

Division of Signal Transduction Therapy

Clone Data Sheet

TYRO3 [468 - 890]

<u>Protein</u>	TYRO3 [468 - 890]
<u>Clone number</u>	DU 61217
<u>Species</u>	Human
<u>Accession number</u>	NM_006293.4
<u>Tags</u>	N-terminal GST
<u>Baculovirus expressed protein</u>	<p>MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFEL GLEFPNLPHYIDGDVKLTQSMAIIRYIADKHNLGGCPKERAESMLE GAVLDIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLN GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPIQIDKY LKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFGPLGSMARGEPAVH FRAARSFNRERPERIEATLDSLGISDELKEKLEDVLIPEQQFTLGRML GKGEFGSVREAQLKQEDGSFVKVAVKMLKADIASSDIEEFLREAACM KEFDHPPHVAKLVGVSLRSRAKGRLPIMVILPFMKHGDHAFLLASRI GENPFNLPLQTLIRFMVDIACGMEYLSSRNF IHRDLAARNCMLAEDMT VCVADFGLSRKIYSGDYRQGCASKLPVKWLALESADNLYTVQSDVW AFGVTMWEIMTRGQTPYAGIENAEIYNYLIGGNRLKQPPECMEDVYDL MYQCWSADPKQRPSTCLRMELNILGQLSVLSASQDPLYINIERAEE PTAGGSLELPGRDQPYSGAGDGS GMGAVGGTPSDCRYILTPGGLAEQP GQAEHQPE SPLNETQRLLLLLQOGLLPHSSC</p>
<u>Native sequence</u>	<p>Amino acids M468 – C890 (end) of human TYRO3.</p> <p>Residue M232 of the fusion protein is equivalent to M468 of the native enzyme. The GST tag is located at residues 1 – 220.</p>
<u>Protease cleavage</u>	PreScission site (<u>LEVLFQGP</u>) residues 221 – 228
<u>Cloning sites</u>	<i>Bam</i> H1 and <i>Not</i> I sites of pFastBac GST 6P1

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**Nucleotide
sequence of
insert**

ggatccATGGCCCGGGGAGAGCCAGCCGTTCACTTCCGGGCAGCCCGG
TCCTTCAATCGAGAAAGGCCCGAGCGCATCGAGGCCACATTGGACAGC
TTGGGCATCAGCGATGAACTAAAGGAAAACTGGAGGATGTGCTCATC
CCAGAGCAGCAGTTCACCTGGGCCGGATGTTGGGCAAAGGAGAGTTT
GGTTCAGTGCGGGAGGCCAGCTGAAGCAAGAGGATGGCTCCTTTGTG
AAAGTGGCTGTGAAGATGCTGAAAGCTGACATCATTGCCTCAAGCGAC
ATTGAAGAGTTCCTCAGGGAAGCAGCTTGCATGAAGGAGTTTGACCAT
CCACACGTGGCCAAACTTGTGGGGTAAGCCTCCGGAGCAGGGCTAAA
GGCCGTCTCCCCATCCCCATGGTCATCTTGCCCTTCATGAAGCATGGG
GACCTGCATGCCTTCCTGCTCGCCTCCCGGATTGGGGAGAACCCCTTT
AACCTACCCCTCCAGACCCTGATCCGGTTCATGGTGGACATTGCCTGC
GGCATGGAGTACCTGAGCTCTCGGAACTTCATCCACCGAGACCTGGCT
GCTCGGAATTGCATGCTGGCAGAGGACATGACAGTGTGTGTGGCTGAC
TTCGGACTCTCCCGGAAGATCTACAGTGGGGACTACTATCGTCAAGGC
TGTGCCTCCAAACTGCCTGTCAAGTGGCTGGCCCTGGAGAGCCTGGCC
GACAACCTGTATACTGTGCAGAGTGACGTGTGGCGTTCGGGGTGACC
ATGTGGGAGATCATGACACGTGGGCAGACGCCATATGCTGGCATCGAA
AACGCTGAGATTTACAACCTACCTCATTGGCGGGAACCGCCTGAAACAG
CCTCCGGAGTGTATGGAGGACGTGTATGATCTCATGTACCAGTGCTGG
AGTGCTGACCCCAAGCAGCGCCGAGCTTTACTTGTCTGCGAATGGAA
CTGGAGAACATCTTGGGCCAGCTGTCTGTGCTATCTGCCAGCCAGGAC
CCCTTATACATCAACATCGAGAGAGCTGAGGAGCCCACTGCGGGAGGC
AGCCTGGAGCTACCTGGCAGGGATCAGCCCTACAGTGGGGCTGGGGAT
GGCAGTGGCATGGGGGCAGTGGGTGGCACTCCCACTGACTGTTCGGTAC
ATACTCACCCCGGAGGGCTGGCTGAGCAGCCAGGGCAGGCAGAGCAC
CAGCCAGAGAGTCCCCTCAATGAGACACAGAGGCTTTTGTGCTGCTGCAG
CAAGGGCTACTGCCACACAGTAGCTGTtaggcggccgc