

Thecocarcelia acutangulata

Taxonomic lineage: Brachycera > Muscomorpha > Oestroidea > Tachinidae > Thecocarcelia

Assembly: GCA_914767995.1_idTheAcut1.1_genomic

The_acu1 | OU612096.1:16704422-16704941 (+) | 520 nt | lncRNA: noe consensus e-value: 1.8e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.94

GGCGGTCTGATGTTCCACTTCGCCATTGGGTTGTACACATCCCCAGACAAAAATGTTGTTCAATAAACTTAAACCTTCGTCAAAAATGATTTTAAACCAATATATAATTGCAAAACAACTACTTTGAATATATAATTTAAAGAACAAACAAGAAAAACATAATTTAAATGTCCCGGCTTTGTATAGGAATATAAAAAACATCCAAAAATGATAAAAAATCATATCTCCTCTCTCATTTCAACAGATGATGTTGTAGTATAGACCAAGAAACGCGTAACCAAAATTTGCAACTGCGCTTTCTGGAAATACATGATGTCTTCAATTTGAGAGAGAGAAATTTTCAGCAGATTTTCAAAAAAATGGTCAAAATCAAAAAACATAAAAACTTAAAACTTAAACCAAGAAAAATGAAATAAACCATAGACATTTTGTGGCAAAAAATAAAAAACGAAAAAATAGCAATAAAAAATGGCGGTCAAAAATATCAACTGAAGTCGTTGGAAATTCGCGTGATCGCCCATTTTTT

The_acu1	----	ttttgccgtt	gtattttcca	taaaattgc	atcttata	taattctc	agattctctttttc	ctgtta	acacacac	ataaat	acaactt	caatttac	acacag	taag
Arthropod_7SK	----	ttatctcc	aaagat	gaattt	gaattt	gaattt	gaattt	gaattt	gaattt	gaattt	gaattt	gaattt	gaattt	gaattt
U6	----	ggtaata	aaaatg	aaatatt	gcacat	gtttgc	gttata	taattc	cgattt	cttttt	ttgtaca	aaattgc	tatatag	ttgtta
U6	----	ggatg	taaacg	aaatatt	ctattt	caatag	ctaaat	taattc	cgattt	cttttt	ttgtaca	aaattgc	tatatag	ttgtta
U6	----	agtaata	aaaatg	aaatatt	gcacat	gtttgc	gttata	taattc	cgattt	cttttt	ttgtaca	aaattgc	tatatag	ttgtta
U6atac	----	aaata	aaaatg	aaatatt	gcacat	gtttgc	gttata	taattc	cgattt	cttttt	ttgtaca	aaattgc	tatatag	ttgtta
tRNAsec	----	ttatattt	ttgaaat	ttcttga	ttac	tttttt	ttata	ttctc	atattg	ttttaa	ctttt	ttgaa	ttat	ttgaa
U1	----	aaagaa	actgtt	ggctg	gaacac	ataata	aaacag	agttta	attt	ctc	atgag	tttg	atattt	tata
U1	----	ctgc	aaaatt	taagca	aatatt	taattg	aaaa	gaatg	ataatt	ctc	atgag	tttg	atattt	tata
U1	----	atgc	aaaatt	taagca	aatatt	taattg	aaaa	gaatg	ataatt	ctc	atgag	tttg	atattt	tata
U1	----	atgc	aaaatt	taagca	aatatt	taattg	aaaa	gaatg	ataatt	ctc	atgag	tttg	atattt	tata
U1	----	atgc	aaaatt	taagca	aatatt	taattg	aaaa	gaatg	ataatt	ctc	atgag	tttg	atattt	tata
U1	----	acac	aaaac	agattt	ctactt	caacat	atgaa	tttca	ataatt	ctc	atgag	tttg	atattt	tata
U1	----	taatt	taaat	attttt	ttttt	ttttt	ttttt	ttttt	ttttt	ttttt	ttttt	ttttt	ttttt	ttttt
U1	----	attt	taaat	attttt	ttttt	ttttt	ttttt	ttttt	ttttt	ttttt	ttttt	ttttt	ttttt	ttttt
U2	----	gac	attaa	gcaag	atata	aaatg	gtttt	catata	attt	ctc	atgag	tttg	atattt	tata
U2	----	ccat	caattt	ccctt	catot	ttttt	aaat	aaat	aaat	aaat	aaat	aaat	aaat	aaat
U2	----	aaat	attt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt
U3	----	ttg	atag	atcc	ctg	atg	atg	atg	atg	atg	atg	atg	atg	atg
U3	----	tttt	attt	ttc	acac	attt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt
U3	----	ttt	atag	atcc	ctg	atg	atg	atg	atg	atg	atg	atg	atg	atg
U4	----	at	catot	at	at	at	at	at	at	at	at	at	at	at
U4	----	at	catot	at	at	at	at	at	at	at	at	at	at	at
U5	----	at	gaag	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt
U5	----	at	gaag	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt
U5	----	at	gaag	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt
U5	----	at	gaag	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt
U5	----	at	gaag	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt
U12	----	tt	caat	gttt	aaatt	agtt	caatt	gttt	aaatt	agtt	caatt	gttt	aaatt	agtt

Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod_7SK, 7SL, RNase_MRP, RNaseP_nuc, U6, U6atac, tRNAsec, snoRNAme18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.