

# *Division of Signal Tranduction Therapy*

## **Standard Operating Procedure**

### **Preparation of active ERBB4 [706 - 991]**

<b><u>Enzyme description:-</u></b>	ERBB4 [706 – 991]
<b><u>Clone number:-</u></b>	DU 9180
<b><u>Source:-</u></b>	Recombinant
<b><u>Expression system:-</u></b>	Baculovirus expression vector system
<b><u>Tag:-</u></b>	N-terminal His(6) tag
<b><u>Purification method:-</u></b>	Ni <sup>2+</sup> -NTA agarose
<b><u>Expression level:-</u></b>	3 mg/L
<b><u>Calculated molecular mass:-</u></b>	
Monoisotopic	35, 963.22 daltons
Average Mass	35, 986.74 daltons
[cysteines reduced, methionines have not been oxidised]	
<b><u>Theoretical pI:-</u></b>	6.31
<b><u>Purity:-</u></b>	75 %
<b><u>Activation protocol:-</u></b>	Constitutively active
<b><u>Enzyme storage buffer:-</u></b>	
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, 0.2 mM PMSF, 1 mM Benzamidine.	
<b><u>Storage temperature:-</u></b>	-70 °C [Long term stability to be determined]
<b><u>Assay:-</u></b>	Standard filter binding assay
<b><u>Assay Buffer:-</u></b>	
50 mM Tris-HCl pH 7.5, 0.1mM EGTA, 0.1 % 2-mercaptoethanol, 10 mM MgAc	
<b><u>Substrate:-</u></b>	
Poly Glu Tyr (4:1)	Final concentration: 1 mg/ml
<b><u>Specific activity range:-</u></b>	To be determined

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**Clone Data Sheet**

**ERBB4 [706 - 991]**

<b><u>Protein</u></b>	ERBB4 [706 – 991]
<b><u>Clone Number</u></b>	DU 9180
<b><u>Species</u></b>	Human
<b><u>Accession number</u></b>	NM_005235
<b><u>Tags</u></b>	N-terminal His(6)
<b><u>Baculovirus expressed protein</u></b>	MSYYHHHHHDYDIPPTENLYFQGAMGS <b>NQAQLRILKETELKRVKVLGS GAFGTVYKGIVWPEGETVKIPVAIKILNETTGPKANVEFMDEALIMASM DPHPLVRLLGVCLSPTIQLVTQLMFHGCLEYVHEHKDNIGSQLLNWC VQIAKGMMYLEERRLVHRDLAARNVLVKSPNHWKITDFGLARLLEGDEK EYNADGGKMPIKWMALCIIHYRKFTHQSDVWSYGVTIWELMTFGGKPYD GIPTREIPDLLEKGERLPQPPICTIDVYVMVMVKCWMIDADSRPKFKELA AEFSRMARDPQRYLVIQGDD</b>
<b><u>Native sequence</u></b>	Amino acids N706 – D991 of human ERBB4. [Full length protein ends at residue V1308] Residue N29 of fusion protein is equilivalent to N706 of the native enzyme. The His(6) tag is located at residues 5 – 10.
<b><u>Protease cleavage</u></b>	rTEV ( <u>ENLYFQG</u> ) residues 18 - 24
<b><u>Cloning sites</u></b>	<i>Bam</i> H1 and <i>Hind</i> III site of pFastBAC HTb

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Nucleotide  
sequence of  
insert

ggatccAATCAAGCACAACCTCGTATTTGAAAGAAACTGAGCTGAAGA  
GGGTAAAAGTCCTGGCTCAGGTGCTTGGAACGGTTATAAAGGTAT  
TTGGGTACCTGAAGGAGAAACTGTGAAGATTCCCTGTGGCTATTAAGATT  
CTTAATGAGACAACTGGTCCAAGGCAAATGTGGAGTTCATGGATGAAG  
CTCTGATCATGGCAAGTATGGATCATCCACACCTAGTCCGGTGCTGGG  
TGTGTGTCCTGAGCCCAACCATCCAGCTGGTTACTCAACTATGCCCAT  
GGCTGCCTGTTGGAGTATGTCCACGAGCACAAGGATAACATTGGATCAC  
AACTGCTGCTTAACCTGGTGTCCAGATAGCTAAGGAAATGATGTACCT  
GGAAGAAAGACGACTCGTCATCGGATTGGCAGCCGTAATGTCTTA  
GTGAAATCTCCAAACCATGTGAAATCACAGATTTGGCTAGCCAGAC  
TCTTGGAAAGGAGATGAAAAAGAGTACAATGCTGATGGAGGAAAGATGCC  
AATTAAATGGATGGCTCTGGAGTGTATACATTACAGGAAATTACCCAT  
CAGAGTGACGTTGGAGCTATGGAGTTACTATATGGGAACGTGACACT  
TTGGAGGAAAACCTATGATGGAATTCCAACCGCGAGAAATCCCTGATT  
ATTAGAGAAAGGAGAACGTTGCCTCAGCCTCCATCTGCACTATTGAC  
GTTTACATGGTCATGGTCAAATGTTGGATGATTGATGCTGACAGTAGAC  
CTAAATTAAAGGAACGGCTGCTGAGTTCAAGGATGGCTCGAGACCC  
CTAAAGATAACCTAGTTATTCAAGGGTGTGATTtaagctt