

Division of Signal Transduction Therapy

Clone Data Sheet

EPH B1 [565 - 984]

<u>Protein</u>	EPH B1 [565 - 984]
<u>Clone number</u>	DU 4455
<u>Species</u>	Human
<u>Accession number</u>	NM_004441
<u>Tags</u>	N-terminal His6
<u>Bacterially expressed protein</u>	<p>MSYYHHHHHDYDIPTTENLYFQGAMDPEFRKRAYSKEAVYSDKLQHY STGRGSPGMKIYIDPFTYEDPNEAVREFAKEIDVSFVKIEEVI GAGEF GEVYKGRLLKLP GKREIYVAIKTLKAGYSEKQRRDFLSEASIMGQFDHP NIIRLEGVVTKSRPVMII TEFMENGALDSFLRQNDGQFTVIQLVGMLR GIAAGMKYLAEMNYVHRDLAARNILVNSNLVCKVSDFGLSRYLQDDTS DPTYTSSLGGKIPVRWTAPEAIAIRKFTSASDVWSYGI VMWEVMSFGE RPYWDMSNQDVINAIEQDYRLPPMDCPAALHQLMLDCWQKDRNSRPR FAEIVNTLDKMIRNPASLKT VATITAVPSQPLLDRSIPDFTAFTTVDD WLSAIKMVQYRDSFLTAGFTSLQLVTQMTSEDLLRIGITLAGHQKKIL NSIHSMRVQISQSPTAMA</p>
<u>Native sequence</u>	<p>Amino acids R565 – A984 (end) of human EPH B1. Residue R31 of the fusion protein is equivalent to R565 of the native enzyme. The His(6) tag is located at residues 5 – 10.</p>
<u>Protease cleavage</u>	rTEV (<u>ENLYFQG</u>) residues 18 - 24
<u>Cloning sites</u>	<i>Eco</i> R1 and <i>Not</i> 1 sites of pFastBAC HTa

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Nucleotide
Sequence

ATGTCGTA
CTACCAT
CACCAT
CACCAT
CACGATT
ACGATAT
CCCAACG
ACCGAAA
ACCTGT
ATTTTC
CAGGGC
GCCATG
GATCCG
GAATTC
CAGGAAA
CGGGCT
TATAGC
AAAGAG
GCTGTG
TACAGC
GATAAG
CTCCAG
CATTAC
AGCACAG
GCCGAG
GCTCCCC
CAGGGAT
GAAGAT
CTACAT
TGACCC
CTTC
ACTTAC
GAGGAT
CCCAAC
GAAGCT
GTCCGG
GAGTTT
GCCAAG
GAGATT
GATGTAT
CTTTT
GTGAAA
ATTGAA
GAGGTC
ATCGG
GAGCAG
GGGGAG
TTTGG
GAGAAG
TGTACA
AGGGGC
GTTTGA
AACTGC
CAGGCA
AGAGGG
GAAATC
TACGTG
GCCATC
AAGACC
CTGAAG
GCAGGG
TACTCG
GAGAAG
CAGCGT
CGGGACT
TTTCTG
AGTGAG
GCGAGC
ATCATG
GGCCAG
TTTCG
ACCATC
CTAAC
ATCATT
CGCCTG
GAGGGT
GTGGTC
ACCAAG
AGTCGG
CCTGTC
ATCATC
ACAGAG
TTCATG
GAGAAT
GGTGC
ATTGG
ATTCTT
TCTCAG
GCAAA
ATGACG
GGCAGT
TCACCG
TGATCC
CAGCTT
GTGGGT
ATGCTC
AGGGC
ATCGCT
GCTGG
CATGA
AGTACC
CTGGCT
GAGATG
AATTAT
GTGCAT
CGGGAC
CTGGCT
GCTAGG
AACATT
CTGGT
CAACAG
TAACCT
GGTGTG
CAAGGT
GTCCG
ACTTTG
GCCTCT
CCCGCT
ACCTCC
CAGGAT
GACACC
CTCA
GATCCC
ACCTAC
ACCAGC
TCCTTG
GGAGGG
AAGATC
CCTGTG
AGATGG
ACAGCT
CCAGAG
GCCATC
GCCTAC
CGCAAG
TTCAC
TTCAGC
CAGCG
ACGTTT
GGAGCT
ATGGG
ATCGT
CATGTG
GGGAAG
TCATG
TCATTT
GGAGAG
AGACC
TATGGG
ATATGT
CCAACC
AAGATG
TCATCA
ATGCC
ATCGAG
CAGGAC
TACCGG
CTGCCCC
ACCCAT
GGACTG
TCAGCT
GCTCTA
CAC
CAGCTC
ATGCTG
GACTGT
TGGCAG
AAGGAC
CCGGA
ACAGCC
GGCCCC
GG
TTTGGC
GGAGAT
TGTCA
ACACC
CTAGAT
AAGATG
ATCCG
GAACCC
GGCA
AGTCT
CAAGAC
TGTGG
CAACC
ATCAC
CGCCG
TGCCTT
CCAGC
CCCTG
CTCGAC
CGCTCC
ATCCC
AGACTT
CACGGC
CTTACC
ACCGT
GGATG
ACTGGC
TCAGC
GCCATC
AAAAT
GGTCC
AGTAC
AGGGAC
AGCTT
CCTCA
CTGCTG
GCTTCA
CCTCC
CTCAG
CTGGT
CACCC
AGATG
ACATC
AGAAG
ACCTC
TGAGAA
TAGGC
ATCAC
CTTGG
CAGGCC
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AGAAG
ATCCTG
AACAGC
ATTCAT
TCTATG
AGGGT
CCAGAT
AAGTC
AGTCAC
CAACG
GGCA
ATGGCA
tgagcggccgc