

## *Division of Signal Transduction Therapy*

### **Standard Operating Procedure**

#### **Preparation of active USP42 [88 – 451]**

**Enzyme description:-** USP42 [88 - 451]

**Clone number:-** DU 61926

**Source:-** Recombinant

**Expression system:-** *E.coli*

**Tag:-** N-terminal GST

**Purification method:-** GSH Sepharose

**Calculated molecular mass:-**

Monoisotopic 67, 739.07 daltons

Average Mass 67, 783.23 daltons

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 8.60

**Purity:-** 80 %

**Activation protocol:-** Constitutively active

**Enzyme storage buffer:-**

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

**Storage temperature:-** -70 °C

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### Clone Data Sheet

USP42 [88 - 451]

<b><u>Protein</u></b>	USP42 [88 - 451]
<b><u>Clone number</u></b>	DU 61926
<b><u>Species</u></b>	Human
<b><u>Accession number</u></b>	Q9H9J4-1
<b><u>Tags</u></b>	N-terminal GST
<b><u>Bacterially expressed protein</u></b>	<p>MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGA VLDIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFGQPLGSP<b>PQKVLFPSEKICL</b> <b>KWQQTHRVGAGLQNLGNTCFANAALQCLTYTPPLANYMLSHEHSKTCHA</b> <b>EGFCMMCTMQAHITQALS</b>NPGDVIKPMFVINEMRRIARHFRFGNQEDAH <b>EFLQYTV</b>DAMQKACLN<b>GSNK</b>LD<b>RHTQ</b>ATTLVCQIFGGYLRSRVKCLNCK GVSDTFDPYLDIT<b>LEIKAAQSV</b>NKALEQFVKPEQLDG<b>ENSYKCSKCKKM</b> VPAS<b>KRFTIHRSS</b>NVLTLSL<b>KRFANFTGGK</b>IAKDVKYPEYLDIRPYMSQ P<b>NGEPIVYVLYAVLVHTGF</b>NCHAGHYFCYIKAS<b>NGLWYQM</b>ND<b>SIVSTSD</b> IRSVLS<b>QQAYVLFYIRSHDV</b>KNGGEL<b>THPTHSPGQSSPRPVISQRVVTN</b> <b>KQAAPGF</b></p>
<b><u>Native sequence</u></b>	<p>Amino acids P88 – F451 (end residue is R1324) of human USP42. Residue P232 of the fusion protein is equivalent to P88 of the native enzyme. The GST tag is located at residues 1 – 220.</p>
<b><u>Protease cleavage</u></b>	PreScission ( <u>LEVLFQGP</u> ) residues 221 - 229
<b><u>Cloning sites</u></b>	<i>Bam</i> H1 and <i>Not</i> 1 sites of pGEX 6P-1

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### Nucleotide Sequence

ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCA  
CTCGACTTCTTTTGGAAATATCTTGAAGAAAAATATGAAGAGCATTTGTA  
TGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTGGGT  
TTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAATTAA  
CACAGTCTATGGCCATCATAACGTTATATAGCTGACAAGCACAAACATGTT  
GGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCG  
GTTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGTAAAGACT  
TTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAA  
AATGTTTGAAGATCGTTTATGTCATAAAACATATTTAAATGGTGATCAT  
GTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTAT  
ACATGGACCCAATGTGCCTGGATGCGTTCCCAAATTAGTTTGTTTTAA  
AAAACGTATTGAAGCTATCCACAAATTGATAAGTACTTGAAATCCAGC  
AAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTG  
GCGACCATCCTCCAAAATCGGATCTGGAAGTTCTGTTCCAGGGGCCCT  
GGGATCCCCTCCACAGAAAGTTCTTTTCCCATCTGAGAAGATTTGTCTT  
AAGTGGCAACAACTCATAGAGTTGGAGCTGGGCTCCAGAATTTGGGCA  
ATACCTGTTTTGCCAATGCAGCACTGCAGTGTTTAACCTACACACCACC  
TCTTGCCAATTACATGCTATCACATGAACACTCCAAAACATGTCATGCA  
GAAGGCTTTTGTATGATGTGTACAATGCAAGCACATATTACCCAGGCAC  
TCAGTAATCCTGGGGACGTTATTAACCAATGTTTGTATCAATGAGAT  
GCGGCGTATAGCTAGGCACCTCCGTTTTTGGAAACCAAGAAGATGCCCAT  
GAATTCCTTCAATACACTGTTGATGCTATGCAGAAAGCATGCTTGAATG  
GCAGCAATAAATTAGACAGACACACCAGGCCACCACTCTTGTTTGTCA  
GATATTTGGAGGATACCTAAGATCTAGAGTCAAATGTTTAAATTGCAAG  
GGCGTTTCAGATACTTTTGTATCCATATCTTGATATAACATTGGAGATAA  
AGGCTGCTCAGAGTGTCAACAAGGCATTGGAGCAGTTTGTGAAGCCGGA  
ACAGCTTGATGGAGAAAACCGTACAAGTGCAGCAAGTGTA AAAAGATG  
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CACTTTCTCTGAAACGTTTTTGCAAATTTTACCGGTGGAAAAATTGCTAA  
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CCCAACGGAGAGCCAATTGTCTACGTCTTGTATGCAGTGCTGGTCCACA  
CTGGTTTTAATTGCCATGCTGGCCATTACTTCTGCTACATAAAAGCTAG  
CAATGGCCTCTGGTATCAAATGAATGACTCCATTGTATCTACCAGTGAT  
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CCCATGATGTGAAAAATGGAGGTGAACTTACTCATCCACCCATAGCCC  
CGGCCAGTCCTCTCCCCGCCCGTCATCAGTCAGCGGGTTGTCACCAAC  
AAACAGGCTGCGCCAGGCTTTtga