

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-USP19 [1 – 1290]

Enzyme description:- GST-USP19 [1 – 1290]

Clone number:- SC20876

Source:- BL21 Recombinant

Tag:- N-terminal GST

Purification method:- GSH-Sepharose

Expression level:- 0.5 mg/L

Calculated molecular mass:-

Monoisotopic 169871 Da

Average Mass 169972 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.89

Purity:- 40%

Enzyme storage buffer:-

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

Storage temperature:- -80°C

Assay:-

Ub-Rho110-Gly cleavage assay monitored by Ex/Em 485/535 nm

Assay buffer:-

40 mM Tris pH 7.5, 100 mM NaCl, 5 mM DTT, 0.01% Triton X-100, 0.005% Ovalbumin, 0.5 µM Ub-Rho110-Gly

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Clone Data Sheet

GST-USP19 [1 – 1290]

<u>Protein</u>	GST-USP19 [1 – 1290]
<u>Synonyms</u>	ZMYMD9, UBP19
<u>Clone Number</u>	SC20876
<u>Species</u>	Human
<u>Accession Number</u>	Protein: O94966 DNA: NM_006677.1
<u>Tags</u>	N-terminal GST tag
<u>Amino acid sequence of expressed protein</u>	<p>MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA WPLQGWQATFGGGDHPKSDLEVLFOGPLGSPNSRVDMMSGGASATGPRRG PPGLEDTTSSKKKQKDRANQESKDGDPKRGKTSRYVAQAGLEPLASGDPSA SASHAAGITGSRHRTRLFFPSSSGSASTPQEEQTKEGACEDPHDLLATPT PELLLDWRQSAEEVIVKLRVGVGPLEQLEDVDAFTDTCVVRFAGGQWG GVFYAEIKSSCAKVQTRKGSLLHLTLPKKVPMLTWPSLLVEADEQLCIPP LNSQTCLLGSEENLAPLAGEKAVPPGNDPVSAMVRSRNPVKDDCAKEEM AVAADAATLVDEPESMVNLAFAVKNDSYKGPDSVVVHVYVKEICRDTSRV LFREQDFTLIFQTRDGNFLRLHPGCGPHTTFRWQVKLRNLIEPEQCTFCF TASRIDICLRKRQSQRWGGLEAPAARVGGAKVAVPTGPTPLDSTPPGGAP HPLTGQEEARAVEKDKSKARSEDGLDSVATRTPMEHVTPKPEHLASPK PTCMVPPMPHSPVSGDSVEEEEEEEKKVCLPGFTGLVNLGNTCFMNSVIO SLSNTRRELDRDFHDRSFEEAEINYNPLGTGGRLAIGFAVLLRALWKGTHH AFQPSKKAIVASKASQFTGYAQHDAQEFMAFLLDGLHEDLNRIQNKPYT ETVSDSGRPDEVVAEEAWQRHKMRNDSFIVDLFOGQYKSKLVCPVCAKVS ITFDPFLLYLPVPLPQKQKVLVVFYFAREPHSKPIKFLVSVSKENSTASEV LDSLSQSVHVKPENLRLAEVINKRFHRVFLPSHSLDTSVSPSDTLLCFELL SSELAKERVVVLEVQORPQVPSVPIKCAACQKQOSEDEKLRCTRRCYR VGVCNQLCQKTHWPDHKGLCRPENIGYPFLVSVPASRLTYARLAOLLEGY ARYSVSVFQPPFQGRMALESQSPGCTTLLSTGSLEAGDSERDPIQPPEL QLVTPMAEGDTGLPRVWAAPDRGVPVSTSGISSEMLASGPIEVGSLPAGE RVSRPEAAVPGYQHPSEAMNAHTPQFFIYKIDSSNREQRLEDKGDTPLEL GDDCSLALVWRNNERLQEFVLVASKLECAEDPGSAGEAARAGHFTLDQC LNLFTRPEVLAPEEAWYCPQCKQHREASKQLLLWRLPNVLIVQLKRFSFR SFIWRDKINDLVEFPVRNLDLSKFCIGQKEEQLP SYDLYAVINHYGGMIG GHYTACARLPNDRSSQRSDVWRLFDSTVTTVDESQVVTRYAYVLFYRR RNSPVERPPRAGHSEHHPDLGPAAEAAAASQASRIWQELEAEEEPVPEGS PLGPWGPQDVGWGLPRGPTTPDEGCLR</p>
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	Precision site underlined
<u>Cloning sites</u>	SalI / NotI

DNA sequence of insert

GTCGACATGTCTGGCGGGGCCAGTGCCACAGGCCCAAGGAGAGGGCCCC
AGGACTGGAGGACACCCTAGTAAGAAGAAGCAGAAGGATCGAGCAAACC
AGGAGAGCAAGGATGGAGATCCTAGGAAAGAGACAGGGTCTCGATATGTT
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