

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of IPA9.8

<u>Enzyme description:-</u>	IPA9.8
<u>Clone number:-</u>	DU32826
<u>Source:-</u>	Recombinant
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH-Sepharose
<u>Expression level:-</u>	3mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	88763
Average Mass	88816
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	5.05
<u>Purity:-</u>	90%
<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>	IPAH9.8 1-545 (full length)
<u>Synonyms</u>	
<u>Clone Number</u>	DU32628
<u>Species</u>	shigella flexneri
<u>Accession Number</u>	AY206445.1
<u>Tags</u>	N-terminal GST-tag
Aminoacid sequence of the expressed protein	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA WPLQGWQATFGGGDHPKSDLEVLFOGPLGSMLP INNNFSLPQNSFYNTI SGTYADYFSAWDKWEKQALPGEERDEAVSRLKECLINNSDELRLDRLNLS SLPDNLPAQITLLNVSYNQLTNLPELPVTLKKLYSASNKLSLPELVLPAL ESLQVQHNELENLPALPDSLLTMNISYNEIVSLPSLPQALKNLRATRNF TELPAFSEGNNPVVREYFFDRNQISHIPESILNLRNECSIHISDNPLSSH ALQALQRLTSSPDYHGPRIFYSMSDGQONTLHRPLADAVTAWFPENKQSD VSQIWHAFEHEEHANTFSAFLDRLSDTVSARNTSGFREQVAAWLEKLSAS AELRQQSFVAADATESCEDRVALTWNLRKTLVHQASEGLFDNDTGAL LSLGREMFRLEILEDIARDKVRTLHFVDEIEVYLAFQTMLAEKLQSTAV KEMRFYGVSGVTANDLRTAEMVRSRENEFTDWFSLWGPWHAVLKRTEA DRWALAEQKYEMLENEYQORVADRLKASGLSGDADAEREAGAQMRETE QQIYRQLTDEVLALRLPENGSQLHHS
Native sequence	in bold
Protease cleavage	Precision Protease site underlined
Cloning sites	BamH1 / NotI

**DNA sequence of
insert**

GGATCCATGTTACCGATAAATAAATAACTTTTCATTGCCCCAAAATTCTTT
TTATAACACTATTTCCGGTACATATGCTGATTACTTTTCAGCATGGGATA
AATGGGAAAAACAAGCGCTCCCCGGTGAAGAGCGTGATGAGGCTGTCTCC
CGACTTAAAGAATGTCTTATCAATAATTCCGATGAACTTCGACTGGACCG
TTTAAATCTGTCTCGCTACCTGACAACCTACCAGCTCAGATAACGCTGC
TCAATGTATCATATAATCAATTAACCTAACCTACCTGAACTGCCTGTTACG
CTAAAAAATTATATTCCGCCAGCAATAAATTATCAGAATTGCCCGTGCT
ACCTCCTGCGCTGGAGTCACTTCAGGTACAACACAATGAGCTGGAAAACC
TGCCAGCTTTACCCGATTTCGTTATTGACTATGAATATCAGCTATAACGAA
ATAGTCTCCTTACCATCGCTCCCACAGGCTCTTAAAAATCTCAGAGCGAC
CCGTAATTTCCCTCACTGAGCTACCAGCATTTTCTGAGGGAAATAATCCCG
TTGTCAGAGAGTATTTTTTTGATAGAAATCAGATAAGTCATATCCCGGAA
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ATTATCATCCCATGCTCTGCAAGCCCTGCAAAGATTAACCTCTTCGCCGG
ACTACCACGGCCACGGATTTACTTCTCCATGAGTGACGGACAACAGAAT
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CAAACAATCTGATGTATCACAGATATGGCATGCTTTTGAACATGAAGAGC
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GCACGCAATACCTCCGGATTCCGTGAACAGGTCGCTGCATGGCTGGAAAA
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CGGAAAACCCTCCTGGTCCATCAGGCATCAGAAGGCCTTTTCGATAATGA
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GCGTGAGACTGAACAGCAGATTTACCGTCAGCTGACTGACGAGGTACTGG
CCCTGCGATTGCCTGAAAACGGCTCACAACCTGCACCATTTCATAAGCGGCC
GC