

Pocota personata

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

Assembly: GCA_963082735.1_idPocPers1.1_genomic

Poc_per1 | OY720430.1:30539990-30540256 (-) | 267 nt | lncRNA:noe consensus e-value: 5.3e-11

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.92

GGGCGGTTGATGCTTACAGTGTGCGGTGGTACATTCCGTTTCCCAATTGTAGCATCTAAACGTATGCTTTGACATCCATACTAAATAAACTGCAAAAAGTGTGTTTGAAAAAGTTTACCACAAAACGACGCAAAACAAAAA
CAAATCTTCTCTATCATAGATAAAAATATATAGAAATATAAGCAATTCATAAAAATTGAGAAAAAAAAGTTTATCAAAAACGGTTTCTGCTGAGGTAGACGCGATCGCCTTTTT

Poc_per1	-----adaccacttaccagtactttcacttttgaatccttTATAGTTCCAGAAATTTattctcatcatocacaacctataaagaaaattcaaacaccctactatc
U6	-----ttgataaaagagatggccgdatattttttttattttTATAATTCATAGTATTTTTtagcatttgcctagatactaataagaatttaacaagactgtaattt-
U6	-----agtcacatatagatgtcgcttatattttattcggtTATGATTCACAGTATTTtattggacaaaatcattgctcatatactgtttatttattgggttacattt-
U6	-----agtgootacaaaattacataaattttacattactTATAATTACAGTATTTTTtgcattttgcctttatcaaatcacattcataaagaatataactt-
U6atac	-----aatgtcaatttgaagaaaaataattttatattcGTATAATTCCAGAAATTTTTtgcctttggttgaaaatgatagttaataatagaacttactaagct
tRNAsec	---taactctattaatttattgttctttatttttaattgaaTATAATTACAGTATTTTTtgcgaattcagcagattgtatacagattctttgaaaacgactgt--
U1	---aatttcctaattttataatttttttttttttactttTACAATTACACATTGCTTTTTtgcgaaaatctactaaaccacacaatttccaatcaaaagc---
U1	---attacgtccgagatcgcccaacccctaaatttcgtttTATAATTACACCAACTTTtagtagtaatttgttaagagaccgactgtgtggcgataaagc---
U1	---caagaacaacaactattggagaatttcattcaattgtACGATTCACATGGTCTTTtgcgagaaataatacaagagataggtcgatagcgagaaaaagc---
U1	---gcatatattttactttttatttttttttttaattTATAATTTCATTCACTTcttgcagaaaatcacaaaacacatttcacaaaccgaaataaac---
U2	---tctaatttttctaagggtgtttatcaaatcattttTATAATTACATTCAATTcctgtagtgtttccaccaagtatcacccctaaaaacggaacagtt-
U2	---ctttaatttttaagggtgttttcaattctctttTATAATTACATTCAATTcctgtagtgtttccaccaagtatcacccctaaaaacggaacagtt-
U4	---tatgcaatgatgtgttgaatttttctgttaattttTACAATTACACATTCAATTcttgcctggcaaatcaactaaagagattgttatgagaaattcatc---
U4	---atttctttctatctaacaattttcattttctataattttTATAGTTCCAGTGGTCTTTtgcagaaaattatgaaadadaaatdaaataaaaaagott---
U4	---attgaaagaaacgaaaaatcttttaccattcaattttTATAATTACATTAACTTTtgcagaaaatcatagaagataatagatgagcagattcgtc---
U4atac	taaggggtgacatttgcggtgagatttttcatatattgtTATAATTACATTCACTTctgcagacattttcgttaagtacaaaacgtgcgtaattct----
U5	---tattttcatcttttcccttttaacatttcccttgcacTCAATTACATTACATTTtatccacaaabacataaagaatttcattotctccttctca---
U5	---acatatggatattgtatttagatttgacattcgtttTATAATTACATTTCATcgttcataaaattctactaaagcacatttcgaagggtggaaaaa---
U5	---ctatttcccttgaaactttatagattttatattttTATAATTACATTCCACTTTtgcgataatttcactagtatatcttcgcatagcaacaactc---
U11	---ccataatcaccacatgccattgcattagttttctTATAATTACATTCTTTtgcgaaaacgaatgaggtatgactgggaatcgaccctccttt---

Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod_7SK, 7SL, RNase_MRP, RNaseP_nuc, U6, U6atac, tRNAsec, snoRNA18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.