Construct information sheet

Gene name	**KIF5A**
Uniprot ID	Q12840
Region	M1 – Q341

Description	kinesin family member 5A
Synonyms	ALS25, D12S1889, MY050, NEIMY, NKHC, SPG10
Construct ID	KIF5AA-c001
Protein sequence	*MHHHHHHSSGVDLGTENLYFQ**SMAETNNECSIKVLCRFRPLNQA EILRGDKFIPIFQGDDSVVIGGKPYVFDRVFPPNTTQEQVYHACA MQIVKDVLAGYNGTIFAYGQTSSGKTHTMEGKLHDPQLMGIIPRI ARDIFNHIYSMDENLEFHIKVSYFEIYLDKIRDLLDVTKTNLSVH EDKNRVPFVKGCTERFVSSPEEILDVIDEGKSNRHVAVTNMNEHS SRSHSIFLINIKQENMETEQKLSGKLYLVDLAGSEKVSKTGAEGA VLDEAKNINKSLSALGNVISALAEGTKSYVPYRDSKMTRILQDSL GGNCRTTMFICCSPSSYNDAETKSTLMFGQRAKTIKNTASVNLEL TAEQS*SKGGYGLNDIFEAQKIEWHE*
DNA sequence (coding sequence)	ATGCACCATCATCATCATCATTCTTCTGGTGTAGATCTGGGTACCGAGAA CCTGTACTTCCAATCCATGGCGGAGACCAACAACGAATGTAGCATCAAGG TGCTCTGCCGATTCCGGCCCCTGAACCAGGCTGAGATTCTGCGGGGAGAC AAGTTCATCCCCATTTTCCAAGGGGACGACAGCGTCGTTATTGGGGGGAA GCCATATGTTTTTGACCGTGTATTCCCCCCAAACACGACTCAAGAGCAAG TTTATCATGCATGTGCCATGCAGATTGTCAAAGATGTCCTTGCTGGCTAC AATGGCACCATTTTTGCTTATGGACAGACATCCTCAGGGAAAACACATAC CATGGAGGGAAAGCTGCACGACCCTCAGCTGATGGGAATCATTCCTCGAA TTGCCCGAGACATCTTCAACCACATCTACTCCATGGATGAGAACCTTGAG TTCCACATCAAGGTTTCTTACTTTGAAATTTACCTGGACAAAATTCGTGA CCTTCTGGATGTGACCAAGACAAATCTGTCCGTGCACGAGGACAAGAACC GGGTGCCATTTGTCAAGGGTTGTACTGAACGCTTTGTGTCCAGCCCGGAG GAGATTCTGGATGTGATTGATGAAGGGAAATCAAATCGTCATGTGGCTGT CACCAACATGAATGAACACAGCTCTCGGAGCCACAGCATCTTCCTCATCA ACATCAAGCAGGAGAACATGGAAACGGAGCAGAAGCTCAGTGGGAAGCTG TATCTGGTGGACCTGGCAGGGAGTGAGAAGGTCAGCAAGACTGGAGCAGA GGGAGCCGTGCTGGACGAGGCAAAGAATATCAACAAGTCACTGTCAGCTC TGGGCAATGTGATCTCCGCACTGGCTGAGGGCACTAAAAGCTATGTTCCA TATCGTGACAGCAAAATGACAAGGATTCTCCAGGACTCTCTCGGGGGAAA CTGCCGGACGACTATGTTCATCTGTTGCTCACCATCCAGTTATAATGATG CAGAGACCAAGTCCACCCTGATGTTTGGGCAGCGGGCAAAGACCATTAAG AACACTGCCTCAGTAAATTTGGAGTTGACTGCTGAGCAGAGCAGTAAAGG TGGATACGGCCTGAATGATATCTTTGAAGCGCAGAAGATTGAATGGCATG AATGA
Construct accession No.	

Opher Gileadi, Structural Genomics Consortium
opher.gileadi@sgc.ox.ac.uk

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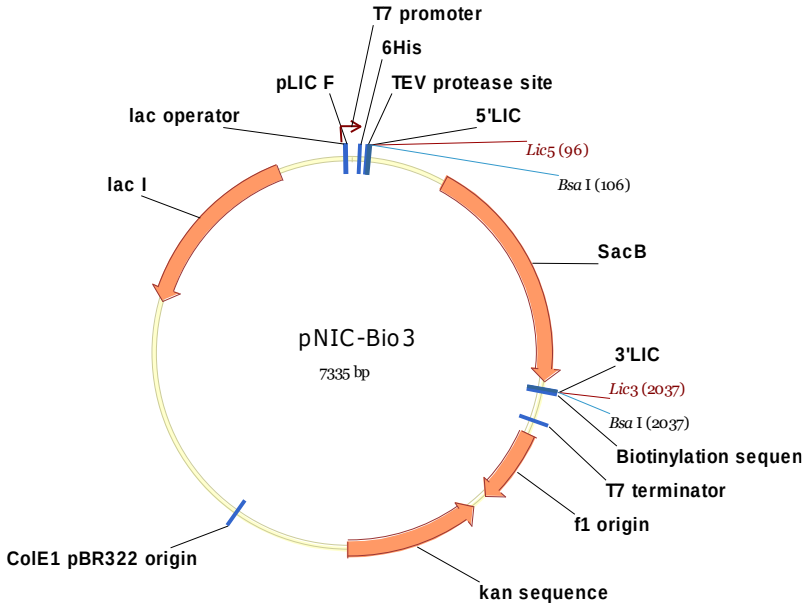
Vector information:

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



Opher Gileadi, Structural Genomics Consortium
opher.gileadi@sgc.ox.ac.uk