

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of hnRNP A0 [2 – 181]

Protein description:- hnRNP A0 [2 - 181]

Clone number:- DU 984

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Expression level:- 15 mg/L

Calculated molecular mass:- 46, 430 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 A0 [2 - 181]

<u>Protein</u>	hnRNP A0 [2 - 181]
<u>Clone number</u>	DU 984
<u>Species</u>	Human
<u>Accession no</u>	NM_006805
<u>Tags</u>	N-terminal GST
<u>Bacterially expressed protein</u>	MSPILGYWKIKGLVQPTRLLEYLEEKYEHLRYERDEGDKW RNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNML GGCPKERAIEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFL SKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLY MDPMCLDAFPKLVCFKKRIEAI PQIDKYLKSSKYIAWPLQG WQATFGGGDHPPKSDLEVLFGGPLGSENSQLCKLFIGGLNV QTSEGLRGHFEAFGTLTDCVVV VNPQTKRSRCFGFVTYSN VEEADAAMAASPHAVDGN TVELKRAVSREDSARPGAHAKVK KLFVGGLKGDVAEGDLIEHFSQFGTVEKAEI IADKQSGKKR GFGFVYFQNHDAADKAAVVKFHP IQGHRVEVKKAVPKEDIY S
<u>Native sequence</u>	Amino acids E2 – S181 of human hnRNP A3. [Full length protein ends at residue F305] Residue E232 of the fusion protein is equivalent to E2 of the native protein. The GST tag is located at residues 1 - 220
<u>Protease cleavage</u>	PreScission (<u>LEVLFQGPL</u>) residues 221 - 229
<u>Cloning sites</u>	<i>Bam</i> H1 and <i>Sal</i> I of pGEX-6P-1

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Nucleotide
sequence of insert

GAGAATTCTCAGTTGTGTAAGCTGTTTCATCGGCGGC
CTCAATGTGCAGACGAGTGAGTCGGGCCTGCGCGG
CCACTTTGAGGCCTTTGGGACTCTGACGGACTGCGT
GGTGGTGGTGAATCCCCAGACCAAGCGCTCCCGTTG
CTTTGGCTTCGTGACCTACTCCAATGTGGAGGAGGC
GGACGCCGCCATGGCCGCCTCGCCCCATGCCGTGG
ACGGCAACACTGTGGAGCTGAAGCGGGCGGTGTCC
CGGGAGGATTCGGCGCGGCCCGGTGCCACGCCAA
GGTTAAGAAGCTCTTTGTCGGAGGCCTTAAAGGAG
ACGTGGCTGAGGGCGACCTGATCGAGCACTTCTCGC
AGTTTGGCACCGTGGAAAAGGCCGAGATTATTGCC
GACAAGCAGTCCGGCAAGAAGCGTGGATTCCGGCTT
CGTGTATTTCCAGAATCACGACGCGGCAGACAAGG
CCGCGGTGGTCAAGTTCCATCCGATTCAGGGCCATC
GCGTGGAGGTGAAGAAAGCAGTCCCCAAGGAGGAT
ATCTACTCCG