

## *Division of Signal Transduction Therapy*

### **Standard Operating Procedure**

#### **Preparation of RBM7 [2 - 100]**

<b><u>Enzyme description:-</u></b>	RBM7 [2 – 100]
<b><u>Clone number:-</u></b>	DU 1661
<b><u>Source:-</u></b>	Recombinant
<b><u>Expression system:-</u></b>	<i>E.coli</i>
<b><u>Tag:-</u></b>	N-terminal GST + HA tag
<b><u>Purification method:-</u></b>	GSH Sepharose

#### **Calculated molecular mass:-**

Monoisotopic            39, 219.08 daltons  
Average Mass            39, 244.40 daltons  
[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-**                                6.17

**Purity:-**    >80 %

#### **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**

#### **RBM7 [2 – 100]**

<b><u>Protein</u></b>	RBM7 [2 – 100]
<b><u>Clone number</u></b>	DU 1661
<b><u>Species</u></b>	Human
<b><u>Accession number</u></b>	AK006755.1
<b><u>Tags</u></b>	N-terminal GST + HA
<b><u>Bacterially expressed protein</u></b>	<p>MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLQSMALIRYIADKHNMLGGCPKERAEISMLEGA VLDIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFFQGPLGSATMYPYDVPDYAGA <b>AAA EADRTL FVGNLETKVTEELLFELFHQAGPVIKVKIPKDKDGKLGKQF</b> <b>AFVNFKHEVSVPYAMNLLNGIKLFGRP I KI QFRSGSSHASQDASVSYPQ</b></p>
<b><u>Native sequence</u></b>	<p>Amino acids G2 – Q100 (end residue is H215) of human RBM7. Residue G244 of the fusion protein is equivalent to G2 of the native enzyme. The GST tag is located at residues 1 – 220 and the HA tag [YPYDVPDYA] is located at residues 235 – 243.</p>
<b><u>Protease cleavage</u></b>	PreScission ( <u>LEVLFQGP</u> ) residues 221 - 228
<b><u>Cloning sites</u></b>	<i>Bam</i> H1 and <i>Eco</i> R1 sites of pGEX6P-1

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**Nucleotide Sequence of Insert:**

ggatccGCCACCATGTACCCATACGATGTGCCAGATTACGCCGGGGCGGC  
GGCCGCAGAGGCGGACCGCACTCTGTTTCGTGGGTAACCTGGAGACGAAGG  
TGACGGAGGAGCTCCTCTTCGAGCTGTTCCACCAGGCTGGGCCGGTAATA  
AAAGTGAAAATCCCGAAAGATAAAGATGGCAAACCTGAAGCAGTTTGCATT  
CGTGAACCTCAAACATGAAGTGTCTGTTCCCTATGCCATGAATCTGCTCA  
ACGGAATCAAACTTTTTCGGGAGGCCTATCAAATTCAGTTTAGATCAGGA  
AGCAGTCACGCCTCTCAGGATGCCAGTGTGTCATATCCCCAGtaagaattc