

Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of active Interleukin-1 Receptor-Associated Kinase 4 (IRAK4) [140 - 460]

Enzyme description:- IRAK4 [140 - 460]

Clone number:- DU 15580

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Expression level:- 2 mg/L

Calculated molecular mass:-

Monoisotopic 60,460.47 daltons

Average Mass 60,499.44 daltons

[cysteines reduced, methionines have not been oxidised

Theoretical pI:- 5.33

Purity:- >80 %

Activation protocol:- Constitutively active

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA,
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF

Storage temperature:- -70 °C

Assay:- Standard filter binding assay

Assay buffer:-

50 mM Tris-HCl pH 7.5, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol, 10 mM magnesium acetate

Substrate:-

MBP Final concentration: 0.3 mg/ml

Specific activity range:- To be determined

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Clone Data Sheet

IRAK4 [140 - 460]

<u>Protein</u>	IRAK4 [140 - 460]
<u>Clone number</u>	DU 15580
<u>Species</u>	Human
<u>Accession number</u>	BC013316.1
<u>Tags</u>	N-terminal GST
<u>Bacterially expressed protein</u>	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHYERDEGDKWRNKKFELG LEFPNLPLYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAESIMLEGA VLDIERYGVSRIAYSKDFETLKVDLFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVLYMDPMCLDAFPKLVCFKKRKRIEAIPQIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSD LEVLFQGPLGS VSDTRFHFSFYEL KNVTNNFDERPISVGGNMGEGGFGVVYKGYVNNTTVAVKKLAAMVDIT TEELKQQFDQEIKVMAKCQHENLVELLGFS SDGDDLCLVYVYMPNGSLL DRLSCLDGTPPPLSWHMRCKIAQGAANGINFLHENHHIHEDIKSANILLD EAFTAKISDFGLARASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSD IYSFGVVLEIITGLPAVDEHREPQLLDIKEEIEDEEKTIEDYIDKMM NNADSTSVEAMYSVASQCLHEKKNRPDIKKVQQLLOEMTAS
<u>Native sequence</u>	Amino acids V140 – S460 (end) of human IRAK4. Residue V232 of the fusion protein is equivalent to V140 of the native enzyme. The GST tag is located at residues 1 – 220.
<u>Protease cleavage</u>	PreScission (LEVLFQGP) residues 221 - 228
<u>Cloning sites</u>	<i>Bam</i> H1 and <i>Not</i> 1 site of pFastBac GST

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<u>Nucleotide Sequence of insert</u>	ggatccGTTAGTGATACACGTTTCACAGTTTCATTATGAATTGA AGAATGTCACAAATAACTTGTGATGAACGACCCATTCTGTTGGTAA TAAAATGGGAGAGGGAGGATTGGAGTTGTATATAAAGGCTACGTAAAT AACACAACGTGGCAGTGAAGAAGCTGCAGCAATGGTGTACATTACTA CTGAAGAACTGAAACAGCAGCTTGATCAAGAAATAAAAGTAATGGCAAA GTGTCAACATGAAAACTTAGTAGAACTACTTGGTTCTCAAGTGATGGA GATGACCTCTGCTTAGTATATGTTACATGCCTAATGGTTATTGCTAG ACAGACTCTTGCTGGATGGTACTCCACCACTTCTGGCACATGAG ATGCAAGATTGCTCAGGGTGCAGCTAATGGCATCAATTCTACATGAA AATCATCATATTCTAGAGATATTAAAAGTCAAATATCTTACTGGATG AAGCTTTACTGCTAAAATATCTGACTTTGCCCTGCACGGCTCTGA GAAGTTGCCAGACAGTCATGACTAGCAGAATTGGAAACACAGCT TATATGGCACCAGAAGCTTGCCTGGAGAAATAACACCCAAATCTGATA TTTACAGCTTGGTGTGGTTACTAGAAATAACTGGACTTCCAGC TGTGGATGAACACCGTGAACCTCAGTTATTGCTAGATATTAAAGAAGAA ATTGAAGATGAAGAAAAGACAATTGAAGATTATATTGATAAAAAGATGA ATGATGCTGATTCCACTTCAGTTGAAGCTATGTAACCTGTTGCTAGTCA ATGTCTGCATGAAAAGAAAAATAAGAGACCAGACATTAAGAAGGTTCAA CAGCTGCTGCAAGAGATGACAGCTTCTtaagcggccgc
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