

Substrate:-
[KKKKERLLDDRHDSGLDSMKDEE]
Residues 21 to 41 of human IKappaB alpha (+ 2 added Lys at N terminus)
Final concentration: 300 μM

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Clone Data Sheet

TANK Binding Kinase 1 K38A [1 - 729]

Protein TBK1 K38A [1 - 729]

Clone number DU 12773

Species Human

Accession number NM_013254

Tags N-terminal GST

Baculovirus expressed protein

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFEL
GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLE
GAVLDIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLN
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAI PQIDKY
LKSSKYIAWPLQGWQATFGGGDHPKSDLEVLFGQPLGSMQSTSNHLW
LLSDILGQGATANVFRGRHKKTGDLFAIKVFNNISFLRPVDVQMRFE
VLKKNHKNIVKLF AIEEETTRHKVLIMEFCPCGSLYTVLEEPSNAY
GLPESEFLIVLRDVVGGMNHLRENGIVHRDIKPGNIMRVIGEDGQSVY
KLTDFGAARELEDDEQFVSLYGTEEYLHPDMYERAVLRKDHQKKYGAT
VDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV MYKIITGKPSGAISGV
QKAENGPIDWSGDMPVSCSLSRGLQVLLTPVLANILEADQEKCWGFDQ
FFAETSDILHRMVIHVFSLQQMTAHKIYIHSYNTATIFHELVYKQTKI
ISSNQELIYEGRRLLVLEPGRLAQHFPKTTEENPIFVVSREPLNTIGLI
YEKISLPKVHPRYDLGDASMAKAITGVVCYACRIASTLLLYQELMRK
GIRWLIELIKDDYNETVHKKTEVVITLDFCIRNIEKTVKVYEKLMKIN
LEAAELGEISDIHTKLLRLSSSQGTIETSLQDIDSRLSPGGSLADAWA
HQEGTHPKDRNVEKLQVLLNCMTEIYYQFKDKAERRLAYNEEQIHKF
DKQKLYYHATKAMTHFTDECVKKYEAFLNKSEEWIRKMLHLRKQLLSL
TNQCFDIEEEVSKYQEYTNELQETLPQKMFTASSGIKHTMTPIYPSSN
TLVEMTLGMKKLKEEMEGVVKELAENNHILERFGSLTMDGGLRNVDCI

Native sequence Amino acids M1 – L729 (end) of human TBK1.
Residue M232 of the fusion protein is equivalent to M1 of TBK1.
The GST tag is located at residues 1 - 220 of the fusion protein.

The enzyme has a K38A mutation.
Residue K38 is equivalent to A269 of the fusion protein.

Protease cleavage PreScission (LEVLFQGP) residues 221 - 228

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Cloning sites

*Bam*H1 of pFastBac GST 6P-1

Nucleotide sequence of insert

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ggatccATGCAGAGCACTTCTAATCATCTGTGGCTTTTATCTGATATTTTAGG
CCAAGGAGCTACTGCAAATGTCTTTCGTGGAAGACATAAGAAAACCTGGTGATT
TATTTGCTATCGCAGTATTTAATAACATAAGCTTCCTTCGTCCAGTGGAATGTT
CAAATGAGAGAATTTGAAGTGTTGAAAAAACTCAATCACAAAAATATTGTCAA
ATTATTTGCTATTGAAGAGGAGACAACAACAAGACATAAAGTACTTATTATGG
AATTTTGTCCATGTGGGAGTTTATACACTGTTTTAGAAGAACCTTCTAATGCC
TATGGACTACCAGAATCTGAATTCTTAATTGTTTTGCGAGATGTGGTGGGTGG
AATGAATCATCTACGAGAGAATGGTATAGTGCACCGTGATATCAAGCCAGGAA
ATATCATGCGTGTTATAGGGGAAGATGGACAGTCTGTGTACAACTCACAGAT
TTTGGTGCAGCTAGAGAATTAGAAGATGATGAGCAGTTTGTCTCTGTATGG
CACAGAAGAATATTTGCACCCTGATATGTATGAGAGAGCAGTGCTAAGAAAAG
ATCATCAGAAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAACA
TTTTACCATGCAGCTACTGGATCACTGCCATTTAGACCCTTTGAAGGGCCTCG
TAGGAATAAAGAAGTGATGTATAAAATAATTACAGGAAAGCCTTCTGGTGCAA
TATCTGGAGTACAGAAAGCAGAAAATGGACCAATTGACTGGAGTGGAGACATG
CCTGTTTCTTGCAGTCTTTCTCGGGGTCTTCAGGTTCTACTTACCCCTGTTCT
TGCAAACATCCTTGAAGCAGATCAGGAAAAGTGTTGGGGTTTTGACCAGTTTT
TTGCAGAAACTAGTGATATACTTCACCGAATGGTAATTCATGTTTTTTCGCTA
CAACAAATGACAGCTCATAAGATTTATATACATAGCTATAATACTGCTACTAT
ATTTTCATGAAGTGGTATATAAACAACCAAAATTATTTCTTCAAATCAAGAAC
TTATCTACGAAGGGCGACGCTTAGTCTTAGAACCTGGAAGGCTGGCACAACAT
TTCCCTAAAACACTACTGAGGAAAACCTATATTTGTAGTAAGCCGGGAACCTCT
GAATACCATAGGATTAATATATGAAAAAATTTCCCTCCCTAAAGTACATCCAC
GTTATGATTTAGACGGGGATGCTAGCATGGCTAAGGCAATAACAGGGGGTTGTG
TGTTATGCCTGCAGAATTGCCAGTACCTTACTGCTTTATCAGGAATTAATGCG
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AGAGTTAGGTGAAATTTGAGACATACACACCAAATTGTTGAGACTTTCAGTT
CTCAGGGAACAATAGAAACAGTCTTCAGGATATCGACAGCAGATTATCTCCA
GGTGGATCACTGGCAGACGCATGGGCACATCAAGAAGGCACTCATCCGAAAGA
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GCACTTTACAGATGAATGTGTTAAAAAGTATGAGGCATTTTTTGAATAAGTCAG
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AATCAGTGTTTTGATATTGAAGAAGAAGTATCAAAATATCAAGAATATACTAA
TGAGTTACAAGAACTCTGCCTCAGAAAATGTTTACAGCTTCCAGTGGAATCA
AACATACCATGACCCCAATTTATCCAAGTTCTAACACATTAGTAGAAATGACT
CTTGGTATGAAGAAATTAAAGGAAGAGATGGAAGGGGTGGTTAAAGAACTTGC
TGAAAAATAACCACATTTTAGAAAGGTTTGGCTCTTTAACCATGGATGGTGGCC
TTCGCAACGTTGACTGTCTTtagggatcc
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