

# Platycheirus albimanus

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Platycheirus

Assembly: GCA\_916050605.2\_idPlaAlba1.2\_genomic

**Pla\_alb1 | OU696697.1:18791016-18791333 (-) | 318 nt | lncRNA: noe consensus e-value: 3.8e-07**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.96

GGGCGGTTGATGCTTCACAGTTGATCGGGTTGTCATTCGGTTCACAAATGTAGTATCAAAATCGTATGCTTTGACATCCATACATGAAAAATCGTAAAACAAAAAACACTGCAAAATTTGTTTGAGAAATAAAATAAGTTTCA  
CCAAAAAATCAACGCAACAAAAACGAATACAAAAACAAAAAACACAAAAACTAAATCCCTCTATCGTATAGATATCTAATATAGAAATAAGCCAAATCAATAAAAATGAGAAAAAATCTATCAAAATGATATCTGCTGAGGT  
AGATGCGATCGCCTTTTTT

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Pla_alb1      ----- tactcagatcgttcaaaaattttcagatcgttATAATTGCGAGATTTTtattgcaacactacatcgttcataaggaaatcatcaagacacataccatc-----
Arthropod_7SK ----- atatttatttatttcatcaaaaatttgacatttctTATAGTTTCACAGTTATTTtttcagcaatagccgtgaataataaaacttccaatttaatttcgac-----
Arthropod_7SK ----- tatttataatttttcaaacactctacatttccTATAGTTTCACAGTTTTTTTTtaacctgaadctgaacatatacaacttccaatttacttccaa-----
RNase_MRP      ----- ttatttttagatctttttcacctctTATAATTACACAGTTTTTTTTtgcgaatgctcgtctatatctgaatcgaatatcacgttagtgaagggttttc-----
U6             ----- ataaacatcatgtgggtataagtttttcactcgtctTACAATTGCGAGTTTTTtattcgaaatattctagataagataattttcaacctaccaacctc-----
U6             ----- tactttaaactcactatgaatttttttaaaaaaaatATAAATTGCGAGTATTTttttcataaagattccattaaatattcttttttattatttttc-----
U6             ----- cgaaaacagatattgtctagtttcatcttctTATAATTACACAGTTTTTTTTtattgctgacaaagatatatacaaaatattgactactacttc-----
U6             ----- gcaaaaacagatgtctctagtttcatcttctTATAATTACACAGTTTTTTTTtattgctgacaaagatatatacaaaatattgactactacttc-----
U6             ----- gcaaaaacagatgtctctagtttcatcttctTATAATTACACAGTTTTTTTTtattgctgacaaagatatatacaaaatattgactactacttc-----
U6             ----- aaaaagagaataatgcataaaaaataccaccgacaaTATAATTACACAGTTTTTTTTtgcgttgtgatgttgggttaagtactatttatgttttctttacgtc-----
U6atac         ----- caaacctttcaaaatgtcacatagttcattcgtttctTATAATTACACAGTATTTttttgctgcgcaaatcactacaattctgtttacatttaactt-----
snoRNAME18SA1806 ----- ttacaaaaaagtgtcagatattttttgcattcaatATAAATTGCGAGTATTTtttttaaggacagagagtaacagattttatgaatccgagagatcggc-----
U1             ----- ttacacactctcactccttaattttaaatcadattatTAAAAATGCGACATAGTTTTttccaataaaatcacaaaacttgaacaaaccttatcaata-----
U1             ----- ccaagaatagcagatgaattattttgttctgtTACAATTACACATTTTgttttgcgtaaaaagtaagtaataagaagatgagagctaaagaaagc-----
U1             ----- ccaagaatagcagatgaattattttgttctgtTACAATTACACATTTTgttttgcgtaaaaagtaagtaataagaagatgagagctaaagaaagc-----
U1             ----- tattcdacatgcacataatattttcatttatttTAAAAATGCGACATAGTAAatgaattgaatttacttctcTcaacaaatccaaagaaagc-----
U1             ----- acgatcatttcgacagatcatttttcgttgtattTAAAAATGCGACATAGTttttagtgaacatttatgagagctcaagcaagatcgaggtgaagc-----
U1             ----- tcatatcacttcttcttaaacactgtaatttgtttttTACAATTGCGATTTTtttactgataattgtatgagagacattgaataacggttaaaagc-----
U2             ----- aaactccttctccttattattttttcttattttTTCACATTACACATTCAATTcttccaacaaatccaatadadaaataatttattttaaagatt-----
U2             ----- ttaaaacaacgttatttattattttttcttaccataTATAATTACACATTTTgttttgcgtaaaaaataagacatttattagttgagtaacgaaagaaagtt-----
U2             ----- cgttattgttgcacacagattttttcagaanaTATAATTACACATTTACTttttgtaagafacacTcaagtaaggaatatttcacgttatgtt-----
U2             ----- tataaataaadaaataaatttttttcaaggtTATAATTACACATTTAGGTGtataaataatataacaaataaataattattattaccattattt-----
U2             ----- tcaagtataagacataaataattgttttcgacgtTACACATTGCGACATAGTTTTtagcaataaataatataagataatcgaatcgagtggaagtt-----
U2             ----- caacacgaattgacatgatttttctcactctctTATTAATGCGACATCGGTTTTgttggaaattgtagtgaaatgaaggtacgttttgatagaagtt-----
U2             ----- tctotdaaadaaandaatttttcttcttaaaaaTATAGTTGCGATGCGtotoadaaaaaatocacaataaataattattattaccattattt-----
U3             ----- aaacaacagcttaatttatttttttcttcttagcaTATAATTACACATTTACTttttgcgtaaaaaataagacatttattagttgagtaacgaaagaaagtt-----
U3             ----- gttgaatgagaaatgacatgtgtttcactactctataTAACTTCACAGTAAgttgcgcacaaactctagttgtgcaagttatttgggtggtgaatt-----
U3             ----- tgaatcctctctcatttcttcttcttcttctcTAACTTCACAGTAAgttgcgcacaaactctagttgtgcaagttatttgggtggtgaatt-----
U3             ----- agaaaaatagggttatgattttgtttcttctctcTACGATTACACAGTACTtttagtagcaaaatttgggttatagaagtgatttggagcggtaaaaatt-----
U3             ----- ttgtgacgtgtcatagattttgtttcttgcgcAAATAATTGCGACATCGGTTTTgcgtttgaaatgtaggtatagagtgaaatcggtgaagaatt-----
U3             ----- ataaaaactaototdaaataatttttcttctctctTATAATTGCGAGTACTttatoccatdaaatttcttattataaataatttcttcttcttcttctt-----
U4             ----- ttgatatttgggtttttttttttttctcgcgcTcaTATAATTACACATTTTAAgttgcaatttttttcaagttacgaataaatttcaacatcctc-----
U4             ----- tgaacgtatagagtaataatttttctcactcatattttTCAATTACACATTCAGTTtagtcataaaactctagtgaaaggtataaaattcagttatcctc-----
U4             ----- gaaatgaagaaataaataatttttcttattattttTATAATTACACATTTGAGTTcaattgaaattttcataaaadaacaaatctgaattgaaataatt-----
U4atac         tgcagggttggtgtcaccttattttttcttataaaaTACAATTGCGATTTGAGTTTTgcagatatatttataagatcacatgcccatgaacaactc-----
U5             ----- aaagaaaagtgtcactcgtatttttttactttcgttttgTAAAAATGCGATTTGGTTTTgtcaggcaatcgataagggtaccccatgattcgtgttataaa-----
U5             ----- catccccTadctgaattcdaatttttacttctcactcaTATAATTGCGATTTGAGTTTTtaattcaaaaattcacaaagcatttcttgaatttgaatt-----
U5             ----- cacaagcatgacacactcttattttgattcgttatTATAATTGCGATTTGAGTTTTtaattcaaaaattcacaaagcatttcttgaatttgaatt-----
U5             ----- ctgacttgcacaggaatgcaatttttttattctctTATAATTGCGATTTGAGTTTTtagcaaaaattggaagtgaggtccataaattggttatataaa-----
U5             ----- tatctotgactttttatccaaatatttcttctcactcaTAAAAATGCGATTTGAGTTctattcaccataaataaadaacaccTcaaatttgaatttataaa-----
U5             ----- agtgattgaaaaatgaacattttttctactttgtttttTATAGTTGCGATTTGAGTTTTtattcaccataaataaadaacaccTcaaatttgaatttataaa-----
U5             ----- ggtgattcacaagtttcaaatttgtacttccaaataaTACAATTGCGATTTGAGTTTTtattaccctgatgtattcttatagatgcaataaaagccacaaca-----
U11            acaataaatttaaaattccatcacacatttcttTACGATTGCGATTTGAGTTTTtccaaaattctcttataaataaccctgaatttgaatttgaatt-----
U12            cttctataatccatcacattttttctttttataaaTATAGTTGCGATTTGAGTTtggtcattttatcatatataaactgtgaaatcgcaatttttaattt-----
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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.