

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of active RIPK2 [2 - 311]

<u>Enzyme description:-</u>	RIPK2 [2 - 311]
<u>Clone number:-</u>	DU 16348
<u>Source:-</u>	Recombinant
<u>Expression system:-</u>	Baculovirus expression vector system
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH Sepharose
<u>Expression level:-</u>	2 mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	63, 537.71 daltons
Average Mass	63, 578.44 daltons
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	6.25
<u>Purity:-</u>	>80 %
<u>Activation protocol:-</u>	Constitutively active
<u>Enzyme storage buffer:-</u>	
50 mM Tris-HCl pH 7.5, 150 mM NaCl, 270 mM sucrose, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF	
<u>Storage temperature:-</u>	-70 °C
<u>Assay buffer:-</u>	
50 mM Tris-HCl pH 7.5, 0.1 % 2-mercaptoethanol, 0.1 mM EGTA, 10 mM MgAc	
<u>Substrate:-</u>	
Myelin Basic Protein	Final concentration: 0.33 mg/ml

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Clone Data Sheet

RIPK2 [2 - 311]

<u>Protein</u>	RIPK2 [2 - 311]
<u>Clone number</u>	DU 16348
<u>Species</u>	Human
<u>Accession number</u>	NM_003821
<u>Tags</u>	N-terminal GST
<u>Bacterially expressed protein</u>	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFEL GLEFPNLPYYIDGDVKLTQSMATIRYIADKHNMLGGCPKERAETSMLE GAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLN GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKY LKSSKYIAWPLQGWQATFGGGDHPKSDLEVLFOGPLGSPEFPGRLER PNGEAICSALPTIPYHKLADRLYLSRGASGTVSSARHADWRVQVAVKH LHIHTPLLDSEKDVLREAEILHKARFSYILPILGICNEPEFLGIVTE YMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPLLH HDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTIIY MPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMY SVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLLI ELEPVLRTFEEITFLEAVIQLKK
<u>Native sequence</u>	Amino acids N2 – K311 of human RIPK2. [Full length protein ends at residue M540] Residue N242 of the fusion protein is equivalent to N2 of the native enzyme. The GST tag is located at residues 1 – 220.
<u>Protease cleavage</u>	PreScission site (<u>LEVLFQGP</u>) residues 221 – 228
<u>Cloning sites</u>	<i>NotI</i> sites of pFB GST 6P-1

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Nucleotide sequence of insert

gcggccgAACGGGGAGGCCATCTGCAGCGCCCTGCCCACCATTCCCTA
CCACAAACTCGCCGACCTGCGCTACCTGAGCCGCGGCGCCTCTGGCAC
TGTGTCGTCCGCCCCGCCACGCAGACTGGCGCGTCCAGGTGGCCGTGAA
GCACCTGCACATCCACACTCCGCTGCTCGACAGTGAAAGAAAGGATGT
CTTAAGAGAAGCTGAAATTTTACACAAAGCTAGATTTAGTTACATTCT
TCCAATTTTGGGAATTTGCAATGAGCCTGAATTTTGGGAATAGTTAC
TGAATACATGCCAAATGGATCATTAATGAACTCCTACATAGGAAAAC
TGAATATCCTGATGTTGCTTGGCCATTGAGATTTTCGCATCCTGCATGA
AATTGCCCTTGGTGTAAATTACCTGCACAATATGACTCCTCCTTTACT
TCATCATGACTTGAAGACTCAGAATATCTTATTGGACAATGAATTTCA
TGTTAAGATTGCAGATTTTGGTTTATCAAAGTGGCGCATGATGTCCCT
CTCACAGTCACGAAGTAGCAAATCTGCACCAGAAGGAGGGACAATTAT
CTATATGCCACCTGAAAACCTATGAACCTGGACAAAAATCAAGGGCCAG
TATCAAGCACGATATATATAGCTATGCAGTTATCACATGGGAAGTGTT
ATCCAGAAAACAGCCTTTTGAAGATGTCACCAATCCTTTGCAGATAAT
GTATAGTGTGTCACAAGGACATCGACCTGTTATTAATGAAGAAAGTTT
GCCATATGATATACCTCACCGAGCACGTATGATCTCTCTAATAGAAAG
TGGATGGGCACAAAATCCAGATGAAAGACCATCTTTCTTAAAATGTTT
AATAGAACTTGAACCAGTTTTGAGAACATTTGAAGAGATAACTTTTCT
TGAAGCTGTTATTTCAGCTAAAGAAAtaa