

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-DEN1 [N91A W103A]

<u>Enzyme description:-</u>	GST-DEN1 [N91A W103A]
<u>Clone number:-</u>	SC20781
<u>Source:-</u>	BL21 Recombinant
<u>Tag:-</u>	N-terminal GST tag
<u>Purification method:-</u>	GSH sepharose
<u>Expression level:-</u>	6 mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	51408 Da
Average Mass	51440 Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	5.65
<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

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Clone Data Sheet

GST-DEN1 [N91A W103A]

<u>Protein</u>	GST-DEN1 [N91A W103A]
<u>Synonyms</u>	SENP8, NEDP1, PRSC2
<u>Clone Number</u>	SC20781
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q96LD8 DNA: NM145204.3
<u>Tags</u>	N-terminal GST tag
<u>Amino acid sequence of expressed protein</u>	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPHYIDGDVKLTSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDLFLSKLPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVLVFOGPLGSPNSRVD MDPVVLSYMSLL RQSDVSLLDPPSWLNDHIIGFAFEYFANSQFHDCSDHVSFISPEVTQFIK CTSNPAEIAMFLEPLDLPNKRVVFLAIADNSNQAAGGTHASLLVYLQDKN SFFHYDSHSRSNSVHAKQVAEKLEAFLGRKGDKLAFVEEKAPAQQNSYDC GMVICNTEALCQNFRRQQTESLLQLLTPAYITKKRGEWKDLITTLAKK
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	site underlined
<u>Cloning sites</u>	Sall/NotI
<u>DNA sequence of insert</u>	GTCGACATGGACCCCGTAGTCTTGAGTTACATGGACAGTCTACTGCGGCA ATCAGATGTCTCACTATTGGATCCGCCAAGCTGGCTCAATGACCATATTA TTGGGTTTTGCGTTTTGAGTACTTTGCCAACAGTCAGTTTCATGACTGCTCT GATCACGTCAGTTTCATCAGCCCTGAAGTCACCCAGTTCATCAAGTGCAC TAGCAACCCAGCAGAGATTGCCATGTTCCCTTGAACCACTGGACCTCCCA ACAAGAGAGTTGTATTTTTAGCCATCGCTGATAACTCCAACCAGGCAGCT GGAGGAACCCACGCGAGTTTATTTGGTCTACCTCCAAGATAAAAAATAGCTT TTTTTATTATGATTCCCATAGCAGGAGCAACTCAGTTCACGCAAAGCAGG TAGCAGAGAAACTGGAGGCTTTCTTAGGCAGAAAAGGAGACAAACTGGCC TTTGTGGAAGAGAAAAGCCCTGCCCAACAAAACAGCTATGACTGTGGGAT GTACGTGATATGTAACACTGAGGCCTTGTGTCAGAACTTCCTTAGGCAAC AGACAGAATCACTGCTGCAGCTACTCACCCCTGCATACATCACAAAGAAG AGGGGAGAATGGAAAGATCTCATTACCACACTTGCTAAAAAGTAGGCGGC CGC