

## *Division of Signal Transduction Therapy*

### **Standard Operation Procedure**

#### **Preparation of GST-PSMD4**

**Enzyme description:-** GST-PSMD4 1-377 (full length)

**Clone number:-** DU34129

**Source:-** BL21 recombinant

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

**Purification method:-** GSH-Sepharose

**Expression level:-** 2mg/L

**Calculated molecular mass:-**

Monoisotopic 67517 Da

Average Mass 67517 Da

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 4.88

**Purity:-** 90%

**Enzyme storage buffer:-**

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

**Storage temperature:-** -80°C

**Assay:-**

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### **Clone Data Sheet**

#### **GST-PSMD4**

<b><u>Protein</u></b>	PSMD4 (1-377 )
<b><u>Synonyms</u></b>	26S proteasome regulatory subunit RPN10, S5A
<b><u>Clone Number</u></b>	DU34129
<b><u>Species</u></b>	Human
<b><u>Accession Number</u></b>	Protein: P55036, DNA: NM_002810
<b><u>Tags</u></b>	N-terminal GST-tag
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEF PNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRY GVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLY DALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLOGWQA TFGGGDHPPKSDLEVL <u>FQGPLGSMVLESTMVCVDNSEYMRNGDFLPTRLQAO</u> <b>QDAVNI</b> VCHSKTRSNPENN <u>VLITLANDCEVLTTLTPDTGRILSKLHTVQPK</u> <b>GKIT</b> TFCTGIRVAHLALKHRQGNHKMRIIAFVGSPVEDNEKDLVKLAKRLKK <b>EKNV</b> DIINFGEEVNT <u>TEKLTAFVNTLNGKDG</u> TGSHLVTVP <b>PGPSLADALIS</b> <b>SPILAGEGGAMLGLGASDFEFGVDPSADPELALALRVSMEEQRQRQEEEAR</b> <b>AAAASAAEAGIATTGTEDSDDALLKMTISQQEFGR</b> TGLPDLSSMTEEEQIAY <b>AMQMSLQGA</b> EFGQAE <b>SADIDASSAMDTSEPAKEEDDYDVMQDPEFLQSVLEN</b> <b>LPGVDPNNEAIRNAMGSLASQATKDGKKDKKEEDKK</b>
Native sequence	in bold, Start Met is missing
Protease cleavage	Prescission site underlined
Cloning sites	BamH1-Age1-Not1 3 way ligation

**DNA sequence of  
insert**

GGATCCATGGTGTGGAAAGCACTATGGTGTGTGTGGACAACAGTGAGTA  
TATGCGGAATGGAGACTTCTTACCCACCAGGCTGCAGGCCCAGCAGGATG  
CTGTCAACATAGTTTGTCAATCAAAGACCCGCAGCAACCCTGAGAACAAC  
GTGGGCCTTATCACACTGGCTAATGACTGTGAAGTGCTGACCACACTCAC  
CCCAGACACTGGCCGTATCCTGTCCAAGCTACATACTGTCCAACCCAAGG  
GCAAGATCACCTTCTGCACGGGCATCCGCGTGGCCCATCTGGCTCTGAAG  
CACCGACAAGGCAAGAATCACAAGATGCGCATCATTGCCTTTGTGGGAAG  
CCCAGTGGAGGACAATGAGAAGGATCTGGTGAAGCTGGCTAAACGCCTCA  
AGAAGGAGAAAGTAAATGTTGACATTATCAATTTTGGGGAAGAGGAGGTG  
AACACAGAAAAGCTGACAGCCTTTGTAAACACGTTGAATGGCAAAGATGG  
AACCGGTTCTCATCTGGTGACAGTGCCTCCTGGGCCAGTTTGGCTGATG  
CTCTCATCAGTTCTCCGATTTTGGCTGGTGAAGGTGGTGCCATGCTGGGT  
CTTGGTGCCAGTGACTTTGAATTTGGAGTAGATCCCAGTGCTGATCCTGA  
GCTGGCCTTGGCCCTTCGTGTATCTATGGAAGAGCAGCGGCAGCGGCAGG  
AGGAGGAGGCCCGGCGGCAGCTGCAGCTTCTGCTGCTGAGGCCGGGATT  
GCTACGACTGGGACTGAAGACTCAGACGATGCCCTGCTGAAGATGACCAT  
CAGCCAGCAAGAGTTTGGCCGCACTGGGCTTCTGACCTAAGCAGTATGA  
CTGAGGAAGAGCAGATTGCTTATGCCATGCAGATGTCCCTGCAGGGAGCA  
GAGTTTGGCCAGGCGGAATCAGCAGACATTGATGCCAGCTCAGCTATGGA  
CACATCTGAGCCAGCCAAGGAGGAGGATGATTACGACGTGATGCAGGACC  
CCGAGTTCTTCAGAGTGTCTTAGAGAACCCTCCAGGTGTGGATCCCAAC  
AATGAAGCCATTTCGAAATGCTATGGGCTCTCTGGCCTCCAGGCCACCAA  
GGACGGCAAGAAGGACAAGAAGGAGGAAGACAAGAAGTGAGCGGCCCGC