



## *Division of Signal Transduction Therapy*

### **Clone Data Sheet**

#### **KIT [544 - 976]**

<b><u>Protein</u></b>	KIT [544 - 976]
<b><u>Clone number</u></b>	DU 9182
<b><u>Species</u></b>	Human
<b><u>Accession number</u></b>	NM_000222.2
<b><u>Tags</u></b>	N-terminal His6
<b><u>Bacterially expressed protein</u></b>	<b>MSYYHHHHHDYDIPPTTENLYFQGAMGSTYKYLQKPMYEVQWKV EEINGNNYVYIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVE ATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELKVL SYLGNH MNI V NLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQE DHAE AALYKNLLH SKESSCSDSTNEYMDMKPGVSYVVPTKADKRR SVRIGSYIERDVTPAIMEDELALDLEDLLSFSYQVAKGMAFLAS KNCIHRDLAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNAR LPVKWMAPE SIFNCVYTFESDVWSYGIFLWELFSLGSSPYPGMPV DSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPLKRPTFKQI VQLIEKQISESTNHIYSNLANCSPNRQKPVVDHSVRINSVGSTAS SSQPLL VHDDV</b>
<b><u>Native sequence</u></b>	Amino acids T544 – V976 (end) of human KIT. Residue T29 of the fusion protein is equivalent to T544 of the native enzyme. The His6 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>Eco</i> R1 sites of pFastBac HTb.

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**Nucleotide  
sequence of insert**

ggatccACCTACAAATATTTACAGAAACCCATGTATGAAGTACAG  
TGGAAGGTTGTTGAGGAGATAAATGGAAACAATTATGTTTACATA  
GACCCAACACAACCTTCCTTATGATCACAAATGGGAGTTTCCCAGA  
AACAGGCTGAGTTTTGGGAAAACCCTGGGTGCTGGAGCTTTCGGG  
AAGGTTGTTGAGGCAACTGCTTATGGCTTAATTAAGTCAGATGCC  
GCCATGACTGTCGCTGTAAAGATGCTCAAGCCGAGTGCCATTTG  
ACAGAACGGGAAGCCCTCATGTCTGAACTCAAAGTCCTGAGTTAC  
CTTGGTAATCACATGAATATTGTGAATCTACTTGGAGCCTGCACC  
ATTGGAGGGCCCACCCTGGTCATTACAGAATATTGTTGCTATGGT  
GATCTTTTGAATTTTTTTGAGAAGAAAACGTGATTCAATTTATTTGT  
TCAAAGCAGGAAGATCATGCAGAAGCTGCACCTTATAAGAATCTT  
CTGCATTCAAAGGAGTCTTCCTGCAGCGATAGTACTAATGAGTAC  
ATGGACATGAAACCTGGAGTTTCTTATGTTGTCCCAACCAAGGCC  
GACAAAAGGAGATCTGTGAGAATAGGCTCATACATAGAAAGAGAT  
GTGACTCCCGCCATCATGGAGGATGACGAGTTGGCCCTAGACTTA  
GAAGACTTGCTGAGCTTTTCTTACCAGGTGGCAAAGGGCATGGCT  
TTCCTCGCCTCCAAGAATTGTATTCACAGAGACTTGGCAGCCAGA  
AATATTCTCCTTACTCATGGTCGGATCACAAAGATTTGTGATTTT  
GGTCTAGCCAGAGACATCAAGAATGATTCCAATTATGTGGTTAAA  
GGAAACGCTCGACTACCTGTGAAGTGGATGGCACCTGAAAGCATT  
TTCAACTGTGTATACACGTTTGAAAGTGACGTCTGGTCCTATGGG  
ATTTTTCTTTGGGAGCTGTTCTCTTTAGGAAGCAGCCCCATCCT  
GGAATGCCGGTTCGATTCTAAGTTCTACAAGATGATCAAGGAAGGC  
TTCCGGATGCTCAGCCCTGAACACGCACCTGCTGAAATGTATGAC  
ATAATGAAGACTTGCTGGGATGCAGATCCCCATAAAAGACCAACA  
TTCAAGCAAATTGTTTCAGCTAATTGAGAAGCAGATTTTCAGAGAGC  
ACCAATCATATTTACTCCAACCTTAGCAAACCTGCAGCCCCAACCGA  
CAGAAGCCCCTGGTAGACCATTCTGTGCGGATCAATTCTGTTCGGC  
AGCACCCTTCCTCCTCCCAGCCTCTGCTTGTGCACGACGATGTC  
tgagaattc