

## *Division of Signal Transduction Therapy*

### **Standard Operation Procedure**

#### **Preparation of GST-ATG10**

**Enzyme description:-** GST-ATG10 1-220 (full length)

**Clone number:-** DU31144

**Source:-** BL21 recombinant

**Tag:-** N-terminal GST-tag

**Purification method:-** GSH-Sepharose

**Expression level:-** 12mg/L

**Calculated molecular mass:-**

Monoisotopic 52068 Da  
Average Mass 52101 Da  
[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 7.8

**Purity:-** 90%

**Enzyme storage buffer:-**

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

**Storage temperature:-** -80°C

**Assay:-**

Not tested yet.

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**Clone Data Sheet**

**GST-ATG10**

**Protein** ATG10  
**Synonyms** APG10L  
**Clone Number** DU31144  
**Species** Human  
**Accession Number** Protein: Q9H0Y0 DNA: NM\_031482  
**Tags** N-terminal GST-tag

Aminoacid sequence of the expressed protein  
MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL  
EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGAVL  
DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH  
PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA  
WPLQGWQATFGGGDHPKSDLEVLFOGPLGSMEDEFI**G**EKT**F**QRY**C**A**E**F  
**I**K**H**S**Q****Q****I**G**D**S**W**E**R**P**S**K**D**C**S**D**G**Y**M**C**K**I**H****F****Q**I**K**N**G**S**V**M**S**H**L**G**A**S**T**H**G****Q****T****C**L  
**P**M**E**E**A**F**E**L**P**L**D**D**C**E**V**I**E**T**A**A**S**E**V**I**K**Y**E**Y**H**V**L**Y**S**C**S**Y**Q**V**P**V**L**Y**F**R**A**S**F**L**D**  
**G**R**P**L**T**L**K**D**I**W**E**G**V**H**E**C**Y**K**M**R**L**L**Q**G**P**W**D**T**I**T**Q****Q****E**H**P**I**L**G**Q**P**F**F**V**L**H**P**C**K**T**N  
**E**F**M**T**P**V**L**K**N**S**Q**K**I**N**K**N**V**N**I**T**S**W**L**S**I**V**G**P**V**V**G**L**N**L**P**L**S**Y**A**K**A**T**S****Q****D**E**R**N**V**  
**P**

Native sequence in bold  
Protease cleavage Precission protease site underlined  
Cloning sites BamH1 / NotI

**DNA sequence of insert**  
GGATCCATGGAAGAAGATGAGTTCATTGGAGAAAAACATTCCAACGTTA  
TTGTGCAGAATTCATTAAACATTCACAACAGATAGGTGATAGTTGGGAAT  
GGAGACCATCAAAGGACTGTTCTGATGGCTACATGTGCAAAATACACTTT  
CAAATTAAGAATGGGTCTGTGATGTCACATCTAGGAGCATCTACCCATGG  
ACAGACATGTCTTCCCATGGAGGAGGCTTTTCGAGCTACCCTTGGATGATT  
GTGAAGTGATTGAAACTGCAGCAGCGTCCGAAAGTGATTAATATGAGTAT  
CATGTCTTATATTCCTGTAGCTACCAAGTGCCCTGACTTTACTTTAGGGC  
AAGCTTTTTAGATGGGAGACCTTTAACTCTGAAGGACATATGGGAAGGAG  
TTCATGAGTGCTATAAGATGCGACTGCTACAGGGACCATGGGACACTATT  
ACGCAACAGGAACATCCAATACTTGGGCAACCCTTTTTTGTACTTCATCC  
CTGCAAGACGAATGAATTCATGACTCCTGTATTAAAGAATTCTCAGAAAA  
TCAATAAGAATGTCAACTATATCACATCATGGCTGAGCATTGTAGGGCCA  
GTTGTTGGGCTGAATCTACCTCTGAGTTATGCCAAAGCAACGTCTCAGGA  
TGAACGAAATGTCCCTTAAGCGGCCGC