

MRCPPU REAGENTS and SERVICES

Standard Operating Procedure

Preparation of KPNA2 [1 – 529]

Enzyme description:- KPNA2 [1 - 529]

Clone number:- DU 42444

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Agarose

Calculated molecular mass:-

Monoisotopic 84, 632.58 daltons

Average Mass 84, 686.08 daltons

[cysteines reduced, methionines have not been oxidized]

Theoretical pI:- 5.41

Purity:- >80 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 0.1 mM EGTA, 150 mM NaCl, 0.1 % 2-mercaptoethanol,
270 mM Sucrose

Storage temperature:- -70 °C

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Clone Data Sheet

KPNA2 [1 - 529]

Protein KPNA2 [1 – 529]

Clone number DU 42444

Species Human

Accession number P52292

Tags N-terminal GST

**Bacterially
expressed protein**

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG
LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAELSMLEGA
VLDIRYGVSR IAYS KDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAI PQIDKYLKSS
KYIAWPLQGWQATFGGGDHPPKSDLEVL FQGPLGSMSTNENANTPAARL
HREFKNKGKDSTEMRRRRIEVNVELRKAKKDDQMLKRRNVSSFPDDATSP
LQENRNNQGTVNWSVDDIVKGINSSNVENQLQATQAARKLLSREKQPP I
DNIIRAGLIPKFVSVFLGRTDCSPIQFESAWALTNIASGTSEQTKAVVDG
GAIPAFISLLASPHAHISEQAVWALGNIAGDGSVFRDLVIKYGAVDPLL
ALLAVPDMSSLACGYLRNLTWTL SNLCRNKNPAPPIDAVEQILPTLVRL
LHHDDPEVLADTCWAI SYLTDGPNERIGMVVKTGVVPQLVKLLGASELP
IVTPALRAIGNIVTGTDEQTQVVIDAGALAVFP SLLTNPKTNIQKEATW
TMSNITAGRQDQIQVVNHGLVPFLVSVLSKADFKTQKEAVWAVTNYTS
GGTVEQIVYLVHCGIIEPLMNL LTAKDTKIILVILDAISNIFQAAEKL G
ETEKLSIMIEECGGLDKIEALQNHENESVYKASLSLIEKYFSVEEEEDQ
NVVPETTSEGYTFQVQD GAPGTFNF

Native sequence Amino acids M1 – F529 (end residue) of human KPNA2.
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 (LEVL FQGP) residues 221 - 229

Cloning sites *Bam*H1 and *Not*1 sites of pGEX 6P-1

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Nucleotide
Sequence of insert

ggatccATGTCCACCAACGAGAATGCTAATACACCAGCTGCCCGTCTTC
ACAGATTCAAGAACAAGGGAAAAGACAGTACAGAAATGAGGCGTCGCAG
AATAGAGGTCAATGTGGAGCTGAGGAAAGCTAAGAAGGATGACCAGATG
CTGAAGAGGAGAAATGTAAGCTCATTTCCTGATGATGCTACTTCTCCGC
TGCAGGAAAACCGCAACAACCAGGGCACTGTAAATTGGTCTGTTGATGA
CATTGTCAAAGGCATAAATAGCAGCAATGTGGAAAATCAGCTCCAAGCT
ACTCAAGCTGCCAGGAACTACTTTCCAGAGAAAAACAGCCCCCATAG
ACAACATAATCCGGGCTGGTTTGATTCCGAAATTTGTGTCCTTCTGGG
CAGAACTGATTGTAGTCCCATTGAGTTTGAATCTGCTTGGGCACTCACT
AACATTGCTTCTGGGACATCAGAACAAACCAAGGCTGTGGTAGATGGAG
GTGCCATCCCAGCATTCAATTTCTCTGTTGGCATCTCCCATGCTCACAT
CAGTGAACAAGCTGTCTGGGCTCTAGGAAACATTGCAGGTGATGGCTCA
GTGTTCCGAGACTTGGTTATTAAGTACGGTGCAGTTGACCCACTGTTGG
CTCTCCTTGCAGTTCCTGATATGTCATCTTTAGCATGTGGCTACTTACG
TAATCTTACCTGGACACTTTCTAATCTTTGCCGCAACAAGAATCCTGCA
CCCCGATAGATGCTGTTGAGCAGATTCTTCCCTACCTTAGTTCCGGCTCC
TGCATCATGATGATCCAGAAGTATTAGCAGATACCTGCTGGGCTATTTT
CTACCTTACTGATGGTCCAAATGAACGAATTGGCATGGTGGTGA AAAACA
GGAGTTGTGCCCCAACTTGTGAAGCTTCTAGGAGCTTCTGAATTGCCAA
TTGTGACTCCTGCCCTAAGAGCCATAGGGAATATTGTCACTGGTACAGA
TGAACAGACTCAGGTTGTGATTGATGCAGGAGCACTCGCCGTCTTTCC
AGCCTGCTCACCAACCCCAAACTAACATTCAGAAGGAAGCTACGTGGA
CAATGTCAAACATCACAGCCGGCCGCCAGGACCAGATACAGCAAGTTGT
GAATCATGGATTAGTCCCATTCCCTTGTGTCAGTGTCTCTCTAAGGCAGAT
TTTAAGACACAAAAGGAAGCTGTGTGGGCCGTGACCAACTATAACCAGTG
GTGGAACAGTTGAACAGATTGTGTACCTTGTTCACTGTGGCATAATAGA
ACCGTTGATGAACCTCTTAACTGCAAAAGATAACCAAGATTATTCTGGTT
ATCCTGGATGCCATTTCAAATATCTTTCAGGCTGCTGAGAACTAGGTG
AAACTGAGAACTTAGTATAATGATTGAAGAATGTGGAGGCTTAGACAA
AATTGAAGCTCTACAAAACCATGAAAATGAGTCTGTGTATAAGGCTTCG
TTAAGCTTAATTGAGAAGTATTTCTCTGTAGAGGAAGAGGAAGATCAAA
ACGTTGTACCAGAACTACCTCTGAAGGCTACACTTTCCAAGTTCAGGA
TGGGCTCCTGGGACCTTTAACTTTTAGGCGGCCGC