

## *Division of Signal Transduction Therapy*

### **Standard Operating Procedure**

#### **Preparation of ABIN3 [1 - 325]**

**Enzyme description:-** ABIN3 [1 – 325]

**Clone number:-** DU 8756

**Source:-** Recombinant

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

**Tag:-** N-terminal GST

**Purification method:-** GSH Sepharose

**Calculated molecular mass:-**

Monoisotopic 66, 643.66 daltons

Average Mass 66, 686.24 daltons

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 6.63

**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**

#### **ABIN3 [1 – 325]**

<b><u>Protein</u></b>	ABIN3 [1 – 325]
<b><u>Clone number</u></b>	DU 8756
<b><u>Species</u></b>	Human
<b><u>Accession number</u></b>	NM_024873.5
<b><u>Tags</u></b>	N-terminal GST
<b><u>Bacterially expressed protein</u></b>	<p>MSPILGYWKIKGLVQPTRLLEYLEEKYEHLIERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGA VLDIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS KYIAWPLQGWQATFGGGDHPKSDLEVL FQG PLGSPGIPGSTRAAAMAH <b>FVQGT SRMIAAES STEHKECAEP STRKNLMNSLEQKIRCLEKQRKELLE</b> <b>VNQWDQQRSMKELYERKVAELKTKLDAAERFLSTREKDPHQQRKDD</b> <b>RQREDDRQRDLTRDLQREEKEKERLNEELHELKEENKLLKGKNTLANK</b> <b>EKEHYECEIKRLNKALQDALNIKCSFSEDCLRKSRVEFCHEEMRTEMEV</b> <b>LKQOVQIYEEDFKKERSDRERLNQEKEELQQINETSQSQNLRLNSQIKA</b> <b>CQMEKEKLEKQLKQMYCPPCNCGLVFHLQDPWVPTGPGAVQKQREHPPD</b> <b>CQWYALDQLPPDVQHKANGLSSVKKVHP</b></p>
<b><u>Native sequence</u></b>	<p>Amino acids M1 – P325 (end) of human ABIN3. Residue M243 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.</p>
<b><u>Protease cleavage</u></b>	PreScission ( <u>LEVLFQGP</u> ) residues 221 - 228
<b><u>Cloning sites</u></b>	<i>Not1</i> sites of pGEX6P-2

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Nucleotide  
Sequence Of  
Insert

gcggccgcgATGGCACATTTTGTACAGGGCACATCTAGAATGATTGCCG  
CAGAAAGTTCTACGGAGCATAAAGAGTGTGCTGAACCATCAACAAGAAA  
GAACTTGATGAATTCTCTTGAACAAAAGATAAGGTGTTTGGAAAAACAA  
AGAAAAGAGCTCCTGGAAGTTAACCAGCAATGGGATCAGCAATTTAGAA  
GTATGAAAGAGTTATATGAAAGAAAGGTAGCAGAGCTGAAGACGAAACT  
GGACGCCGCGGAAAGATTCTCAGCACGCGGGAGAAGGATCCGCATCAG  
AGGCAGAGAAAGGACGACAGGCAGAGAGAGGACGACAGGCAGCGCGACC  
TGACCCGGGACCGGCTGCAGCGGGAGGAGAAGGAAAAGGAACGCCTAAA  
TGAAGAATTACATGAATTGAAAGAAGAGAATAAACTTTTTAAAGGGAAAA  
AATACTCTTGCGAACAAGGAAAAGGAACATTACGAATGTGAAATAAAAC  
GCCTCAATAAGGCTCTTCAGGATGCCTTGAATATCAAGTGTTCAATTTTC  
CGAGGACTGTTTGAGGAAGTCTCGAGTGGAATTCTGCCATGAGGAGATG  
AGAACAGAAATGGAAGTTCTGAAGCAGCAGGTGCAAATATACGAAGAAG  
ACTTCAAAAAGGAACGATCGGATCGAGAGAGACTTAATCAAGAGAAAGA  
GGAGCTACAGCAAATTAATGAAACTTCCCAATCCCAGTTGAACAGGCTG  
AATCCCAGATAAAAAGCTTGTCAGATGGAGAAAAGAAAAGCTAGAAAAGC  
AATAAAACAGATGTATTGCCACCCTGTAAGTGGGCTTGGTTTTCCA  
CCTGCAAGATCCATGGGTACCAACAGGCCCTGGAGCTGTGCAGAAGCAA  
CGGGAGCACCCACCAGACTGTCAGTGGTATGCTCTTGACCAGCTTCCGC  
CAGATGTACAACACAAGGCAAATGGTTTTATCCTCAGTAAAGAAAGTCCA  
TCCGtaggcggccgc