

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of CUGBP2 [2 - 521]

Enzyme description:- CUGBP2 [2 – 521]

Clone number:- DU 1397

Source:- Recombinant

Expression system:- *E.coli*,

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-

Monoisotopic 82, 394.60 daltons

Average Mass 82, 447.46 daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 8.41

Purity:- >80 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 150 mM NaCl, 270 mM sucrose, 0.1 mM EGTA,
0.1 % 2-mercaptoethanol, 0.03 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF

Storage temperature:- -70 °C

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Clone Data Sheet

CUGBP2 [2 - 521]

Protein CUGBP2 [2 - 521]

Clone number DU 1397

Species Human

Accession number BC036391

Tags N-terminal GST

**Bacterially
expressed protein**

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFEL
GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLE
GAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLN
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKY
LKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFOGPLGSMVEGRLLVP
DRINGTANKMNGALDHSQDPDAIKMFVGQIPRSWSEKELKELFEPY
GAVYQINVLDRSQNPQSKGCCFVTFYTRKAALQAQNALHNIKTLPG
MHHP IQMKPADSEKSNAVEDRKLFIGMVSKKCNENDIRVMFSPFGQIE
ECRILRGPDGLSRGCAFVTFSTRAMAQNAIKAMHQSQTMEGCSSPIVV
KFADTQKDKEQRRLOQLAQOMQQLNTATWGNLTGLGGLTPQYLALLO
QATSSSNLGA FSGIQOMAGMNALQQLONLATLAAAAAAQTSATSTNAN
PLSTTSSALGALTSPVAASTPNSTAGAAMNSLTSLGTLQGLAGATVGL
NNINALAGTINTPRSKRLLLPKDNNGMAALNGGLGATGLTNGTAGTMD
ALTQAYSGIQQYAAAALPTLYSQSLLOQQAAGSQKEGPEGANLF IYH
LPQEFGDQDILQMFMPFGNVI SAKVFI DKQTNLSKCFGFVSYDNPVSA
QAAIQAMNGFQIGMKRLKVQLKRSKNDSKPY

Native sequence Amino acids M2 – Y521 (end) of human CUGBP2.
Residue M232 of fusion protein is equivalent to M1 of the native
enzyme. The GST tag is located at residues 1 – 220.

Protease cleavage Precission site (LEVLFGQP) at residues 221 – 228

Cloning sites *Bam*H1 sites of pGex6P-1

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Nucleotide
sequence of insert

ggatccATGGTCGAGGGCCGCCTGCTCGTTCCTGACAGAATTAACGGC
ACAGCCAACAAGATGAACGGAGCTTTGGATCACTCAGACCAACCAGAC
CCAGATGCCATTAAGATGTTTGTTCGGACAGATCCCCCGTTCATGGTTCG
GAAAAGGAGCTGAAAGAACTTTTTGAGCCTTACGGAGCCGTCTACCAG
ATCAACGTCCTCCGGGACCGGAGTCAGAACCCCTCCGCAGAGTAAAGGT
TGTTGTTTCGTAACATTTTATACAAGAAAAGCTGCACTTGAGGCCAG
AATGCACTGCACAATATTA AAACTTTACCTGGGATGCATCATCCCATT
CAGATGAAACCTGCAGATAGTGAAAAGTCCAACGCTGTGGAAGACAGA
AAATTGTTTCATAGGAATGGTATCGAAGAAATGTAATGAGAACGCATC
AGGGTGATGTTCTCTCCATTTGGCCAGATAGAAGAATGCCGGATACTC
CGGGGACCTGATGGGCTGAGTCGAGGCTGTGCGTTTGTCCACATTTTCT
ACAAGGGCAATGGCACAGAATGCAATCAAAGCCATGCATCAGTCTCAG
ACCATGGAGGGCTGCTCTTACCTATCGTGGTGAAGTTTGCTGACACT
CAGAAGGACAAAGAGCAAAGGCGCCTCCAGCAGCAGCTCGCTCAGCAG
ATGCAGCAGCTCAACACTGCCACCTGGGGGAACCTGACAGGGCTGGGC
GGACTGACCCACAGTATCTGGCGCTCCTGCAGCAGGCCACCTCCTCC
AGCAACCTGGGTGCGTTCAGCGGCATTCAACAAATGGCAGGCATGAAT
GCTTTACAGTTGCAGAACCTGGCGACGCTGGCTGCTGCTGCAGCTGCG
GCCAGACCTCAGCCACCAGCACCAATGCAAACCCTCTCTCTACCACG
AGCAGCGCCCTGGGAGCCCTCACGAGTCCCGTGGCTGCTTCAACCCCC
AACTCCACTGCTGGTGCAGCCATGAACTCCTTGACCTCTCTCGGGACT
CTGCAAGGACTGGCTGGAGCCACTGTTGGACTGAATAATATTAATGCA
CTAGCAGGTACCATCAACACTCCCAGAAGCAAAGGCTTTTACTTCCA
AAAGATAACAACGGTATGGCGGCTCTGAATGGAGGACTTGGCGCCACA
GGCTTGACGAATGGCACGGCTGGCACCATGGACGCCCTCACCCAGGCC
TACTCAGGAATTCAACAGTACGCAGCCGCCGCGCTGCCCACTCTGTAC
AGCCAGAGCCTGCTGCAGCAGCAGAGCGCTGCAGGCAGCCAGAAGGAA
GGTCCAGAGGGGGCAAACCTCTTTATTTACCACCTTCCACAGGAATTT
GGAGACCAGGACATCTGCAGATGTTTCATGCCTTTTGGAAATGTTATC
TCTGCTAAAGTCTTCATTGACAAACAGACCAATCTGAGCAAGTGCTTT
GGTTTTGTTAGCTACGACAATCCAGTCTCTGCACAAGCTGCTATCCAA
GCTATGAATGGCTTTCAGATCGGCATGAAACGCTTGAAGGTGCAGCTG
AAGCGTTCCAAAACGACAGCAAACCTTACTgagatcc