

Division of Signal Transduction Therapy

Standard Operation Procedure

GST-OTUD3

<u>Enzyme description:-</u>	GST-OTUD3
<u>Clone number:-</u>	DU21323
<u>Source:-</u>	BL21 Recombinant
<u>Tag:-</u>	N-terminal GST tag
<u>Purification method:-</u>	GSH sepharose
<u>Expression level:-</u>	0.8 mg/L

Calculated molecular mass:-

Monoisotopic	71903 Da
Average Mass	71945 Da
[cysteines reduced, methionines have not been oxidised]	

Theoretical pI:- 7.32

Purity:- 50%

Enzyme storage buffer:-

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

Storage temperature:- -80°C

Assay:-

Ub-Rho110-Gly cleavage assay monitored by Ex/Em 485/535 nm

Assay buffer:-

40 mM Tris pH 7.5, 100 mM NaCl, 5 mM DTT, 0.01% Triton X-100, 0.005% Ovalbumin, 0.5 µM Ub-Rho110-Gly

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Clone Data Sheet

GST-OTUD3

Protein GST-OTUD3

Synonyms

Clone Number DU21323

Species Human

Accession Number Protein: Q5T2D3 DNA: NM_015207

Tags N-terminal GST tag

Amino acid sequence of expressed protein MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFP
NLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGV
SRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDAL
DVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLOGWQATFGG
GDHPPKSDLEVLFOGPLGSM**SRKQAAKSRPGSGSRKAEAERKRD**ERAARRALA
KERRNRPESGGGGG**C**EEEFV**S**FAN**Q**L**Q**AL**G**L**K**L**R**EV**P**GD**G**N**C**L**F**R**A**L**G**D**Q**LE**G**
HSR**N**HL**K**HR**Q**ET**V**D**Y**MI**K**Q**R**ED**F**EP**F**VED**D**IP**F**E**K**H**V**AS**L**AK**P**GT**F**AG**N**DA**I**V
AF**A**R**N**H**Q**L**N**V**V**I**H**Q**L**N**A**P**L**W**Q**I**R**G**T**E**K**S**S**V**R**E**L**H**I**A**Y**R**Y**G**E**H**Y**D**S**V**R**R**I**N**D**N**S**
EAP**A**H**L**Q**T**D**F**Q**M**L**H**Q**D**ES**N**K**R**E**K**I**K**T**K**G**M**D**S**E**D**D**L**R**D**E**V**E**D**A**V**Q**K**V**C**N**A**T**G**C**S**
DF**N**L**I**V**Q**N**L**E**A**E**N**Y**N**I**E**S**A**I**I**A**V**L**R**M**N**Q**G**K**R**N**A**E**N**L**E**P**S**G**R**V**L**K**Q**C**G**P**L**W**E**
EG**G**S**G**A**R**I**F**G**N**Q**L**N**E**G**R**T**E**N**N**K**A**Q**A**S**P**S**E**E**N**K**A**N**K**N**Q**L**A**K**V**T**N**K**Q**R**R**E**Q**Q**W**M
EK**K**K**R**Q**E**E**R**H**R**H**K**A**L**E**S**R**G**S**H**R**D**N**N**R**S**E**A**E**A**N**T**Q**V**T**L**V**K**T**F**A**A**L**N**I

Native sequence in bold

Protease cleavage Precision site underlined

Cloning sites BamH1 / Not1

**DNA sequence of
insert**

GGATCCATGTCCCGAAAGCAGGCGGGCGAAGAGCCGGCCGGGCAGCGGCAGCCG
GAAAGCCGAGGCCGAGCGCAAGCGGGACGAGCGGGCGGGCGCCGGGCCCTGG
CCAAGGAGCGGGCGGAATCGGCCGGAGTCTGGCGGGCGGGCGGGCTGCGAGGAG
GAGTTCGTCAGCTTCGCCAACAGCTGCAGGCCCTGGGGCTGAAGCTGCGGGA
GGTGCCGGGGGACGGCAATTGCTTGTTTCAGAGCTCTTGGTGATCAATTGGAGG
GACTCACGAAATCATCTCAAGCACAGACAGGAGACAGTGGACTACATGATA
AAGCAGCGGGAAGATTTTGAACCCTTTGTAGAAGATGACATTCCTTTTGAGAA
GCATGTGGCCAGTTTGGCAAAGCCTGGTACTTTTGTGGCAATGATGCAATTG
TAGCCTTTGCAAGAAATCATCAGTTGAATGTAGTGATTCATCAACTTAATGCC
CCTTTGTGGCAGATTCGTGGTACAGAGAAAAGCAGCGTGAGGGAGTTACACAT
CGCATATCGGTATGGAGAGCACTACGACAGTGTTCCGGAGGATCAATGACAAC
CAGAGGCACCTGCACATCTCCAGACGGATTTTCAGATGCTTCATCAAGATGAA
TCAAATAAAAAGAGAAAAGATCAAGACAAAGGGAATGGACTCTGAAGACGACCT
GAGAGATGAAGTAGAGGATGCTGTCCAGAAAGTTTGTAATGCAACTGGATGTT
CAGATTTTAATTTAATAGTCCAGAACCTGGAAGCTGAAAATTATAATATTGAA
TCTGCAATAATTGCCGTGCTTCGGATGAACCAAGGGAAGAGAAATAATGCAGA
AGAGAATCTTGAGCCCAGTGGTCGAGTGCTGAAGCAGTGTGGCCCTTTGTGGG
AGGAGGGTGGCAGTGGTGCCAGAATCTTTGGAAATCAGGGCTTAAATGAAGGC
AGGACCGAAAACAATAAGGCACAGGCCAGCCCTAGTGAAGAAAACAAAGCAA
TAAAACCAGCTCGCAAAGGTCACAAACAAACAGAGGCGAGAACAGCAGTGGA
TGGAGAAGAAGAAGCGGCAGGAGGAGAGGCACCGCCACAAAGCCCTGGAGAGC
AGAGGTAGCCACAGGGACAATAACAGAAGCGAAGCAGAGGCGAACACGCAGGT
CACCTTGGTGAAGACCTTCGCCGCTCTCAACATCTGAGCGGCCGC