINCGD SRAVLYRNGQVCFSTQDHKPNCNPREKERIQNAGGSVMIQRVNGLAVS RALGDYDYKCVDGKGPTEQLVSPPEVYEILRAEDEFIILACDGIWD VMSNEELCEYVKSRL EVSDDENVCNWVVTCLHKGSRDNMSIVLVCF SNAPKVSDEAVKKDSELDKHLESRVEEIMEKSGEEGMPDLAHVRILS AENIPNLPPGGGLAGKRNVIEAVYSRLNPRESDGASDEAEESGSQGK LVEALRQMRINHRGNYRQLLEEMTSYRLAKVEGEESPAEPATATSS NSDAGNPVTMQESHTESGELDSSNEDAGTKMSGEKI
<u>Native sequence</u>	Amino acids G2 – I479 (end) of human PPM1 beta isoform 1. Residue G235 of the fusion protein is equivalent to G2 of the native enzyme. The GST tag is located at residues 1 - 220.
<u>Protease cleavage</u>	PreScission (<u>LEVLFQGPL</u>) at residues 221 - 229
<u>Cloning sites</u>	<i>Eco</i> RI and <i>Not</i> I sites of pGEX-6P-1

Division of Signal Tranduction Therapy

Nucleotide sequence of insert

gaattcGGTGCATTTGGATAAACCCAAACTGAAAAACATAATGCT
CATGGTGCTGGGAATGGTTACGTTATGGCCTGAGCAGCATGCAAGGA
TGGAGAGTGGAAATGGAAGATGCACACACAGCTGTTTAGGTATTCC
CACGGCTTGGAAAGACTGGTCATTTGCAGTTATGATGGTCATGCT
GGATCCCAGTGGCAAATTACTGCTCAACACACATTATTAGAACACATC
ACTACTAACGAAGACTTTAGGGCAGCTGGAAAATCAGGATCTGCTCTT
GAGCTTCAGTGGAAAATGTTAAGAATGGTATCAGAACTGGATTTTG
AAAATTGATGAATACATGCGTAACCTTCAGACCTCAGAAACGGGATG
GACAGGAGTGGTCAACTGCAGTGGAGTTATGATTTCACCTAACATC
ATCTACTTTATCAACTGTGGTATTACGTGCTGTTCTGTATAGGAAT
GGACAAGTCTGCTTTCTACCCAGGATCACAAACCTGCAATCCAAGG
GAAAAGGAGCGAACCCAAATGCAGGAGGCAGCGTGTGATGATAACAGT
GTTAATGGTCATTAGCAGTATCTCGTCTGGGGACTATGATTAC
AAAGTGTGTTGATGGCAAGGGCCAACAGAACAAACTTGTTCAGAG
CCTGAGGTTATGAAATTAAAGAGCAGAACAGGATGAATTATCATC
TTGGCTTGTGATGGATCTGGATGTTATGAGTAATGAGGAGCTCTGT
GAATATGTTAAATCTAGGCTTGAGGTATCTGATGACCTGGAAAATGTG
TGCAATTGGTAGTGGACACTTGTACACAAGGGAGTCGAGATAAC
ATGAGTATTGTAAGTTGCTTTCAAATGCTCCAAAGGTCTCAGAT
GAAGCGGTGAAAAAAGATTCAAGAGTTGGATAAGCACCTGGAAATCACGG
GTTGAAGAGATTATGGAGAAGTCTGGCGAGGAAGGAATGCCTGATCTT
GCCCATGTCATGCGCATTTGTCTGCAGAAAATATCCAAATTGCT
CCTGGGGAGGTCTGCTGGCAAGCGTAATGTTATTGAAGCTGTTAT
AGTAGACTGAATCCACATAGAGAAAGTGTGATGGGCCTCGATGAAGCA
GAGGAAAGTGGATCACAGGGAAAATTGGTGAAGCTCTCAGGCAAATG
AGAATTAAATCATAGGGAAACTACCGACAACCTCTGGAGGAGATGCTG
ACTAGTTACAGGCTAGCTAAAGTAGAGGGAGAAGAAAGCCCTGCTGAA
CCAGCTGCCACAGCTACTTCTCGAACAGTGATGCTGGAAACCCAGTG
ACAATGCAGGAAAGCCATACTGAATCAGAAAGTGGCTTGCTGAATTA
GACAGCTCTAATGAAGATGCAGGGACAAAGATGAGTGGTGGAAAAATA
tgagcgccgc