

Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of active EPH B4 [561 – 987]

<u>Enzyme description:-</u>	EPH B4 [561 - 987]
<u>Clone number:-</u>	DU 4864
<u>Source:-</u>	Recombinant
<u>Expression system:-</u>	Baculovirus expression vector system
<u>Tag:-</u>	N-terminal His(6) tag
<u>Purification method:-</u>	Ni ²⁺ -NTA agarose
<u>Calculated molecular mass:-</u>	
Monoisotopic	50, 954.36 daltons
Average Mass	50, 986.91 daltons
	[cysteines reduced, methionines have not been oxidised]
<u>Theoretical pI:-</u>	6.44
<u>Purity:-</u>	85 %
<u>Activation protocol:-</u>	Constitutively active
<u>Enzyme storage buffer:-</u>	
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	
<u>Storage temperature:-</u>	-80 °C
<u>Assay buffer:-</u>	
50 mM Tris-HCl pH 7.5, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol, 10 mM MgAc	
<u>Substrate:-</u>	
Poly Glu Tyr (4:1)	Final concentration: 0.1 mg/ml

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Clone Data Sheet

EPH B4 [561 - 987]

<u>Protein</u>	EPH B4 [561 - 987]
<u>Clone number</u>	DU 4864
<u>Species</u>	Human
<u>Accession number</u>	NP_004435.3
<u>Tags</u>	N-terminal His(6)
<u>Bacterially expressed protein</u>	MSYYHHHHHDYDIPPTENLYFQGAM GSL CLR KQS NGRE AEY SDK HG QY LIGH GT KV YID PFT YEDP NEAV REFA KE IDV SY VK IEE VIG AGE FGE VC RG RL KAP GKK ESC VAI KTL KGG YTER QRREF LSE AS IM QF EHP NI I RL EG VVT NSMP VMIL TE FMENG ALDS FLRL NDG QFT VI QLV GML RG IA SGM RY LAEM SY VRD LAAR NIL VNS NL VCK VSDF GLS RFL EEN SS DPT YT SS LGG KI PIR WT APE AIA FRK FT SAS DAW SY GIV MWE VMS FG ERY WD MSN QDV INAI EQDY RL PPPP DC PT SL HQ LML DC WQ KDR NAR PRF PQ VVS ALD KM IRN PA SLK IV ARE NGGA SHPL LDQ RQPH YSA FG SV GE WL RAI KM GR Y EES FA AAG FGS FEL VSQ I SAED LL RIG VT LAG H QK KI LAS VQ HM KS QAK PGT PGG TGG PAP QY
<u>Native sequence</u>	Amino acids L561 – Y987 (end) of human EPH B4. Residue L29 of fusion protein is equilivalent to L561 of the native enzyme. The His(6) tag is located at residues 5 – 10.
<u>Protease cleavage</u>	rTEV (<u>ENLYFQG</u>) residues 18 - 24
<u>Cloning sites</u>	<i>Bam</i> H1 and <i>Not</i> 1 site of pFBHTb

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<u>Nucleotide sequence of insert</u>	ggatccCTCTGCCTCAGGAAGCAGAGCAATGGAGAGAAGCAGAAATT CGGACAAACACGGACAGTATCTCATCGGACATGGTACTAAGGTCTACAT CGACCCCTTCACTTATGAAGACCCTAATGAGGCTGTGAGGGAATTGCA AAAGAGATCGATGTCTCCTACGTCAAGATTGAAGAGGTGATTGGTCAG GTGAGTTGGCGAGGTGTGCCGGGGCGGCTCAAGGCCCCAGGGAAAGAA GGAGAGCTGTGTGGCAATCAAGACCCCTGAAGGGTGGCTACACGGAGCAG CAGCGGCGTGAGTTCTGAGCGAGGCCTCCATCATGGGCCAGTCGAGC ACCCCAATATCATCCGCCTGGAGGGCGTGGTCACCAACAGCATGCCGT CATGATTCTCACAGAGTTCATGGAGAACGGGCCCTGGACTCCTCCTG CGGCTAAACGACGGACAGTTCACAGTCATCCAGCTCGTGGCATGCTGC GGGGCATCGCCTCGGCATCGGTACCTGGCGAGATGAGCTACGTCCA CCGAGACCTGGCTGCTCGAACATCCTAGTCAACAGCAACCTCGTCTGC AAAGTGTCTGACTTGGCCTTCCCATTCCCTGGAGGAGAACTCTTCCG ATCCCACCTACACGAGCTCCCTGGAGGAAAGATTCCCATCCGATGGAC TGCCCCGGAGGCCATTGCCTTCCGGAAGTTCACTTCCGCCAGTGATGCC TGGAGTTACGGGATTGTGATGTGGAGGTGATGTCAATTGGGGAGAGGC CGTACTGGGACATGAGCAATCAGGACGTGATCAATGCCATTGAACAGGA CTACCGGCTGCCCGCCCCCAGACTGTCCCACCTCCCTCCACCAGCTC ATGCTGGACTGTTGGCAGAAAGACCGGAATGCCGGCCAGCCTCC AGGTGGTCAGGCCCTGGACAAGATGATCCGAACCCGCCAGCCTCAA AATCGTGGCCCGGGAGAATGGCGGGCCTCACACCCCTCTGGACCAAG CGGCAGCCTCACTACTCAGTTGGCTCTGTGGCGAGTGGCTTGGG CCATCAAAATGGGAAGATACTGAAGAAAGTTCGCAGCCGCTGGCTTG CTCCTTCGAGCTGGTCAGCCAGATCTCTGCTGAGGACCTGCTCCGAATC GGAGTCACTCTGGCGGGACACCAGAAGAAAATCTTGGCCAGTGTCCAGC ACATGAAGTCCCAGGCCAAGCCGGAAACCCGGGTGGACAGGGAGGACC GGCCCCGCAGTACTgagcggccgc
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