Construct information sheet

Gene name	**UBQLN2**
Uniprot ID	Q9UHD9
Region	M1 - S624

Description	Ubiquilin 2
Synonyms	ALS15, CHAP1, DSK2, HRIHFB2157, N4BP4, PLIC2.
Construct ID	UBQLN2A-c000
Protein sequence	*MHHHHHHSSGVDLGTENLYFQ*SM*AENGESSGPPRPSRGPAAAQG SAAAPAEPKIIKVTVKTPKEKEEFAVPENSSVQQFKEAISKRFKS QTDQLVLIFAGKILKDQDTLIQHGIHDGLTVHLVIKSQNRPQGQS TQPSNAAGTNTTSASTPRSNSTPISTNSNPFGLGSLGGLAGLSSL GLSSTNFSELQSQMQQQLMASPEMMIQIMENPFVQSMLSNPDLMR QLIMANPQMQQLIQRNPEISHLLNNPDIMRQTLEIARNPAMMQEM MRNQDLALSNLESIPGGYNALRRMYTDIQEPMLNAAQEQFGGNPF ASVGSSSSSGEGTQPSRTENRDPLPNPWAPPPATQSSATTSTTTS TGSGSGNSSSNATGNTVAAANYVASIFSTPGMQSLLQQITENPQL IQNMLSAPYMRSMMQSLSQNPDLAAQMMLNSPLFTANPQLQEQMR PQLPAFLQQMQNPDTLSAMSNPRAMQALMQIQQGLQTLATEAPGL IPSFTPGVGVGVLGTAIGPVGPVTPIGPIGPIVPFTPIGPIGPIG PTGPAAPPGSTGSGGPTGPTVSSAAPSETTSPTSESGPNQQFIQQ MVQALAGANAPQLPNPEVRFQQQLEQLNAMGFLNREANLQALIAT GGDINAAIERLLGSQPSS*SKGGYGLNDIFEAQKIEWHE*
DNA sequence (coding sequence)	ATGCACCATCATCATCATCATTCTTCTGGTGTAGATCTGGGTACC GAGAACCTGTACTTCCAATCCATGGCTGAGAATGGCGAGAGCAGC GGCCCCCCGCGCCCCTCCCGCGGCCCTGCTGCGGCCCAAGGCTCG GCTGCTGCCCCGGCTGAGCCTAAAATCATCAAAGTCACGGTGAAG ACTCCCAAAGAGAAAGAGGAGTTCGCGGTGCCCGAGAACAGCTCG GTTCAGCAGTTTAAGGAAGCGATTTCGAAACGCTTCAAATCCCAA ACCGATCAGCTAGTGCTGATTTTTGCCGGAAAAATCTTAAAAGAT CAAGATACCTTGATCCAGCATGGCATCCATGATGGGCTGACTGTT CACCTTGTCATCAAAAGCCAGAACCGACCTCAGGGCCAGTCCACG CAGCCTAGCAATGCCGCGGGAACTAACACTACCTCGGCGTCGACT CCCAGGAGTAACTCCACACCTATTTCCACAAATAGCAACCCGTTT GGGTTGGGGAGCCTGGGAGGACTTGCAGGCCTTAGCAGCCTGGGC TTGAGCTCGACCAACTTCTCTGAGCTCCAGAGCCAGATGCAGCAG CAGCTTATGGCCAGCCCTGAGATGATGATCCAAATAATGGAAAAT CCCTTTGTTCAGAGCATGCTTTCGAATCCCGATCTGATGAGGCAG CTCATTATGGCTAATCCACAGATGCAGCAATTGATTCAGAGAAAC CCAGAAATCAGTCACCTGCTCAACAACCCAGACATAATGAGGCAG ACACTCGAAATTGCCAGGAATCCAGCCATGATGCAAGAGATGATG AGAAATCAAGACCTGGCTCTTAGCAATCTAGAAAGCATCCCAGGT GGCTATAATGCTTTACGGCGCATGTACACTGACATTCAAGAGCCG ATGCTGAATGCCGCACAAGAGCAGTTTGGGGGTAATCCATTTGCC TCCGTGGGGAGTAGTTCCTCCTCTGGGGAAGGTACGCAGCCTTCC CGCACAGAAAATCGCGATCCACTACCCAATCCATGGGCACCACCG CCAGCTACCCAGAGTTCTGCAACTACCAGCACGACCACAAGCACT GGTAGTGGGTCTGGCAATAGTTCCAGCAATGCTACTGGGAACACC GTTGCTGCCGCTAATTATGTCGCCAGCATCTTTAGTACCCCAGGC ATGCAGAGCCTGCTGCAACAGATAACTGAAAACCCCCAGCTGATT CAGAATATGCTGTCGGCGCCCTACATGAGAAGCATGATGCAGTCG CTGAGCCAGAATCCAGATTTGGCTGCACAGATGATGCTGAATAGC CCGCTGTTTACTGCAAATCCTCAGCTGCAGGAGCAGATGCGGCCA CAGCTCCCAGCCTTCCTGCAGCAGATGCAGAATCCAGACACACTA TCAGCCATGTCAAACCCAAGAGCAATGCAGGCTTTAATGCAGATC CAGCAGGGGCTACAGACATTAGCCACTGAAGCACCTGGCCTGATT

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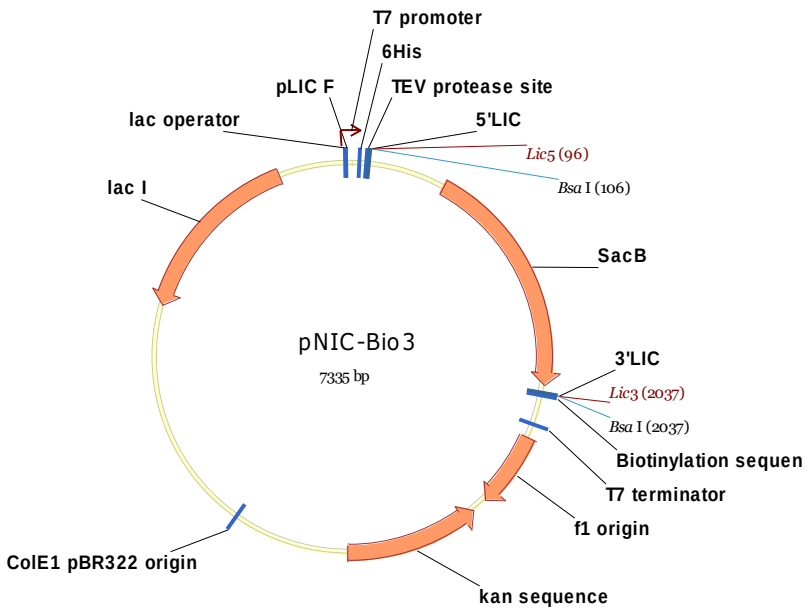
	CCGAGCTTCACTCCAGGTGTGGGGGTGGGGGTGCTGGGAACCGCT ATAGGCCCTGTAGGCCCAGTCACCCCCATAGGCCCCATAGGCCCT ATAGTCCCTTTTACCCCCATAGGCCCCATTGGGCCCATAGGACCC ACTGGCCCTGCAGCCCCCCCTGGCTCCACCGGCTCTGGTGGCCCC ACGGGGCCTACTGTGTCCAGCGCTGCACCTAGTGAAACCACGAGT CCTACATCAGAATCTGGACCCAACCAGCAGTTCATTCAGCAAATG GTGCAGGCCCTGGCTGGAGCAAATGCTCCACAGCTGCCGAATCCA GAAGTCAGATTTCAGCAACAACTGGAACAGCTCAACGCAATGGGG TTCTTAAACCGTGAAGCAAACTTGCAGGCCCTAATAGCAACAGGA GGCGACATCAATGCAGCCATTGAAAGGCTGCTGGGCTCCCAGCCA TCGAGCAGTAAAGGTGGATACGGCCTGAATGATATCTTTGAAGCG CAGAAGATTGAATGGCATGAATGA
Construct accession No.	

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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