Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of hnRNP A3 [3 - 188]

Protein description:- hnRNP A3 [3 - 188]

Clone number:- DU 251

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Expression level:- 15 mg/L

Calculated molecular mass:- 48, 082 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 A3 [3 – 188]

Protein	hnRNP A3 [3 - 188]
Clone number	DU 251
Species	Mouse
Accession no	AF463524
Tags	N-terminal GST
Bacterially expressed prtoein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKW RNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNML GGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFL SKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLY MDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQG WQATFGGGDHPPKSDLEVLFQGPLGS**GHDPKEPEQLRKLFI** **GGLSFETTDDSLREHFEKWGTLTDCVVMRDPQTKRSRGFGF** **VTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA** **HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDRQ** **SGKKRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS** **KQEMQSA**
Native sequence	Amino acids G3 – A188 of mouse hnRNP A3. [Full length protein ends at residue F357] Residue G232 of the fusion protein is equivalent to G3 of the native protein. The GST tag is located at residues 1 - 220
Protease cleavage	PreScission (LEVLFQGPL) residues 221 - 229
Cloning sites	*Bam*H1 and *Eco*R1 of pGEX-6P-1

Nucleotide sequence of insert

GGATCCGGCCATGATCCAAAGGAACCAGAGCAGCTGAGGAA
GCTATTTATTGGTGGTCTGAGCTTTGAAACCACAGATGATA
GCTTAAGAGAACATTTTGAGAAATGGGGCACACTTACAGAC
TGTGTGGTAATGAGAGATCCCCAAACAAAACGTTCCAGAGG
CTTTGGTTTTGTGACCTACTCTTGTGTTGAAGAGGTGGATG
CTGCAATGTGTGCTCGGCCACACAAGGTTGATGGGCGTGTG
GTGGAACCGAAGAGAGCTGTTTCTAGAGAGGATTCTGTAAA
GCCTGGTGCCCATTTAACGGTGAAGAAAATTTTTGTTGGTG
GTATTAAAGAGGATACGGAAGAATATAACCTGAGAGACTAC
TTTGAAAAGTATGGCAAGATTGAAACCATAGAGGTTATGGA
AGACAGGCAGAGTGGGAAAAAGAGAGGATTTGCTTTTGTAA
CTTTTGATGATCATGACACAGTTGATAAAATTGTTGTTCAG
AAATACCACACTATTAATGGGCATAATTGTGAAGTGAAAAA
GGCCCTTTCTAAACAAGAGATGCAGTCTGCTGA