Construct information sheet

Gene name	**HNRNPA1**
Uniprot ID	P09651
Region	M1 – F320

Description	heterogeneous nuclear ribonucleoprotein A1
Synonyms	ALS19, ALS20, HNRPA1, HNRPA1L3, IBMPFD3, UP 1, hnRNP A1, hnRNP-A1
Construct ID	HNRNPA1A-c000
Protein sequence	*MHHHHHHSSGVDLGTENLYFQ**SMSKSESPKEPEQLRKLFIGGLS FETTDESLRSHFEQWGTLTDCVVMRDPNTKRSRGFGFVTYATVEE VDAAMNARPHKVDGRVVEPKRAVSREDSQRPGAHLTVKKIFVGGI KEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFDDHD SVDKIVIQKYHTVNGHNCEVRKALSKQEMASASSSQRGRSGSGNF GGGRGGGFGGNDNFGRGGNFSGRGGFGGSRGGGGYGGSGDGYNGF GNDGSNFGGGGSYNDFGNYNNQSSNFGPMKGGNFGGRSSGPYGGG GQYFAKPRNQGGYGGSSSSSSYGSGRRFS*SKGGYGLNDIFEAQKI* *EWHE*
DNA sequence (coding sequence)	ATGCACCATCATCATCATCATTCTTCTGGTGTAGATCTGGGTACCGAGAA CCTGTACTTCCAATCCATGTCTAAGTCAGAGTCTCCTAAAGAGCCCGAAC AGCTGAGGAAGCTCTTCATTGGAGGGTTGAGCTTTGAAACAACTGATGAG AGCCTGAGGAGCCATTTTGAGCAATGGGGAACGCTCACGGACTGTGTGGT AATGAGAGATCCAAACACCAAGCGCTCCAGGGGCTTTGGGTTTGTCACAT ATGCCACTGTGGAGGAGGTGGATGCAGCTATGAATGCAAGGCCACACAAG GTGGATGGAAGAGTTGTGGAACCAAAGAGAGCTGTCTCCAGAGAAGATTC TCAAAGACCAGGTGCCCACTTAACTGTGAAAAAGATATTTGTTGGTGGCA TTAAAGAAGACACTGAAGAACATCACCTAAGAGATTATTTTGAACAGTAT GGAAAAATTGAAGTGATTGAAATCATGACTGACCGAGGCAGTGGCAAGAA AAGGGGCTTTGCCTTTGTAACCTTTGACGACCATGACTCCGTGGATAAGA TTGTCATTCAGAAATACCATACTGTGAATGGCCACAACTGTGAAGTTAGA AAAGCCCTGTCAAAGCAAGAGATGGCTAGTGCTTCATCCAGCCAAAGAGG TCGAAGTGGTTCTGGAAACTTTGGTGGTGGTCGTGGAGGTGGTTTCGGTG GGAATGACAACTTCGGTCGTGGAGGAAACTTCAGTGGTCGTGGTGGCTTT GGTGGCAGCCGTGGTGGTGGTGGATATGGTGGCAGTGGGGATGGCTATAA TGGATTTGGTAATGATGGAAGCAATTTTGGAGGTGGTGGAAGCTACAATG ATTTTGGGAATTACAACAATCAGTCTTCAAATTTTGGACCCATGAAGGGA GGAAATTTTGGAGGCAGAAGCTCTGGCCCCTATGGCGGTGGAGGCCAATA CTTTGCAAAACCACGAAACCAAGGTGGCTATGGCGGTTCCAGCAGCAGCA GTAGCTATGGCAGTGGCAGAAGATTTAGCAGTAAAGGTGGATACGGCCTG AATGATATCTTTGAAGCGCAGAAGATTGAATGGCATGAATGA
Construct accession No.	

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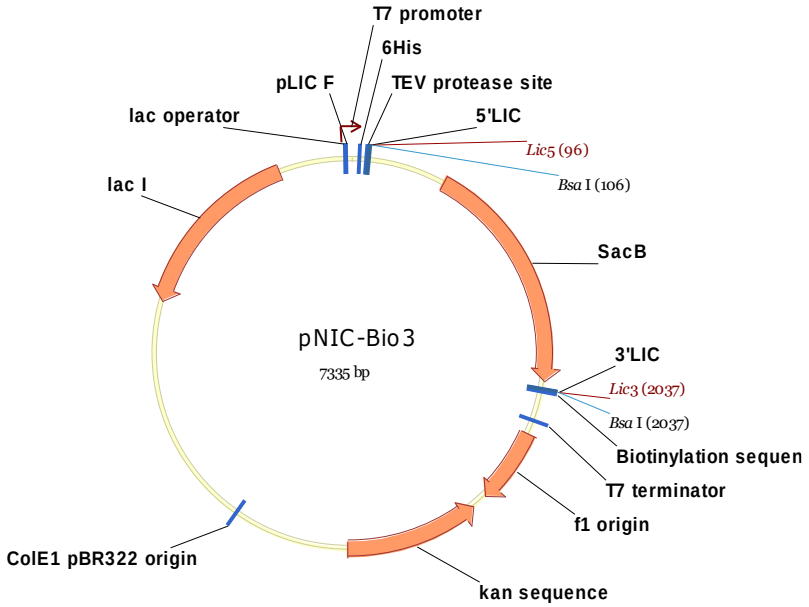
Vector information:

pNIC-Bio3	Expression vector with N-terminal His6-TEV and C-terminal avi-tag
Antibiotic resistance	Kanamycin, 50 μg/ml
Promoter	T7 - lacO
N-terminal fusion – seq.	MHHHHHHSSGVDLGTENLYFQ*SM (* - TEV cleavage site)
N-terminal fusion – MW	2684.1 Da including Met (2465.8 Da removed by TEV cleavage)
C-terminal fusion – seq.	GSKGGYGLNDIFEAQ**K***IEWHE (* biotinylation site)
C-terminal fusion - MW	2396.57 Da, +226 Da for biotinylation
Protease cleavage	TEV protease
Preferred expression host	DE3 hosts: BL21, Rosetta, etc. MUST express T7 RNA polymerase. For effective biotinylation, the host should overexpress BirA (e.g. from plasmid pCDF-BIRA, GenBank: JF914075)
Genebank: JN792439	Reference: PMID: 22027370



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