

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of Beta-Catenin [2 – 1011]

Protein description:- Beta-Catenin [2 – 1011]

Clone number:- DU 1105

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Expression level:- 4 mg/L

Calculated molecular mass:- 112, 117 daltons

Purity:- > 95 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 50 % glycerol, 150 mM NaCl, 0.1 mM EGTA,
0.1 % 2- mercaptoethanol, 0.02 % Brij-35, 0.2 mM PMSF, 1 mM Benzamidine.

Storage temperature:- –20 °C

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CLONE DATA SHEET

Beta-Catenin [2 – 1011]

<u>Protein</u>	Beta-Catenin [2 – 1011]
<u>Clone number</u>	DU 1105
<u>Species</u>	Human
<u>Accession no</u>	NM_001904
<u>Tags</u>	N-terminal GST
<u>Bacterially expressed protein</u>	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKF ELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNLGGCPKERA EI SMLEGAVLDIRYGVSR IAYSKDFETLKVDFLSKLPEMLKMFEDRLC HKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIE AIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVL FQGPLG SATQADLMELDMAMEPDRKAAVSHWQQQSYLD SGIHSGATTTAPSL SGKGNPEEEDVDTSQVLYEWEQGFSQSFTQE QVADIDGQYAMTRAQ RVRAAMFPETLDEGMQIPSTQFDAAHPTNVQRLAEPSQMLKHAVVN LINYQDDAELATRAIPELTKLLNDEDQVVVNKAAMVHQLSKKEAS RHAIMRSPQMVS AIVRTM QNTNDVETARCTAGTLHNL SHHREGLLA IFKSGGIPALVKMLGSPVDSVLFYAITTLHNL LLHQEGAKMAVRLA GGLQKMVALLNKTNVKFLAITTDCLQILAYGNQESKL IILASGGPQ ALVNIMRTYTYEKLLWTTSRVLKVL SVCSSNKPAIVEAGGMQALGL HLTDPSQRLVQNCLWTLRNLSDAATKQEGMEGL LGTLVQLLGSDDI NVVTCAAGILSNLTCNNYKNKMMVCQVGGIEALVRTVLRAGDREDI TEPAICALRH LTSRHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPL IKATVGLIRNLALCPANHAPLREQGAIPRLVQLLVRAHQDTQRRTS MGGTQQQFVEGVRMEEIVEGCTGALHILARDVHN RIVIRGLNTIPL FVQLLYSPIENIQRVAAGVLC ELAQDKEAAEAIEAEGATAPL TELL HSRNEGVATYAAAVLFRMSEDKPQDYKKRLSVELTSSLFRTEPMAW NETADLGLDIGAQGEPLGYRQDDPSYRSFHSGGYGQDALGMDPMME HEMGGHHPGADYPVDGLPDLGHAQDLMDGLPPGDSNQLAWFDTDL
<u>Native sequence</u>	Amino acids A2 – L1011 (end) of human beta-catenin. Residue A232 of the fusion protein is equivalent to A2 of the native protein. The GST tag is located at residues 1 - 220

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Protease cleavage PreScission (LEVLFQGPL) residues 221 - 229

Cloning sites *Bam*H1 and *Sma*I of pGEX-6P-1

Nucleotide GGATCCGCTACTCAAGCTGATTTGATGGAGTTGGACATG
sequence of insert GCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGG
CAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGT
GCCACTACCACAGCTCCTTCTCTGAGTGGTAAAGGCAAT
CCTGAGGAAGAGGATGTGGATACCTCCCAAGTCCTGTAT
GAGTGGGAACAGGGATTTTCTCAGTCCTTCACTCAAGAA
CAAGTAGCTGATATTGATGGACAGTATGCAATGACTCGA
GCTCAGAGGGTACGAGCTGCTATGTTCCCTGAGACATTA
GATGAGGGCATGCAGATCCCATCTACACAGTTTGATGCT
GCTCATCCCATAATGTCCAGCGTTTGGCTGAACCATCA
CAGATGCTGAAACATGCAGTTGTAACTTGATTA ACTAT
CAAGATGATGCAGAACTTGCCACACGTGCAATCCCTGAA
CTGACAAAAGTCTAAATGACGAGGACCAGGTGGTGGTT
AATAAGGCTGCAGTTATGGTCCATCAGCTTTCTAAAAAG
GAAGCTTCCAGACACGCTATCATGCGTTCTCCTCAGATG
GTGTCTGCTATTGTACGTACCATGCAGAATACAAATGAT
GTAGAAACAGCTCGTTGTACCGCTGGGACCTTGCATAAC
CTTTCCCATCATCGTGAGGGCTTACTGGCCATCTTTAAG
TCTGGAGGCATTCTGCCCTGGTGAAAATGCTTGGTTCA
CCAGTGGATTCTGTGTTGTTTTATGCCATTACAACTCTC
CACAACCTTTTATTACATCAAGAAGGAGCTAAAATGGCA
GTGCGTTTAGCTGGTGGGCTGCAGAAAATGGTTGCCTTG
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TGGACCACAAGCAGAGTGCTGAAGGTGCTATCTGTCTGC
TCTAGTAATAAGCCGGCTATTGTAGAAGCTGGTGGAATG
CAAGCTTTAGGACTTCACCTGACAGATCCAAGTCAACGT
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TGCAATAATTATAAGAACAAGATGATGGTCTGCCAAGTG
GGTGGTATAGAGGCTCTTGTGCGTACTGTCCTTCGGGCT
GGTGACAGGGAAGACATCACTGAGCCTGCCATCTGTGCT
CTTCGTCATCTGACCAGCCGACACCAAGAAGCAGAGATG
GCCCAGAATGCAGTTCGCCTTCACTATGGACTACCAAGT

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GTGGTTAAGCTCTTACACCCACCATCCCACTGGCCTCTG
ATAAAGGCTACTGTTGGATTGATTGAAATCTTGCCCTT
TGTCCCGCAAATCATGCACCTTTGCGTGAGCAGGGTGCC
ATTCCACGACTAGTTCAGTTGCTTGTTCTGTCACATCAG
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GCTTGGAATGAGACTGCTGATCTTGGAACCTTGATATTGGT
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