

Division of Signal Transduction Therapy

Clone Data Sheet

Vascular Endothelial Growth Factor Receptor [784 - 1338]

<u>Protein</u>	VEGFR [784 - 1338]
<u>Clone number</u>	DU 8999
<u>Species</u>	Human
<u>Accession number</u>	NM_002019.3
<u>Tags</u>	N-terminal GST
<u>Baculovirus expressed protein</u>	<p>MSPILGYWKIKGLVQPTRLLEYLEEKYEHLIERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAETSMLEGA VLDIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVL FQG PLGSKRSSEIKTDYLSI IMDPDEVPLDEQCERLPYDASKWEFARERLKLGKSLGRGAFGKVVQASA FGIKKSPTCRTVAVKMLKEGATASEYKALMTELKILTHIGHHLNVNLL GACTKQGGPLMVIVEYCKYGNLSNYLKS KRDLFFLNKDAALHMEPKKEK MEPGLEQGGKPRLDSVTSSSEFASSGFQEDKSLSDVEEEEDSDGFYKEP ITMEDLISYSFQVARGMEFLSSRKC IHRDLAARNILLSENNVVKICDFG LARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVWSYGVLLWE IFSLGGSPYPGVQMD EDFCSRLREGMRRAPEYSTPEIYQIMLDCWHRD PKERPRFAELVEKLGDLLQANVQD GKDYIPINAILTGNSGFTYSTPAF SEDFFKESISAPKFNSGSSDDVRYVNAFKFMSLERIKTFEELLPNATSM FDDYQGDSSTLLAS PMLKRFTWTD SKPKASLKIDLRVTSKSKESGLSDV SRPSFCHSSCGHVSEGKRRFTYDHAELERKIACCSPPPDYNSVVLYSTP PI</p>
<u>Native sequence</u>	Amino acids K784 – I1338 (end) of human VEGFR. Residue K232 of the fusion protein is equivalent to K784 of the native enzyme. The GST tag is located at residues 1 – 220.
<u>Protease cleavage</u>	PreScission (<u>LEVLFQGPL</u>) residues 221 - 229
<u>Cloning sites</u>	<i>Bam</i> H1 and <i>Not</i> I sites of pFastBAC GEX6P-1

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Nucleotide
Sequence of insert

ggatccAAAAGGTCTTCTTCTGAAATAAAGACTGACTACCTATCAATTA
TAATGGACCCAGATGAAGTTCCTTTGGATGAGCAGTGTGAGCGGCTCCC
TTATGATGCCAGCAAGTGGGAGTTTGCCCGGGAGAGACTTAAACTGGGC
AAATCACTTGGAAGAGGGGCTTTTGGAAAAGTGGTTCAAGCATCAGCAT
TTGGCATTAAAGAAATCACCTACGTGCCGGACTGTGGCTGTGAAAATGCT
GAAAGAGGGGGCCACGGCCAGCGAGTACAAAGCTCTGATGACTGAGCTA
AAAATCTTGACCCACATTGGCCACCATCTGAACGTGGTTAACCTGCTGG
GAGCCTGCACCAAGCAAGGAGGGCCTCTGATGGTGATTGTTGAATACTG
CAAATATGGAAATCTCTCCAACCTCAAGAGCAAACGTGACTTATTT
TTTCTCAACAAGGATGCAGCACTACACATGGAGCCTAAGAAAGAAAAA
TGGAGCCAGGCCTGGAACAAGGCAAGAAACCAAGACTAGATAGCGTCAC
CAGCAGCGAAAGCTTTGCGAGCTCCGGCTTTCAGGAAGATAAAAAGTCTG
AGTGATGTTGAGGAAGAGGAGGATTCTGACGGTTTCTACAAGGAGCCCA
TCACTATGGAAGATCTGATTTCTTACAGTTTTTCAAGTGGCCAGAGGCAT
GGAGTTCCTGTCTTCCAGAAAGTGCATTCATCGGGACCTGGCAGCGAGA
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GCGCAGGTTACCTACGACCACGCTGAGCTGGAAAGGAAAATCGCGTGC
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CCATCtaggcggccgcg