

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of USP30 (57-517)

Enzyme description:- USP30 57- 517 (end) = Δ TM

Clone number:- DU36294

Source:- Recombinant from bacteria

Tag:- cleaved from GST-

Purification method:- GSH-agarose

Expression level:- 0.8mg/L

Calculated molecular mass:-

Monoisotopic 52962

Average Mass 52995

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 8.14

Purity:- 50%

Enzyme storage buffer:-

50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT

Storage temperature:- -80°C

Assay:-

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Clone Data Sheet

Protein name

<u>Protein</u>	USP30 (57-517)
<u>Synonyms</u>	UBP30
<u>Clone Number</u>	DU36294
<u>Species</u>	Human
<u>Accession Number</u>	Q70CQ3
<u>Tags</u>	cleaved from GST-
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGKWRNK KFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPK ERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEML KMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAF PKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHP PKSDLEVL<u>FQGPLGSTERKKRRKGLVPGLVNLGNTCFMNSLLQ</u> GLSACPAFIRWLEEFTSQYSRDQKEPPSHQYLSLTLLHLLKAL SCQEVTDDEVLDASCLLDVLRMYRWQISSFEEQDAHELFHVIT SSLEDERDRQPRVTHLFDVHSLEQQSEITPKQITCRTRGSPHP TSNHWKSQHPFHGRLTSNMVCKHCEHQSPVRFDTFDSLSLSIP AATWGHPLTLDHCLHHFISSESVRDVVCDNCTKIEAKGTLNGE KVEHQRTTFVKQLKLGKLPQCLCIHLQRLSWSSHGTPLKRHEH VQFNEFLMDIYKYHLLGHKPSQHNPKLNKNPGPTLELQDGPG APTPVLNQPGAPKTQIFMNGACSPSLLPTLSAPMPFFLPVVPD YSSSTYLFRMAVVVHHGDMHSGHFVTYRRSPPSARNPLSTSN QWLWVSDDTVRKASLQEVLSSSAYLLFYERVLSRMQHQSQECK SEE
Native sequence	
Protease cleavage	Prescission protease site underlined
Cloning sites	BamH1/Not1

**DNA sequence of
insert**

ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCAC
TCGACTTCTTTTGGAAATATCTTGAAGAAAAATATGAAGAGCATTGTATG
AGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTGGGTTTG
GAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAATTAACACA
GTCTATGGCCATCATACTGTTATATAGCTGACAAGCACACATGTTGGGTG
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GATATTAGATACGGTGTTCGAGAATTGCATATAGTAAAGACTTTGAAAC
TCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTTCG
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CCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATACATGGACCC
AATGTGCCTGGATGCGTTCCCAAATTAGTTTGTTTAAAAAACGTATTG
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TGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACCATCCTCC
AAAATCGGATCTGGAAGTTCTGTTCCAGGGGCCCCCTGGGATCCACAGAAA
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CATCAGGTGGCTGGAAGAGTTCACCTCCCAGTACTCCAGGGATCAGAAGG
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CGTGCAGTTCAATGAGTTCCTGATGATGGACATTTACAAGTACCACCTCC
TTGGACATAAAACCTAGTCAACACAACCCTAAACTGAACAAGAACCCAGGG
CCTACACTGGAGCTGCAGGATGGGCCGGGAGCCCCCACACCAGTTCTGAA
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CATCTTTATTGCCAACGCTGTCAGCGCCGATGCCCTTCCCTCTCCAGTT
GTTCCCGACTACAGCTCCTCCACATACCTCTTCCGGCTGATGGCAGTTGT
CGTCCACCATGGAGACATGCACTCTGGACACTTTGTCACTTACCGACGGT
CCCCACCTTCTGCCAGGAACCTCTCTCAACTAGCAATCAGTGGCTGTGG
GTCTCCGATGACACTGTCCGCAAGGCCAGCCTGCAGGAGTCTGTCTC
CAGCGCCTACCTGCTGTTCTACGAGCGCGTCCTTTCCAGGATGCAGCACC
AGAGCCAGGAGTGCAAGTCTGAAGAATGA