

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of active B-Raf [2 – 766]

<u>Enzyme description:-</u>	B-Raf [2 – 766]
<u>Clone number:-</u>	DU 15484
<u>Source:-</u>	Recombinant
<u>Expression system:-</u>	Baculovirus expression vector system
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH Sepharose

Calculated molecular mass:-

Monoisotopic 111,727.51 daltons
Average Mass 111,798.57 daltons
[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.62

Purity:- 85 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA,
0.1 % 2-mercaptoethanol, 0.03 % Brij-35, 0.2 mM PMSF, 1 mM Benzamidine

Storage temperature:- -70 °C

Assay buffer:-

50 mM Tris-HCl pH 7.5, 10 mM DTT, 0.1 mM EGTA, 10 mM MgAc

Substrate:-

Three step assay in which B-Raf activates inactive MKK1, which in turn activates inactive p42MAPKinase. Activity of p42MAPKinase is then assayed against myelin basic protein as substrate (final concentration of 0.3 mg/ml), in a standard filter binding assay.

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Clone Data Sheet

B-Raf [2 – 766]

Protein B-Raf [2 – 766]

Clone number DU 15484

Species Human

Accession number NM_004333.4

Tags N-terminal GST

**Bacterially
expressed protein**

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKK
FELGLEFPNLPYYIDGDVKLQSMAIIRYIADKHNMLGGCPKERA
EISMLEGAVLDIRYGVSRIAYS KDFETLKVDFLSKLPPEMLKMFED
RLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFK
KRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPKSDLEVL
QGPLGSPNSRVD**DAALSGGGGGAEPGQALFNGDMEPEAGAGAGAA**
ASSAADPAIPEEVWNIKQMIKLTQEHIEALLDKFGGEHNPPSIYL
EAYEYTSKLDALQOREQQLLESLGNGTDFSVSSASMDTVTSSS
SSSLSVLPSSLSVFNPTDVARSNPKSPQKPIVRVFLPNKQRTVV
PARCGVTVRDSLKKALMMRGLIPECCAVYRIQDGEKKPIGWTDI
SWLTGEELHVEVLENVPLTTHNFVRKTFFTLAFCDFCRLLFQGF
RCQTCGYKFHQRCSTEVPLMCVNYDQLDLLFVSKFFEHHPIPOEE
ASLAETALTSGSSPSAPASDSIGPQILTSPSPSKSIPIPOPFRA
DEDHRNQFGQDRSSAPNVHINTIEPVNIDDLIRDQGFRGDGGS
TTGLSATPPASLPGSLTNVKALQKSPGPQERKSSSSSEDRNRMK
TLGRRDSSDDWEIPDGQITVGQRIIGSGSFGTVYKWKWHDVAVKM
LNVTAPTPOQLQAFKNEVGVLKTRHVNILLFMGYSTKPQLAIVT
QWCEGSSLYHHLHI IETKFEMI KLID IARQTAQGMDYLHAKSI IH
RDLKSNNIFLHEDLTVKIGDFGLATVKS RWSGSHQFEQLSGSILW
MAPEVIRMQDKNPYSFQSDVYAFGIVLYELMTGQLPYSNINNRDQ
IIFMVGRGYLSPDLKSVRSNCPKAMKRLMAECLKKRDERPLFPQ
ILASIELLARS LPKIHR SASEPSLN RAGFQTEDFSLYACASPKTP
IQAGGYGAFPVH

Native sequence Amino acids A2 – H766 (end) of human B-Raf.
Residue A238 of the fusion protein is equivalent to A2 of the native

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enzyme. The GST tag is located at residues 1 - 220.

Protease cleavage PreScission (LEVLFQGP) residues 221 - 228

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**Nucleotide
sequence of insert**

gtcgacGCGGCGCTGAGCGGTGGCGGTGGTGGCGGCGCGGAGCCG
GGCCAGGCTCTGTTCAACGGGGACATGGAGCCCAGGCCGGCGCC
GGCGCCGGCGCCGCGGCCTCTTCGGCTGCGGACCCTGCCATTCCG
GAGGAGGTGTGGAATATCAAACAAATGATTAAGTTGACACAGGAA
CATATAGAGGCCCTATTGGACAAATTTGGTGGGGAGCATAATCCA
CCATCAATATATCTGGAGGCCTATGAAGAATACACCAGCAAGCTA
GATGCACTCCAACAAAGAGAACAACAGTTATTGGAATCTCTGGGG
AACGGAAC TGATTTTTCTGTTTCTAGCTCTGCATCAATGGATACC
GTTACATCTTCTTCTCTTCTAGCCTTTCAGTGCTACCTTCATCT
CTTTCAGTTTTTCAAATCCACAGATGTGGCACGGAGCAACCCC
AAGTCACCACAAAACCTATCGTTAGAGTCTTCCTGCCCAACAAA
CAGAGGACAGTGGTACCTGCAAGGTGTGGAGTTACAGTCCGAGAC
AGTCTAAAGAAAGCACTGATGATGAGAGGTCTAATCCCAGAGTGC
TGTGCTGTTTACAGAATTCAGGATGGAGAGAAGAAACCAATTGGT
TGGGACACTGATATTTCTGGCTTACTGGAGAAGAATTGCATGTG
GAAGTGTTGGAGAATGTTCCACTTACAACACACAACCTTGTACGA
AAAACGTTTTTTCACCTTAGCATTTTGTGACTTTTGTGAAAGCTG
CTTTTCCAGGGTTTCCGCTGTCAAACATGTGGTTATAAATTTTAC
CAGCGTTGTAGTACAGAAGTTCCTACTGATGTGTGTTAATTATGAC
CAACTTGATTTGCTGTTTGTCTCCAAGTCTTTGAACACCACCCA
ATACCACAGGAAGAGGCGTCCTTAGCAGAGACTGCCCTAACATCT
GGATCATCCCCTCCGCACCCGCTCGGACTCTATTGGGCCCCAA
ATTCTCACCAGTCCGTCTCCTTCAAATCCATTCCAATTCCACAG
CCCTTCCGACCAGCAGATGAAGATCATCGAAATCAATTTGGGCAA
CGAGACCGATCCTCATCAGCTCCCAATGTGCATATAAACACAATA
GAACCTGTCAATATTGATGACTTGATTAGAGACCAAGGATTTCTGT
GGTGTGGAGGATCAACCACAGGTTTGTCTGCTACCCCCCTGCC
TCATTACCTGGCTCACTAACTAACGTGAAAGCCTTACAGAAATCT
CCAGGACCTCAGCGAGAAAGGAAGTCATCTTCATCCTCAGAAGAC
AGGAATCGAATGAAAACACTTGGTAGACGGGACTCGAGTGATGAT
TGGGAGATTCCTGATGGGCAGATTACAGTGGGACAAAGAATTGGA
TCTGGATCATTGGAACAGTCTACAAGGGAAAGTGGCATGGTGAT
GTGGCAGTGAAAATGTTGAATGTGACAGCACCTACACCTCAGCAG
TTACAAGCCTTCAAATGAAGTAGGAGTACTCAGGAAAACACGA
CATGTGAATATCCTACTCTTCATGGGCTATTCCACAAAGCCACAA
CTGGCTATTGTTACCCAGTGGTGTGAGGGCTCCAGCTTGTATCAC
CATCTCCATATCATTGAGACCAAATTTGAGATGATCAAACCTTATA
GATATTGCACGACAGACTGCACAGGGCATGGATTACTTACACGCC
AAGTCAATCATCCACAGAGACCTCAAGAGTAATAATATATTTCTT
CATGAAGACCTCACAGTAAAAATAGGTGATTTTGGTCTAGCTACA
GTGAAATCTCGATGGAGTGGGTCCCATCAGTTTGAACAGTTGTCT
GGATCCATTTTGTGGATGGCACCAGAAGTCATCAGAATGCAAGAT
AAAAATCCATACAGCTTTCAGTCAGATGTATATGCATTTGGGATT
GTTCTGTATGAATTGATGACTGGACAGTTACCTTATTCAAACATC
ACAACAGGGACCAGATAATTTTTATGGTGGGACGAGGATACCTG
TCTCCAGATCTCAGTAAGGTACGGAGTAACTGTCCAAAAGCCATG
AAGAGATTAATGGCAGAGTGCCTCAAAGAAAAGAGATGAGAGA

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CCACTCTTCCCAAATTCTCGCCTCTATTGAGCTGCTGGCCCGC
TCATTGCCAAAAATTCACCGCAGTGCATCAGAACCCTCCTTGAAT
CGGGCTGGTTTCCAAACAGAGGATTTTAGTCTATATGCTTGTGCT
TCTCCAAAAACACCCATCCAGGCAGGGGATATGGTGCCTTTCCT
GTCCACTgagcggccgc