

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of ZNF216 [1 - 213]

Enzyme description:- ZNF216 [1 - 213]

Clone number:- DU 8901

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-

Monoisotopic 49, 865.68 daltons

Average Mass 49, 898.21 daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 8.06

Purity:- >80 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA,
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF

Storage temperature:- -70 °C

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Clone Data Sheet

ZNF216 [1 - 213]

<u>Protein</u>	ZNF216 [1 - 213]
<u>Clone number</u>	DU 8901
<u>Species</u>	Human
<u>Accession number</u>	NM_001278245.1
<u>Tags</u>	N-terminal GST
<u>Bacterially expressed protein</u>	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPPYYIDGDVKLTQSMATIRYIADKHNMLGGCPKERAETSMLEGA VLDIRYGVSR IAYS KDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS KYIAWPLQGWOATFGGGDHPPKSDLEVLFGQPLGSMAQETNQTGPMLC STGCGFYGNPRTNGMCSVCYKEHLQRQNSGRMSPMG TASGSNSPTSGS ASVQRADTSLNNCEGAAGSTSEKSRNVPVAALPVTQOMTEMSISREDKI TTPKTEVSEPVVTQPSPSVSQPSTSQSEEKAPELPKPKKNRCFMCRKKV GLTGFDRCRGNLFCGLHRYSDKHNC PYDYKAEAAAKIRKENPVVVAEKI QRI
<u>Native sequence</u>	Amino acids M1 – I213 (end) of human ZNF216. Residue M232 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.
<u>Protease cleavage</u>	PreScission (LEVLFGQP) residues 221 - 228
<u>Cloning sites</u>	<i>Bam</i> H1 and <i>Not</i> I of pGEX6P-1

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Nucleotide

Sequence of insert

gatccATGGCTCAGGAGACTAACCAGACCCCGGGGCCCATGCTGTGTAG
CACAGGATGTGGCTTTTATGGAAATCCTAGGACAAATGGAATGTGTTCA
GTTTGCTACAAAGAACATCTTCAGAGGCAGCAAAATAGTGGCAGAATGA
GCCCAATGGGGACAGCTAGTGGTTCCAACAGTCCTACCTCAGGTTCTGC
ATCTGTACAGAGAGCAGACACTAGCTTAAACAACGTGAAGGTGCTGCT
GGCAGCACATCTGAAAAATCAAGAAATGTGCCTGTGGCTGCCTTGCCCTG
TAACTCAGCAAATGACAGAAATGAGCATTTCAAGAGAGGACAAAATAAC
TACCCCGAAAACAGAGGTGTCAGAGCCAGTTGTCACTCAGCCCAGTCCA
TCAGTTTCTCAGCCCAGTACTTCTCAGAGTGAAGAAAAAGCTCCTGAAT
TGCCCAAACCAAAGAAAAACAGATGTTTCATGTGCAGAAAGAAAGTTGG
TCTTACAGGGTTTGACTGCCGATGTGGCAATTTGTTTTGTGGACTTCAC
CGT TACTCTGACAAGCACAACTGTCCGTATGATTACAAAGCAGAAGCTG
CAGCAAAAATCAGAAAAGAGAATCCAGTTGTTGTGGCTGAAAAAATTCA
GAGAATAtaagcggccgc