

MRC PPU Reagents and Services

Standard Operating Procedure

Preparation of active USP38 [1 – 1042]

Enzyme description:- USP38 [1 - 1042]

Clone number:- DU 35473

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-

Monoisotopic 144, 257.22 daltons

Average Mass 144, 349.40 daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.84

Purity:- >85 %

Activation protocol:- Constitutively active

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA,
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF

Storage temperature:- -70 °C

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Clone Data Sheet

USP38 [1 - 1042]

Protein USP38 [1 - 1042]

Clone number DU 35473

Species Human

Accession number NM_032557.6

Tags N-terminal GST

**Bacterially
expressed protein**

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG
LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGA
VLDIRYGVSR IAYS KDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS
KYIAWPLQGWQATFGGGDHPPKSDLEVLFGQPLGSPGIPGSTRAAAMDK
ILEGLVSS**S**HPLPLKRVIVRKV**V**ESA**E**HWLDEA**Q**CEAMFDLT**T**RL**I**LEG
QDPF**Q**R**Q**VGH**Q**VLEAYARYHRPEFESFFNKTFVLG**L**LH**Q**GYHSLDRKDV
AILDY**I**H**N**GLKLIMSCPSVLDL**F**SLL**Q**VEVLRMVCERPE**P**QLCARLS**D**L
LTDFV**Q**CIPKGKLSIT**F**C**Q**QLV**R**TIGHF**Q**CVST**Q**ERELREYVS**Q**VT**K**VS
NLL**Q**NIWKAEPATLLPS**L**QEVFASISSTDASFEP**S**VALASLV**Q**HIPL**Q**M
ITVLIRSLT**T**DPNVKDASMT**Q**ALCRMIDWLSWPLA**Q**HVDTWVIAL**L**KGL
AAV**Q**KFTILIDVTL**L**KIELVF**N**RLWFPLVRPGALAVLS**H**MLLS**F**QHS**P**E
AFHLIVPHVVNLVHS**F**KNDGLPSSTAFLV**Q**LTEL**I**HCM**M**YHYS**G**FPDLY
EP**I**LEAIKDFPK**P**SEEKIKLIL**N**QSAWTS**Q**SN**S**LASCL**S**R**L**SGK**S**ET**G**K
TGLINLGNTCYMNSV**I**QALF**M**ATDFRR**Q**VLSL**N**LG**C**NSL**M**KK**L**QHL**F**A
FLAHT**Q**REAYAPR**I**FF**E**ASRPPWFT**P**RS**Q**QDCSEYLR**F**LLDR**L**HEE**E**K**I**
LK**V**QASHKPSE**I**ECSET**S**LQEVASKAAVLTET**P**RTSDGEKT**L**IEKM**F**G
GKL**R**THIRCLNCRSTS**Q**KVEAF**T**DSLAF**C**PSS**S**LENMSV**Q**DPASS**P**SI
QDGGL**Q**ASVPG**P**SEEPVVYN**P**TTAA**F**ICDSL**V**NEKTIGSP**P**NEFY**C**SE
NTSV**P**NESNKILVNKDVP**Q**KPGGET**P**SVTDLL**N**YFLA**P**EIL**T**GD**N**Q**Y**Y
CENCAS**L**QNAEK**T**MQITEE**P**EYLIL**T**LLR**F**SYD**Q**KYHVR**R**KILD**N**VS**L**P
LVLELPV**K**RITS**F**SSLSESWSVDV**D**FTD**L**SEN**L**AK**K**L**P**SG**T**DEAS**C**TK
LVPYLLSSVV**V**HSGISSES**G**HYY**S**YARNITSTDSSY**Q**MYH**Q**SEAL**A**LAS
S**Q**SHLLGRD**S**PAVFE**Q**DLENK**E**MSKEWFL**F**ND**S**RV**T**FT**S**F**Q**SV**Q**K**I**TS
R**F**PKDTAYVLLY**K**K**Q**HST**N**GLSG**N**NP**T**SG**L**WING**D**P**P**L**Q**KELMD**A**IT**K**D
NKLY**L**Q**E**QELNARARAL**Q**AASAS**C**S**F**RPNG**F**DDND**P**PG**S**CG**P**TGGGGGG
GFNTV**G**RL**V**F

Native sequence Amino acids M1 – F1042 (end) of human USP38.
Residue M243 of the fusion protein is equivalent to M1 of the native
enzyme. The GST tag is located at residues 1 – 220.

Protease cleavage PreScission (**LEVLFGQP**) residues 221 - 229

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Cloning sites

Not1 site of pGEX6P-2

Nucleotide Sequence of Insert

gcggccgcgATGGACAAGATCCTGGAGGGCCTTGTGAGTTCCTCGCATCCCCTGCCCCTCAAGCGG
GTGATTGTGCGGAAGGTGGTGGGAATCGGCGGAGCACTGGCTAGACGAGGCGCAGTGCAGAGGCCATG
TTTGACCTGACGACCCGGCTCATCCTGGAGGGCCAGGACCCTTTCCAGCGGCAGGTGGGGCACCAG
GTGCTGGAGGCCCTACGCACGATACCACCGGCCAGAGTTCGAGTCCTTCTTCAACAAGACCTTCGTG
TTGGGCCCTCCTTCATCAGGGCTACCACTCTCTGGACAGGAAGGATGTAGCCATCCTGGACTACATT
CACAACGGCCTGAAGCTGATTATGAGCTGTCCGTCCGTGCTGGATCTCTTTAGCCTCCTGCAGGTA
GAGGTGTTACGGATGGTGTGTGAGAGGCCGGAGCCGCAGCTCTGTGCCCAGCTGAGCGACCTTCTG
ACCGACTTTGTGCAATGCATCCCCAAGGGGAAATTGTCCATCACGTTCTGTCAACAGCTGGTTCGA
ACGATAGGCCATTTCCAGTGCCTGTCCACCCAGGAAAGAGAGCTGCGGGAATATGTCTCCAGGTG
ACAAAAGTGAGTAACTTGCTGCAGAACATCTGGAAGGCCGAGCCTGCCACACTACTGCCTTCCCTG
CAAGAAGTTTTTGCAAGCATCTCTTCCACAGATGCATCATTTGAACCTTCTGTAGCATTGGCAAGC
CTTGTGCAGCATATTCCCTCTTCAGATGATTACAGTTCTCATCAGGAGCCTTACTACGGATCCAAAT
GTAAAAGATGCAAGTATGACCCAAGCCCTTTGCAGAATGATTGACTGGCTATCCTGGCCATTGGCT
CAGCATGTGGATACATGGGTAATTGCACTCCTGAAAGGACTGGCAGCTGTCCAGAAGTTTACTATT
TTGATAGATGTTACTTTGCTGAAAATAGAACTGGTTTTTAATCGACTTTGGTTTCTCTTGTGAGA
CCTGGTGCTCTTGCAGTTCTTTCTCACATGCTGCTTAGCTTTCAGCATTTCTCCAGAGGCGTTCCAT
TTGATTGTTCCCTCATGTGGTTAATTTGGTTCAATTCTTTCAAAAATGATGGTCTGCCTTCAAGTACA
GCCTTCTTAGTACAATTAACAGAATTGATACACTGTATGATGTATCATTATTCTGGATTTCCAGAT
CTCTATGAACCTATTCTGGAGGCAATAAAGGATTTTCCTAAGCCCAGTGAAGAGAAGATTAAAGTTA
ATTCTCAATCAAAGTGCCTGGACTTCTCAATCCAATTCTTTGGCGTCTTGCTTGTCTAGACTTTCT
GGAAAATCTGAAACTGGGAAAATGGTCTTATTAACCTAGGAAATACATGTTATATGAACAGTGTT
ATACAAGCCTTGTTTATGGCCACAGATTTCCAGGAGACAAGTATTATCTTTAAATCTAAACGGGTGC
AATTCATTAATGAAAAAATTACAGCATCTTTTTGCCTTTCTGGCCCATACACAGAGGGAAGCATAC
GCACCTCGGATATTCTTTGAGGCTTCCAGACCTCCATGGTTTACTCCCAGATCACAGCAAGACTGT
TCTGAATACCTCAGATTTCTCCTTGACAGGCTCCATGAAGAAGAAAAGATCTTGAAAAGTTCAGGCC
TCACACAAGCCTTCTGAAATTCTGGAATGCAGTGAACTTCTTTACAGGAAGTAGCTAGTAAAGCA
GCAGTACTAACAGAGACCCCTCGTACAAGTGACGGTGAGAAGACTTTAATAGAAAAAATGTTTGA
GGAAAATACGAACCTACATACGTTGTTTGAAGTGCAGGAGTACCTCACAAAAAGTGGAAGCCTTT
ACAGATCTTTTCGCTTGCCTTTTGTCTTCTCTTCTTTGGAAAACATGTCTGTCCAAGATCCAGCA
TCATCACCCAGTATACAAGATGGTGGTCTAATGCAAGCCTCTGTACCCGGTCTTTCAGAAGAACCA
GTAGTTTATAATCCAACAACAGCTGCCTTCATCTGTGACTCACTTGTGAATGAAAAAACCATAGGC
AGTCCTCCTAATGAGTTTACTGTTCTGAAAACACTTCTGTCCCTAACGAATCTAACAAGATTCTT
GTTAATAAAGATGTACCTCAGAAACCAGGAGGTGAAACCACACCTTCAGTAACTGACTTACTAAAT
TATTTTTTGGCTCCAGAGATTCTTACTGGTGATAACCAATATATTGTGAAAACGTGTGCCTCTCTG
CAAAATGCTGAGAAAACATGCAAATCACGGAGGAACCTGAATACCTTATTCTTACTCTCCTGAGA
TTTTTCATATGATCAGAAGTATCATGTGAGAAGGAAAATTTTAGACAATGTATCACTGCCACTGGTT
TTGGAGTTGCCAGTTAAAAGAATTACTTCTTTCTCTTCATTGTCAGAAAGTTGGTCTGTAGATGTT
GACTTCACTGATCTTAGTGAGAACCTTGCTAAAAAATTAAAGCCTTCAGGGACTGATGAAGCTTCC
TGCACAAAATTGGTGCCCTATCTATTAAGTTCCGTTGTGGTTCCTCTGGTATATCCTCTGAAAGT
GGGCATTACTATTCTTATGCCAGAAATATCACAAAGTACAGACTCTTCATATCAGATGTACCACCAG
TCTGAGGCTCTGGCATTAGCATCCTCCCAGAGTCATTTACTAGGGAGAGATAGTCCCAGTGCAGTT
TTTGAACAGGATTTGGAAAATAAGGAAATGTCAAAAGAATGGTTTTTATTTAATGACAGTAGAGTG
ACATTTACTTTCATTTTCAGTCAGTCCAGAAAATTACGAGCAGGTTTCCAAAGGACACAGCTTATGTG
CTTTTGTATAAAAAACAGCATAGTACTAATGGTTTAAAGTGGTAATAACCCAACCAGTGGACTCTGG
ATAAATGGAGACCCACCTCTACAGAAAGAACTTATGGATGCTATAACAAAAGACAATAAACTATAT
TTACAGGAACAAGAGTTGAATGCTCGAGCCCGGGCCCTCCAAGCTGCATCTGCTTCATGTTTCAATTT
CGGCCCAATGGATTTGATGACAACGACCCACCAGGAAGCTGTGGACCAACTGGTGGAGGGGGTGA
GGAGGATTTAATACAGTTGGCAGACTCGTATTTtgagcggcc

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