Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of hnRNP A1 [2 - 189]

Protein description:- hnRNP A1 [2 - 189]

Clone number:- DU 4003

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST and HA

Purification method:- GSH Sepharose

Expression level:- 10 mg/L

Calculated molecular mass:- 49, 552 daltons

Purity:- 95 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 50 % glycerol, 150 mM NaCl, 0.1 mM EGTA,
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 0.2 mM PMSF, 1 mM Benzamidine.

Storage temperature:- –20 °C

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CLONE DATA SHEET

hnRNP A1 [2 – 189]

Protein	hnRNP A1 [2 - 189]
Clone number	DU 4003
Species	Human
Accession no	NM_031157
Tags	N-terminal GST and HA
Bacterially expressed prtoein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKW RNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNML GGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFL SKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLY MDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQG WQATFGGGDHPPKSDLEVLFQGPLGSATMYPYDVPDYA**SKS** **ESPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCVV** **MRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEP** **KRAVSREDSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQ** **YGKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIVIQKYH** **TVNGHNCEVRKALSKQEMASA**
Native sequence	Amino acids S2 – A189 of human hnRNP A1. [Full length protein ends at residue F372] Residue G244 of the fusion protein is equivalent to S2 of the native protein. The GST tag is located at residues 1 – 220 and the HA tag is located at residues 235 – 243.
Protease cleavage	PreScission (LEVLFQGPL) residues 221 - 229
Cloning sites	*Bam*H1 of pGEX-6P-1

Complete nucleotide sequence

ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGT
GCAACCCACTCGACTTCTTTTGGAATATCTTGAAGAAAAAT
ATGAAGAGCATTTGTATGAGCGCGATGAAGGTGATAAATGG
CGAAACAAAAAGTTTGAATTGGGTTTGGAGTTTCCCAATCT
TCCTTATTATATTGATGGTGATGTTAAATTAACACAGTCTA
TGGCCATCATACGTTATATAGCTGACAAGCACAACATGTTG
GGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGA
AGGAGCGGTTTTGGATATTAGATACGGTGTTTCGAGAATTG
CATATAGTAAAGACTTTGAAACTCTCAAAGTTGATTTTCTT
AGCAAGCTACCTGAAATGCTGAAAATGTTCGAAGATCGTTT
ATGTCATAAAACATATTTAAATGGTGATCATGTAACCCATC
CTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATAC
ATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTAGTTTG
TTTTAAAAAACGTATTGAAGCTATCCCACAAATTGATAAGT
ACTTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGC
TGGCAAGCCACGTTTGGTGGTGGCGACCATCCTCCAAAATC
GGATCTGGAAGTTCTGTTCCAGGGGCCCCTGGGATCCGCCA
CCATGTACCCATACGATGTGCCAGATTACGCCTCTAAGTCA
GAGTCTCCTAAAGAGCCCGAACAGCTGAGGAAGCTCTTCAT
TGGAGGGTTGAGCTTTGAAACAACTGATGAGAGCCTGAGGA
GCCATTTTGAGCAATGGGGAACGCTCACGGACTGTGTGGTA
ATGAGAGATCCAAACACCAAGCGCTCCAGGGGCTTTGGGTT
TGTCACATATGCCACTGTGGAGGAGGTGGATGCAGCTATGA
ATGCAAGGCCACACAAGGTGGATGGAAGAGTTGTGGAACCA
AAGAGAGCTGTCTCCAGAGAAGATTCTCAAAGACCAGGTGC
CCACTTAACTGTGAAAAAGATATTTGTTGGTGGCATTAAAG
AAGACACTGAAGAACATCACCTAAGAGATTATTTTGAACAG
TATGGAAAAATTGAAGTGATTGAAATCATGACTGACCGAGG
CAGTGGCAAGAAAAGGGGCTTTGCCTTTGTAACCTTTGACG
ACCATGACTCCGTGGATAAGATTGTCATTCAGAAATACCAT
ACTGTGAATGGCCACAACTGTGAAGTTAGAAAAGCCCTGTC
AAAGCAAGAGATGGCTAGTGCTtaa