Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of ZNRF1

Enzyme description:- GST-ZNRF1 1-227

Clone number:- DU33621

Source:- Recombinant

Tag:- N-terminal GST

Purification method:- GSH-Sepharose

Expression level:- 1 mg/L

Calculated molecular mass:-

Monoisotopic	50573 Da
Average Mass	50605 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.28

Purity:- 60%

Enzyme storage buffer:-

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

Storage temperature:- -80ºC

Assay:-

Division of Signal Transduction Therapy

Clone Data Sheet

Protein name ZNRF1

Protein	GST-ZNRF1 1-227 (full length)
Synonyms	NIN283
Clone Number	DU33621
Species	human
Accession Number	Protein: Q8ND25 DNA: NM_032268.4
Tags	N-terminal GST
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGS**MGGKQSTAARSRGPFPGVSTDDSAVPPPGGAPHFGHYRTGGGAMGLRSRSVSSVAGMGMDPSTAGGVPFGLYTPASRGTGDSERAPGGGGSASDSTYAHGNGYQETGGGHHRDGMLYLGSRASLADALPLHIAPRWFSSHSGFKCPICSKSVASDEMEMHFIMCLSKPRLSYNDDVLTKDAGECVICLEELLQGDTIARLPCLCIYHKSCIDSWFEVNRSCPEHPAD**
Native sequence	in bold
Protease cleavage	Prescission site underlined
Cloning sites	BamH1 Not1
DNA sequence of insert	GGATCCATGGGGGGCAAGCAGAGCACGGCGGCCCGCTCCCGGGGCCCCTTCCCGGGGGTCTCCACCGATGACAGCGCCGTGCCGCCGCCGGGAGGGGCGCCCCATTTCGGGCACTACCGGACGGGCGGCGGGGCCATGGGGCTGCGCAGCCGCTCGGTCAGCTCGGTGGCAGGCATGGGCATGGACCCCAGCACGGCCGGGGGGGTGCCCTTTGGCCTCTACACCCCCGCCTCCCGGGGCACCGGCGACTCCGAGAGGGCGCCCGGCGGCGGAGGGTCTGCGTCCGACTCCACCTATGCCCATGGCAATGGTTACCAGGAGACGGGCGGCGGTCACCATAGAGACGGGATGCTGTACCTGGGCTCCCGAGCCTCGCTGGCGGATGCTCTACCTCTGCACATCGCACCCAGGTGGTTCAGCTCGCATAGTGGTTTCAAGTGCCCCATTTGCTCCAAGTCTGTGGCTTCTGACGAGATGGAAATGCACTTTATAATGTGTTTGAGCAAACCTCGCCTCTCCTACAACGATGATGTGCTGACTAAAGACGCGGGTGAGTGTGTGATCTGCCTGGAGGAGCTGCTGCAGGGGGACACGATAGCCAGGCTGCCCTGCCTGTGCATCTATCACAAAAGCTGCATAGACTCGTGGTTTGAAGTGAACAGATCTTGTCCGGAACACCCTGCGGACTGAGCGGCCGC