



*Division of Signal Transduction Therapy*

**Clone Data Sheet**

**USP30 [1 - 517]**

**Protein** USP30 [1 - 517]

**Clone number** DU 36244

**Species** Human

**Accession number** NM\_032663.4

**Tags** N-terminal GST

**Baculovirus  
expressed protein**

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFEL  
GLEFPNLPYYIDGDVKLTSMAIIRYIADKHNMLGGCPKERAIEISMLE  
GAVLDIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLN  
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKY  
LKSSKYIAWPLQGWQATFGGGDHPKSDLEVL FQGPLGSMLSSRAEAA  
**MTAADRAIQRFLRTGAAVRYKVMKNWGVIGGIAAALAAGIYVIWGPIT**  
**ERKKRRKGLVPLVNLGNTCFMNSLLQGLSACPAFIRWLEEFTSQYSR**  
**DQKEPPSHQYLSLTLHLLKALSCQEVTDDEVLDASCLLDVLRMYRWQ**  
**ISSFEEQDAHEL FHVITSSLEDERDRQPRVTHLFDVHSLEQOSEITPK**  
**QITCRTRGSPHPTS NHWKSQHPPFHGRLTSNMVCKHCEHQSPVRFDTFD**  
**SLSLSIPAATWGHPLTLDHCLHFFISSESVRDVVCDNCTKIEAKGTLN**  
**GEKVEHQRTTFVKQLKLGKLPQCLCIHLQRLSWSSHGTPLKRHEHVQF**  
**NEFLMMDIYKYHLLGHKPSQHNPKNKPNPGPTLELQDGGAPT PVLNQ**  
**PGAPKTQIFMNGACSPSLLPTLSAPMPFPLPVVPDYSSSTYLFRLMAV**  
**VVHHGDMHSGHFV TYRRSPPSARNPLSTSNQWLWVSDDTV RKASLQEV**  
**LSSAYLLFYERVLSRMQHQSQECKSEE**

**Native sequence** Amino acids M1 – E517 (end) of human USP30.

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 site (LEVLFQGP) residues 221 – 228

**Cloning sites** *Bam*H1 and *Not*1 sites of pFastBac GST 6P1

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**Nucleotide  
sequence of  
insert**

ggatccATGCTGAGCTCCCGGGCCGAGGCGGCGATGACCGCGGCCGAC  
AGGGCCATCCAGCGCTTCCTGCGGACCGGGGCGGCCGTCAGATATAAA  
GTCATGAAGAAGTGGGGAGTTATAGGTGGAATTGCTGCTGCTCTTGCA  
GCAGGAATATATGTTATTTGGGGTCCCATTACAGAAAGAAAGAAGCGT  
AGAAAAGGGCTTGTGCCTGGCCTTGTTAATTTAGGGAACACCTGCTTC  
ATGAACTCCCTGCTACAAGGCCTGTCTGCCTGCTCCTGCTTTTCATCAGG  
TGGCTGGAAGAGTTCACCTCCCAGTACTCCAGGGATCAGAAGGAGCCC  
CCCTCACACCAGTATTTATCCTTAACACTCTTGACCTTCTGAAAGCC  
TTGTCCTGCCAAGAAGTTACTGATGATGAGGTCTTAGATGCAAGCTGC  
TTGTTGGATGTCTTAAGAATGTACAGATGGCAGATCTCATCATTTGAA  
GAACAGGATGCTCACGAATTATTCATGTACATTACCTCGTCATTGGAA  
GATGAGCGAGACCGCCAGCCTCGGGTCACACATTTGTTTGATGTGCAT  
TCCCTGGAGCAGCAGTCAGAAATAACTCCCAAACAAATTACCTGCCGC  
ACAAGAGGGTCACCTCACCCCTACATCCAATCACTGGAAGTCTCAACAT  
CCTTTTCATGGAAGACTCACTAGTAATATGGTCTGCAAACACTGTGAA  
CACCAGAGTCCTGTTTCGATTTGATACCTTTGATAGCCTTTCACTAAGT  
ATTCCAGCCGCCACATGGGGTCACCCATTGACCTGGACCACTGCCTT  
CACCCTTCATCTCATCAGAATCAGTGCGGGATGTTGTGTGTGACAAC  
TGTACAAAGATTGAAGCCAAGGGAACGTTGAACGGGGAAAAGGTGGAA  
CACCAGAGGACCACTTTTGTAAACAGTTAAAACCTAGGGAAGCTCCCT  
CAGTGTCTCTGCATCCACCTACAGCGGCTGAGCTGGTCCAGCCACGGC  
ACGCCTCTGAAGCGGCATGAGCACGTGCAGTTCAATGAGTTCCTGATG  
ATGGACATTTACAAGTACCACCTCCTTGGACATAAACCTAGTCAACAC  
AACCCTAAACTGAACAAGAACCAGGGCTACACTGGAGCTGCAGGAT  
GGGCCGGGAGCCCCACACCAGTTCTGAATCAGCCAGGGGCCCCAAA  
ACACAGATTTTTTATGAATGGCGCCTGCTCCCATCTTTATTGCCAACG  
CTGTCAGCGCCGATGCCCTTCCCTCTCCAGTTGTTCCCGACTACAGC  
TCCTCCACATACCTCTTCCGGCTGATGGCAGTTGTCGTCCACCATGGA  
GACATGCACTCTGGACACTTTGTCACTTACCGACGGTCCCCACCTTCT  
GCCAGGAACCCTCTCTCAACTAGCAATCAGTGGCTGTGGGTCTCCGAT  
GACACTGTCCGCAAGGCCAGCCTGCAGGAGGTCCTGTCTCCAGCGCC  
TACCTGCTGTTCTACGAGCGGTCCTTTCCAGGATGCAGCACCAGAGC  
CAGGAGTGCAAGTCTGAAGAAatgagcggccgc