

Division of Signal Transduction Therapy

Clone Data Sheet

AZK [1 - 455]

<u>Protein</u>	AZK [1 - 455]
<u>Clone number</u>	DU 42048
<u>Species</u>	Human
<u>Accession number</u>	NM_133646.2
<u>Tags</u>	N-terminal GST
<u>Baculovirus expressed protein</u>	<p>MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKK FELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERA EISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFED RLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFK KRIEAIPOIDKYLKSSKYIAWPLQGQWQATFGGGDHPPKSDLEVL FQGPLGSMSSLGASVQIKFDDLQFFENC GGGSFGSVYRAKWI SQD KEVAVKLLKIEKEAEILSVLSHRNI IQFYGVILEPPNYGIVTEY ASLGSLYDYINSNRSEEMDMDHIMTWATDVAKGMHYLHMEAPVKV IHRDLKSRNVVIAADGVLKICDFGASRFHNHTTHMSLVGTFPWMA PEVIQSLPVSETCDTYSYGVVLWEMLTREVPFKGLEGLQVAWL VVEKNERLTIPSSCPRSFAELLHQCWEADAKKRPSFKQIISILESMS NDTSLPDKCNFLHNKAEWRCIEATLERLKKLERDLSFKEQELK ERERRLKMWEQKLTQSNTPLLLPLAARMSEESYFESKTEESNSA EMSCQITATSNGEGHGMNPSLQAMMLMGFGDIFSMNKAGAVMHSG MQINMQAKQNSSKTTSKRRGKKVNMALGFSDFDLSEGDDDDDDG EEDNDMDNSE</p>
<u>Native sequence</u>	<p>Amino acids M1 – E455 (end) of human AZK. Residue M232 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 - 220.</p>
<u>Protease cleavage</u>	PreScission (<u>LEVLFQGP</u>) residues 221 - 228
<u>Cloning sites</u>	<i>Bam</i> H1 and <i>Not</i> I sites of pFastBac Dual.

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**Nucleotide
sequence of insert**

ggatccATGTCGTCTCTCGGTGCCTCCTTTGTGCAAATTAATTT
GATGACTTGCAGTTTTTTGAAAAC TCGGTGGAGGAAGTTTTGGG
AGTGTTTATCGAGCCAAATGGATATCACAGGACAAGGAGGTGGCT
GTAAAGAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGT
GTCCCTCAGTCACAGAAACATCATCCAGTTTTTATGGAGTAATTCTT
GAACCTCCCAACTATGGCATTGTACAGAATATGCTTCTCTGGGA
TCACTCTATGATTACATTAACAGTAACAGAAGTGAGGAGATGGAT
ATGGATCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATG
CATTATTTACATATGGAGGCTCCTGTCAAGGTGATTCACAGAGAC
CTCAAGTCAAGAAACGTTGTTATAGCTGCTGATGGAGTATTGAAG
ATCTGTGACTTTGGTGCCTCTCGGTTCCATAACCATAACAACACAC
ATGTCCTTGGTTGGAAC TTTCCCATGGATGGCTCCAGAAGTTATC
CAGAGTCTCCCTGTGT CAGAACTTGTGACACATATTCCTATGGT
GTGGTTCTCTGGGAGATGCTAACAAGGGAGGTCCCTTTAAAGGT
TTGGAAGGATTACAAGTAGCTTGGCTTGTAGTGAAAAAACGAG
AGATTAACCATTCCAAGCAGTTGCCCCAGAAGTTTTGCTGAACTG
TTACATCAGTGTTGGGAAGCTGATGCCAAGAAACGGCCATCATTC
AAGCAAATCATTTCAATCCTGGAGTCCATGTCAAATGACACGAGC
CTTCCTGACAAGTGTAAC TCAATTCCTACACAACAAGGCGGAGTGG
AGGTGCGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAG
CGTGATCTCAGCTTTAAGGAGCAGGAGCTTAAAGAACGAGAAAGA
CGTTTAAAGATGTGGGAGCAAAGCTGACAGAGCAGTCCAACACC
CCGCTTCTCTTGCCCTTTGCTGCAAGAATGTCTGAGGAGTCTTAC
TTTGAATCTAAAACAGAGGAGTCAAACAGTGCAGAGATGTCATGT
CAGATCACAGCAACAAGTAACGGGGAGGGCCATGGCATGAACCCA
AGTCTGCAGGCCATGATGCTGATGGGCTTTGGGGATATCTTCTCA
ATGAACAAAGCAGGAGCTGTGATGCATTCTGGGATGCAGATAAAC
ATGCAAGCCAAGCAGAATTCTTCCAAAACCATCTAAGAGAAGG
GGGAAGAAAGTCAACATGGCTCTGGGGTTCAGTGATTTTACTTG
TCAGAAGGTGACGATGATGATGATGATGACGGTGAGGAGGAGGAT
AATGACATGGATAATAGTGAAtgagcggccgc