

## *Division of Signal Transduction Therapy*

### **Standard Operating Procedure**

#### **Preparation of TAPP1 PH domain [182 – 303]**

**Protein description:-** TAPP1 PH domain [182 – 303]

**Clone number:-** DU 2033

**Source:-** Recombinant

**Expression system:-** *E.coli*

**Tag:-** N-terminal GST

**Purification method:-** GSH Sepharose

**Expression level:-** 3 mg/L

**Calculated molecular mass:-** 40, 872 daltons

**Purity:-** 90 %

**Enzyme storage buffer:-**

50 mM Tris-HCl pH 7.5, 50 % glycerol, 150 mM NaCl, 0.1 mM EGTA,  
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 0.2 mM PMSF, 1 mM Benzamidine.

**Storage temperature:-** –20 °C

**Assay:-** Sensor for PI3,4P2

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**CLONE DATA SHEET**

**TAPP1 PH domain [182 - 303]**

<b><u>Protein</u></b>	TAPP1 PH domain [182 - 303]
<b><u>Clone number</u></b>	DU 2033
<b><u>Species</u></b>	Human
<b><u>Accession no</u></b>	NM_021622
<b><u>Tags</u></b>	N-terminal GST
<b><u>Bacterially expressed protein</u></b>	<p>MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKW RNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNML GGCPKERAIEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFL SKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLY MDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQG WQATFGGGDHPPKSDLEVLFOGPLGSM<b>FTPKPPQDSAVIKA</b> <b>GYCVKQGAVMKNWKRRYFQLDENTIGYFKSELEKEPLRVIP</b> <b>LKEVHKVQECKQSDIMMRDNLFEIVTTSRTFYVQADSPEEM</b> <b>HSWIKAVSGAIVAQRGPGRSASSEHP</b></p>
<b><u>Native sequence</u></b>	<p>Amino acids F182 – P303 (V404 end) of human TAPP1. Residue F233 of the fusion protein is equivalent to F182 of the native protein. The GST tag is located at residues 1 - 220</p>
<b><u>Protease cleavage</u></b>	PreScission ( <u>LEVLFQGPL</u> ) residues 221 - 229
<b><u>Cloning sites</u></b>	<i>Bam</i> H1 of pGEX-6P

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**Nucleotide**  
**sequence of insert**

GGATCCATGTTTACTCCTAAACCACCTCAAGATAGTGCGGT  
TATCAAAGCTGGATATTGTGTAACAAGGAGCAGTGATGA  
AAAAGTGAAGAGAAGATATTTCAATTGGATGAAACACA  
ATAGGCTACTTCAAATCTGAACTGGAAAAGGAACCTCTTCG  
TGTAATACCACTTAAAGAGGTTCATAAAGTCCAGGAATGTA  
AGCAAAGCGACATAATGATGAGGGACAACCTCTTTGAAATT  
GTAACAACGTCTCGAACTTTCTATGTGCAGGCTGATAGCCC  
TGAAGAGATGCACAGTTGGATTAAAGCAGTCTCTGGCGCCA  
TTGTAGCACAGCGGGTCCCGGCAGATCTGCGTCTTCTGAG  
CATCCCtgaggatcc