

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of

<u>Enzyme description:-</u>	BIRC3
<u>Clone number:-</u>	DU32417
<u>Source:-</u>	Recombinant
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH-Sepharose
<u>Expression level:-</u>	0.1mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	95134
Average Mass	95193
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	5.64
<u>Purity:-</u>	50%-70% variable
<u>Enzyme storage buffer:-</u>	
50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT	
<u>Storage temperature:-</u>	-80°C
<u>Assay:-</u>	

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Clone Data Sheet

Protein name

<u>Protein</u>	BIRC3 1-604 (full length)
<u>Synonyms</u>	IAP1, API2, MIHC, RNF49
<u>Clone Number</u>	DU32417
<u>Species</u>	Human
<u>Accession Number</u>	Protein Q13489
<u>Tags</u>	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAESIMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA WPLQGWQATFGGGDHPKSDLEVLFOGPLGSMNIVENSIFLSNLMKSANT FELKYDLSCELYRMSTYSTFPAGVPVSERSLARAGFYITGVNDKVKCFCC GLMLDNWKRGDSPTEKHKKLYPSCRFOQLNSVNNLEATSQPTFPSSVTN STHSLLPGTENSGYFRGSYSNSPSNPVNSRANQDF SALMRSSYHCAMNE NARLLTFQTWPLTFLSPTDLAKAGFYIIGPDRVACFACGGKLSNWEPKD NAMSEHLRHFPKCPFIENQLQDTSRYTVSNLSMOTHAARFKTFFNWPSSV LVNPEQLASAGFYVGNSSDDVKCFCCDGGRLCWESGDDPWVQHAKWFPRC EYLIRIKGQEFIRQVQASYPHLLEQLLSTSDSPGDENAESSIHFEPGED HSEDAIMMNTPVINA AAVEMGFSRSLVKQTVQRKILATGENYRLVNDLVLD LLNAEDEIREEERERATEEKESNDLLLIRKNRMALFOHLTCVIPILDSLL TAGINEQEHDVIKQKTQTSLQARELIDTILVKGNI AATVFRNSLQEAEA VLYEHLFVQODIKYIPTEDVSDLPVEEQLRRLQEERTCKVCMDKEVSIVF IPCGHLVVCKDCAPSLRKCPICRSTIKGTVRTFLS
Native sequence	1-604 in bold
Protease cleavage	Prescission site underlined
Cloning sites	BamH1 / Not1

**DNA sequence of
insert**

GGATCCATGAACATAGTAGAAAACAGCATATTCTTATCAAATTTGATGAAA
AGCGCCAACACGTTTGAAGTAAAATACGACTTGTTCATGTGAAGTGTACCG
AATGTCTACGTATTCCACTTTTCTGCTGGGGTTCCTGTCTCAGAAAGGA
GTCTTGCTCGTGTGGTTTCTATTACACTGGTGTGAATGACAAGGTCAAA
TGCTTCTGTTGTGGCCTGATGCTGGATAACTGGAAAAGAGGAGACAGTCC
TACTGAAAAGCATAAAAAGTTGTATCCTAGCTGCAGATTTCGTTTCAGAGTC
TAAATTCGGTTAACAACCTTGGAAAGCTACCTCTCAGCCTACTTTTCTTCT
TCAGTAACAAATTCACACACTCATTACTTCCGGGTACAGAAAACAGTGG
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TCCTTCTTTAAGAAAAGTGTCTATTGTAGGAGTACAATCAAGGGTACAG
TTCGTACATTTCTTTCATGAGCGGCCGC