Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-DEN1 [N91A W103A C163A]

Enzyme description:- GST-DEN1 [N91A W103A C163A]

Clone number:- SC20825

Source:- BL21 Recombinant

Tag:- N-terminal GST tag

Purification method:- GSH sepharose

Expression level:- 6 mg/L

Calculated molecular mass:-

Monoisotopic 51376 Da
Average Mass 51408 Da
[cycsteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.65

Purity:- 90%

Enzyme storage buffer:-

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

Storage temperature:- -80ºC

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Clone Data Sheet

GST-DEN1 [N91A W103A C163A]

Protein	GST-DEN1 [N91A W103A C163A]
Synonyms	SENP8, NEDP1, PRSC2
Clone Number	SC20825
Species	Human
Accession Number	Protein: Q96LD8 DNA: NM145204.3
Tags	N-terminal GST tag
Amino acid sequence of expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGSPNSRVD**MDPVVLSYMDSLLRQSDVSLLDPPSWLNDHIIGFAFEYFANSQFHDCSDHVSFISPEVTQFIKCTSNPAEIAMFLEPLDLPNKRVVFLAIADNSNQAAGGTHASLLVYLQDKNSFFHYDSHSRSNSVHAKQVAEKLEAFLGRKGDKLAFVEEKAPAQQNSYDAGMYVICNTEALCQNFFRQQTESLLQLLTPAYITKKRGEWKDLITTLAKK**
Native sequence	in bold
Protease cleavage	Precission site underlined
Cloning sites	Sal1/Not1
DNA sequence of insert	GTCGACATGGACCCCGTAGTCTTGAGTTACATGGACAGTCTACTGCGGCAATCAGATGTCTCACTATTGGATCCGCCAAGCTGGCTCAATGACCATATTATTGGGTTTGCGTTTGAGTACTTTGCCAACAGTCAGTTTCATGACTGCTCTGATCACGTCAGTTTCATCAGCCCTGAAGTCACCCAGTTCATCAAGTGCACTAGCAACCCAGCAGAGATTGCCATGTTCCTTGAACCACTGGACCTCCCCAACAAGAGAGTTGTATTTTTAGCCATCGCTGATAACTCCAACCAGGCAGCTGGAGGAACCCACGCGAGTTTATTGGTCTACCTCCAAGATAAAAATAGCTTTTTTCATTATGATTCCCATAGCAGGAGCAACTCAGTTCACGCAAAGCAGGTAGCAGAGAAACTGGAGGCTTTCTTAGGCAGAAAAGGAGACAAACTGGCCTTTGTGGAAGAGAAAGCCCCTGCCCAACAAAACAGCTATGACGCTGGGATGTACGTGATATGTAACACTGAGGCCTTGTGTCAGAACTTCTTTAGGCAACAGACAGAATCACTGCTGCAGCTACTCACCCCTGCATACATCACAAAGAAGAGGGGAGAATGGAAAGATCTCATTACCACACTTGCTAAAAAGTAGGCGGCCGC