

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-ABIN2

Enzyme description:- GST-ABIN2 1-429 (full length)

Clone number:- DU3714

Source:- BL21 recombinant

Tag:- N-terminal GST

Purification method:- GSH-Sepharose

Expression level:- 0.1mg/L

Calculated molecular mass:-

Monoisotopic 75561 Da

Average Mass 75605 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.15

Purity:- 90%

Enzyme storage buffer:-

50mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT

Storage temperature:- -80°C

Assay:-

Division of Signal Transduction Therapy

Clone Data Sheet

GST-ABIN2

<u>Protein</u>	ABIN2 (1-429)
<u>Synonyms</u>	TNFAIP3 interacting protein 2 (TNIP2), A20-binding inhibitor of NF-kappaB activation 2 (ABIN2)
<u>Clone Number</u>	DU3714
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q8NFZ5
<u>Tags</u>	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEHLIERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIRYIADKHNMLGGCPKERAIEISMLEGAVLDIRYGVSR IAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFGPLGSMRDPGSGGWEEAPRAAAALCTLYHEAGQRLRRLQDQLAARDALIARLRARLAALEGDAAPSLVDALLEQVARFREQLRRQEGGAAEAQMRQEI ERLTERLEEKEREMOQLLSQPQHER EKEVLLRRSMAEGERARAASDVLCRSLANETHQLRRTL TATAHMCQH LAKCLDERQHAQRNVGERSPDQSEHTDGHTSVQSVIEKLOEENRLLKQKVTHVEDLNKAWQRYNASRDEYV RGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDCAEVKQELAASRTARDAALERVQMLEQQI LAYKDDFMSEADRER AQSRIQELEEKVASLLHQVSWRQDSREP DAGRIHAGSKTAKYLAADALEL M VPGGWRPGTGSQQPEPPAEGGHPGAVQRGQGD LQCPHCLQCF SDEQGEELLRHVAECCQ
Native sequence	in bold
Protease cleavage	Prescission protease site underlined
Cloning sites	BamHI / NotI
<u>DNA sequence of insert</u>	GGATCCATGTCCCGGGACCCGGGGTTCGGGCGGCTGGGAGGAGGCCCCGCGCGCAGCTGCCGCGCTCTGCACCCGTGTACCACGAGGCCGGACAGCGGCTGCCGCTGCAGGACCAGCTCGCTGCCCCGCGACGCCCTCATCGCTCGCCTCCGCGCCCGCTGGCCGCGCTGGAGGGGACGCCGCGCCGTCCCTAGTGGA CGCGCTGCTGGAGCAGGTTGCGCGCTTCCGGGAGCAGCTGCGAAGGCAGGAGGGCGGCGCCGCGAGGCCAGATGCGCCAGGAAATTGAGAGGCTGACTGAGCGACTAGAAGAAAAGAGAGGGAGATGCAGCAGCTGCTGAGCCAGCCCAACACGAGCGAGAGAAGGAAGTCGTCCTGCTACGGAGGAGCATGGCAG AAGGGGAGCGCGCCCGGGCCGCCAGTGACGTCCTGTGCCGCTCCTTGGCC AACGAGACCCATCAGCTGCGGAGGACGCTGACCGCCACCGCCACATGTGTCAGCATCTGGCCAAGTGTCTGGATGAACGACAGCATGCACAAAGGAATG TGGGGGAGAGAAGTCCTGACCAGTCGGAACACACAGATGGGCACACCTCTGTCCAGAGTGTTATTGAGAAGTTGCAGGAAGAAAATCGACTGTTAAACA

GAAGGTGACTCACGTTGAAGACCTCAATGCCAAGTGGCAGCGCTACAACG
CCAGCAGGGACGAATACGTGAGGGGGCTCCATGCGCAGCTCAGGGGGCTG
CAGATCCCCACGAGCCGAGCTGATGAGGAAGGAGATCTCCCGGCTCAA
CAGACAGTTGGAAGAGAAAATAAATGACTGTGCCGAAGTGAAGCAGGAGC
TGGCGGCCTCCAGGACGGCCCCGGGATGCTGCGTTGGAGCGGGTGCAGATG
CTGGAACAGCAGATTCTCGCTTACAAGGATGACTTCATGTCAGAAAGGGC
CGATCGGGAACGGGCTCAAAGTAGGATTCAAGAAGTGGAGGAAAAGGTG
CCTCTTTGCTGCACCAGGTGTCCTGGAGACAGGATTCTCGAGAGCCAGAC
GCCGGCCGGATTACGCTGGGAGCAAACTGCCAAGTATTTGGCCGCCGA
CGCATTAGAGCTTATGGTGCCTGGTGGCTGGAGGCCTGGGACTGGGTCCC
AGCAGCCAGAACCCCTGCAGAGGGCGGGCATCCTGGCGCGGTCCAGAGA
GGCCAGGGGGACCTTCAGTGCCCTCACTGCCTGCAGTGCTTCAGTGACGA
GCAAGGGGAAGAGCTCCTCAGGCATGTGGCCGAGTGCTGCCAGTGAGCGG
CCGC