

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of

<u>Enzyme description:-</u>	BIRC2 1-618 (full length)
<u>Clone number:-</u>	DU32469
<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	97639
Average Mass	97700
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	6.44
<u>Purity:-</u>	50%-70% varies with expression
<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

Protein BIRC2 1-618
Synonyms cIAP1, AIP1
Clone Number DU32469
Species Human
Accession Number Protein: NP_001157 or Q13490
Tags N-terminal GST

Aminoacid sequence
of the expressed
protein

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGL
EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAESMLEGAVL
DIRYGVSRIAYSDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH
PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA
WPLQGWQATFGGGDHPKSDLEVLFOGPLGSPGIPGSTRAAAMHKTASQR
LFPGPSYQNIKSIMEDSTILSDWTNSNKQMKYDFSCELYRMSTYSTFPA
GVPVSESLARAGFYITGVNDKVKCFCCGLMLDNWKLGDSPIQKHKQLYP
SCSFIQNLVSASLGSTSKNTSPMRNSFAHLSPTLEHSSLFSGSYSSLSP
NPLNSRAVEDISSRTNPYSYAMSTEEARFLTYHMWPLTFLSPSELARAG
FYYIGPGRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPFLNSLETLR
FSISNLSMQTHAARMRTFMYWPSSVPVQPEQLASAGFYVGRNDDVKCFC
CDGGLRCWESGDDPWVEHAKWFPRCEFLIRMKGQEFVDEIQGRYPHLEQ
LLSTSDTTGEENADPPIIHFGPGESSEDAVMNTPVVKSALEMGFNRDL
VKQTVQSKILTTGENYKTVNDIVSALLNAEDEKREEEKEKQAEEMASDDL
SLIRKNRMALFQQLTCVLPILDNLLKANVINKQEHDIKQKTQIPLQARE
LIDTILVKGNAANIFKNCLKEIDSTLYKNLFVDKNMKYIPTEDVSGLSL
EEQLRRLQEERTCKVCMDEKVSVVFIPCGHLVVCQECAPSLRKCPICRGI
IKGTVRTFLS

Native sequence 1-618 (full length in bold)
Protease cleavage Precission site underlined
Cloning sites Not1 / Not1

**DNA sequence of
insert**

GCGGCCGCGATGCACAAAACACTGCCTCCCAAAGACTTTTCCCAGGTCCCTC
GTATCAAAACATTAAGAGTATAATGGAAGATAGCACGATCTTGTTCAGATT
GGACAAACAGCAACAAACAAAAAATGAAGTATGACTTTTCCCTGTGAACTC
TACAGAATGTCTACATATTCAACTTTCCCGCCGGGGTGCCTGTCTCAGA
AAGGAGTCTTGCTCGTGTGGTTTTTTATTATACTGGTGTGAATGACAAGG
TCAAATGCTTCTGTTGTGGCCTGATGCTGGATAACTGGAACTAGGAGAC
AGTCTTATTCAAAAGCATAAACAGCTATATCCTAGCTGTAGCTTTTATTCA
GAATCTGGTTTCAGCTAGTCTGGGATCCACCTCTAAGAATACGTCTCCAA
TGAGAAACAGTTTTGCACATTCATTATCTCCACCTTGGAACATAGTAGC
TTGTTTCAGTGGTCTTACTCCAGCCTTTCTCCAAACCCTCTTAATTCTAG
AGCAGTTGAAGACATCTCTTCATCGAGGACTAACCCCTACAGTTATGCAA
TGAGTACTGAAGAAGCCAGATTTCTTACCTACCATATGTGGCCATTAACT
TTTTTGTCCACATCAGAATTGGCAAGAGCTGGTTTTTTATTATATAGGACC
TGGAGATAGGGTAGCCTGCTTGCCTGTGGTGGGAAGCTCAGTAACTGGG
AACCAAGGATGATGCTATGTCAGAACACCGGAGGCATTTTCCCAACTGT
CCATTTTTGGAAAATTCTCTAGAACTCTGAGGTTTAGCATTTCAAATCT
GAGCATGCAGACACATGCAGCTCGAATGAGAACATTTATGTACTGGCCAT
CTAGTGTTCAGTTCAGCCTGAGCAGCTTGCAAGTGTGGTTTTTTATTAT
GTGGGTCGCAATGATGATGTCAAATGCTTTTGTGTGATGGTGGCTTGAG
GTGTTGGGAATCTGGAGATGATCCATGGGTAGAACATGCCAAGTGGTTTC
CAAGGTGTGAGTCTTGATACGAATGAAAGGCCAAGAGTTTGTGTGATGAG
ATTCAAGGTAGATATCCTCATCTTCTTGAACAGCTGTTGTCAACTTCAGA
TACCACTGGAGAAGAAAATGCTGACCCACCAATTATTCAATTTGGACCTG
GAGAAAGTTCTTCAGAAGATGCTGTCATGATGAATACACCTGTGGTTAAA
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TCTCTAAGAAAATGCCCTATTTGCAGGGGTATAATCAAGGGTACTGTTTCG
TACATTTCTCTCTTAAGCGGCCGC