

## *Division of Signal Transduction Therapy*

### **Standard Operating Procedure**

#### **Preparation of IkappaB alpha S32A S36A [2 - 54]**

**Enzyme description:-** IkappaB alpha S32A S36A [2 – 54]

**Clone number:-** DU 1445

**Source:-** Recombinant

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

**Tag:-** N-terminal GST

**Purification method:-** GSH Sepharose

**Calculated molecular mass:-**

Monoisotopic 33, 118.72 daltons

Average Mass 33, 140.22 daltons

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 5.24

**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

*Division of Signal Transduction Therapy*

**Clone Data Sheet**

**IkappaB alpha S32A S36A [2 – 54]**

<b><u>Protein</u></b>	IkappaB alpha S32A S36A [2 – 54]
<b><u>Clone number</u></b>	DU 1445
<b><u>Species</u></b>	Human
<b><u>Accession number</u></b>	BC004983
<b><u>Tags</u></b>	N-terminal GST
<b><u>Bacterially expressed protein</u></b>	MSPILGYWKIKGLVQPTRLLEYLEEKYEHLIERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGA VLDIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS KYIAWPLQGWQATFGGGDHPKSDLEVLV FQGPLGS <b>FQAAERPQEWAMEG</b> <b>PRDGLKKERLLDDRHDAGLDAMKDEEYEQMVKELQEIRL</b>
<b><u>Native sequence</u></b>	Amino acids F2 – L54 (end residue is L317) of human IkappaB alpha. Residue F232 of the fusion protein is equivalent to F2 of the native enzyme. The GST tag is located at residues 1 – 220. The protein has an S32 <b>A</b> and an S36 <b>A</b> mutation. Residue S32 is equivalent to residue <b>A262</b> of the fusion protein. Residue S36 is equivalent to residue <b>A266</b> of the fusion protein.
<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

*Division of Signal Transduction Therapy*

Nucleotide  
Sequence Of  
Insert

ggatccTTCCAGGCGGCCGAGCGCCCCAGGAGTGGGCCATGGAGGGCC  
CCCGCGACGGGCTGAAGAAGGAGCGGCTACTGGACGACCGCCACGACgc  
CGGCCTGGACgcCATGAAAGACGAGGAGTACGAGCAGATGGTCAAGGAG  
CTGCAGGAGATCCGCCTctgagaattc