

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of NLEL

Enzyme description:- GST-NLEL 60-782

Clone number:- DU39419

Source:- Recombinant

Tag:- N-terminal GST

Purification method:- GSH-Sepharose

Expression level:- 3mg/L

Calculated molecular mass:-

Monoisotopic 107864 Da

Average Mass 107932 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 4.68

Purity:- 90%

Enzyme storage buffer:-

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

Storage temperature:- -80°C

Assay:-

Division of Signal Transduction Therapy

Clone Data Sheet

Protein name NLEL

Protein GST-NLEL 60-782

Synonyms

Clone Number DU39419

Species Escherichia Coli

Accession Number Protein: NP_309587.1

Tags N-terminal GST

Aminoacid sequence
of the expressed
protein

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL
EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGAVL
DIRYGVSR IAYS KDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTH
PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA
WPLQGWQATFGGGDHPKSDENLYFOGGS**NGETLSISEPITTLPDLLPGS**
LKELVLNGCTELKSINCLPPNLSSLSMVGCSSEVINCSIPENVINSLC
HCSLKHIEGSFPEALRNSVYLNGCNSLNESQCQFLAYDVSQGRACLSKA
ELTADLIWLSANRTGEESAEEELNYSGCDLSGLSLVGLNLSSVNFSGAVLD
DTDLRMSDLSQAVLENCSEFKNSILNECNFCYANLSNCIIRALFENSFN
SNLKNASFKGSSYIQYPPILNEADLTGAIIPGMVLSGAILGDVKELFSE
KSNTINLGGCYIDLSDIQENILSVLDNYTKSNKSILLTMNTSDDKYNHDK
VRAAEELIKKISLDELAAFRPYVKMSLADSFSIHPYLNANIQWLEPIC
DDFFDTIMSWFNNSIMMYMENGSLLOAGMYFERHPGAMVSYNSSFIQIVM
NGSRRDGMQERFRELYEVYLKNEKVYPVTQOSDFGLCDGSGKPDWDDSD
LAYNWVLLSSQDDGMAMMCSLSHMVDMLSPNTSTNWMSFFLYKDGEVQNT
FGYLSNLFSESFPIFSIPYHKAFSQNFVSGILDILISDNELKERFIEAL
NSNKSDYKMIADDQQRKLACVWNPFLDGWELNAQHVDMIMGSHVLKDMPL
RKQAEILFCLGGVFCYSSSDMFGTEYDSPEILRRYANGLIEQAYKTDPQ
VFGSVYYYNDILDRLOGRNNVFTCTAVLTDMLTEHAKESFPEIFSLYYPV
AWR

Native sequence Residues 60-782 in bold

Protease cleavage Precission site underlined

Cloning sites BamH1 Not1

DNA sequence of insert

GGATCCAACGGCGAAACCCTGAGCATTAGCGAACCGATTACCACCCTGCCG
GATCTGCTGCCGGGCAGCCTGAAAGAAGCTGGTGTGAACGGCTGCACCGAA
CTGAAAAGCATTAACTGCCTGCCGCCGAACCTGAGCAGCCTGAGCATGGTG
GGCTGCAGCAGCCTGGAAGTGATTAAGTGCAGCATTCCGGAAAACGTGATT
AACCTGAGCCTGTGCCATTGCAGCAGCCTGAAACATATTGAAGGCAGCTTT
CCGGAAGCGCTGCGCAACAGCGTGTATCTGAACGGCTGCAACAGCCTGAAC
GAAAGCCAGTGCCAGTTTCTGGCGTATGATGTGAGCCAGGGCCGCGCGTGC
CTGAGCAAAGCGGAACTGACCGCGGATCTGATTTGGCTGAGCGCGAACCGC
ACCGGCGAAGAAAGCGCGGAAGAAGCTGAACTATAGCGGCTGCGATCTGAGC
GGCCTGAGCCTGGTGGGCCTGAACCTGAGCAGCGTGAACCTTAGCGGCGCG
GTGCTGGATGATAACCGATCTGCGCATGAGCGATCTGAGCCAGGCGGTGCTG
GAAAACCTGCAGCTTTAAAAACAGCATTCTGAACGAATGCAACTTTTGCTAT
GCGAACCTGAGCAACTGCATTATTCGCGCGCTGTTTAAAAACAGCAACTTT
AGCAACAGCAACCTGAAAAACGCGAGCTTTAAAGGCAGCAGCTATATTCAG
TATCCGCCGATTCTGAACGAAGCGGATCTGACCGGCGCGATTATTATTCCG
GGCATGGTGCTGAGCGGCGCGATTCTGGGCGATGTGAAAGAAGCTTTTAGC
GAAAAAAGCAACACCATTAACCTGGGCGGCTGCTATATTGATCTGAGCGAT
ATTCAGGAAAACATTCTGAGCGTGTGGATAACTATAACAAAAGCAACAAA
AGCATTCTGCTGACCATGAACACCAGCGATGATAAATATAACCATGATAAA
GTGCGCGCGGCGGAAGAAGCTGATTAAAAAAATTAGCCTGGATGAACTGGCG
GCGTTTCGCCCGTATGTGAAAATGAGCCTGGCGGATAGCTTTAGCATTTCAT
CCGTATCTGAACAACGCGAACATTCAGCAGTGGCTGGAACCGATTTGCGAT
GATTTTTTTGATAACCATTTAGAGCTGGTTTAAACAACAGCATTATGATGTAT
ATGAAAACGGCAGCCTGCTGCAGGCGGGCATGTATTTTGAACGCCATCCG
GGCGCGATGGTGAGCTATAACAGCAGCTTTATTCAGATTGTGATGAACGGC
AGCCGCCGCGATGGCATGCAGGAACGCTTTCGCGAACTGTATGAAGTGTAT
CTGAAAACGAAAAGTGTATCCGGTGACCCAGCAGAGCGATTTTGGCCTG
TGCGATGGCAGCGGCAAACCGGATTGGGATGATGATAGCGATCTGGCGTAT
AACTGGGTGCTGCTGAGCAGCCAGGATGATGGCATGGCGATGATGTGCAGC
CTGAGCCATATGGTGGATATGCTGAGCCGAACACCAGCACCAACTGGATG
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CTGAGCAACCTGTTTAGCGAAAAGCTTTCCGATTTTTAGCATTCCGTATCAT
AAAGCGTTTAGCCAGAAGCTTTGTGAGCGGCATTCTGGATATTCTGATTAGC
GATAACGAAGTGAAGAAGCTTTATTGAAGCGCTGAACAGCAACAAAAGC
GATTATAAATGATTGCGGATGATCAGCAGCGCAAACCTGGCGTGCCTGTGG
AACCCGTTTTCTGGATGGCTGGGAAGTGAACGCGCAGCATGTGGATATGATT
ATGGGCAGCCATGTGCTGAAAAGATATGCCGCTGCGCAAACAGGCGGAAATT
CTGTTTTGCTGGGCGGCGTGTGTTTGCAAAATATAGCAGCAGCGATATGTTT
GGCACCGAATATGATAGCCCGGAAATTCTGCGCCGCTATGCGAACGGCCTG
ATTGAACAGGCGTATAAAACCGATCCGCAGGTGTTTGGCAGCGTGTATTAT
TATAACGATATTCTGGATCGCCTGCAGGGCCGCAACAACGTGTTTACCTGC
ACCGCGGTGCTGACCGATATGCTGACCGAACATGCGAAAAGAAAGCTTTCCG
GAAATTTTTAGCCTGTATTATCCGGTGGCGTGGCGCTAAGCGGCCGC