

Syritta pipiens

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

Assembly: GCA_905187475.1_idSyrPipi1.1_genomic

Syr_pip1 | LR994571.1:19390290-19390567 (+) | 278 nt | lncRNA:noe consensus e-value: 1.7e-11

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

666C66TTC6ATGCCTCACAGTGGATC66TGGTACATCCC6TTTCCCAATTTGTAGCATCCAAATC6TATGCTTTGACATCCATACTAAATAAAATCTGAAAAAGTGT6TTTGA AAAAG6TTTACCAACAAAAACGGCAAAAAACA

AAAATCTTTCTTCTATCTCATATAAGATAAAAAGTAAAAAGTATATAGAAATAAAGCAATTCAATTAAAAATTGAGAAAAAGATTATCAAAACGGTTCTGCTGAGGTAGATGCGATCGCCTTTTT

Syr_pip1	-----aaacTcaaadcdcccccattotttcaactacotATAATTCCAGAAATTCatttctccadaaatgaatataaaatdaaaatdcaaaccccataccatc
U6	-----CgaccaacagatggccttaggttcctccacttaaaTACAATTCACAGAAATCTctttgtccatcgctaaaccaatcaccctgggaacattcaacctc--
tRNAsec	-----gtgttttactttgtttaccattfaaatttttatagcaCATAAATTCACAGTAATTTttttactgtgggtfaaatttcatagatcatcattgaatcagatggt--
U1	---ctaccatcactdaaaadaaaaadttcdaataaafcaTATAATTCACACCTATTCCctccaaaaaagctacagaactcaacattcaacggaatcaagc--
U1	---aaccaatggcgacgtcagttgttttttccactcatTAATAATTCACAGTTAGTTggtgtgaaaaaagtatatagatggtttggtgtgagcggttaagc--
U1	---tcgaagtgtgcctttttcttttttatctgttttgAATAATTCACAGGCACTTgtgtgaaaaaatatcaaatgtcaaaagctaacgcgaagaagc--
U2	-----cttttctccctcdaataaatttttttttcccaotATAAATTCACACCCGAAGtttcattttctttctcaaaataaodaaatattotactacaaaattt--
U2	-----aaaaacaagctagacgccgctttttcgtttgtgtTAGAATTCACAGCTGGCGcgtgtaggaatacgtttgaatagcaggtagtttgacggtgaaaattt--
U2	-----tttgaacgataaaatgagaaattcttccagtagttTATAAATTCACATCCAAATtcgtgcgaattttctataagttaaccgatttgggggtgttctagtt--
U3	-----cttcgaacaaatcaatttcaatttctctgctatTATAATTCACAGTTAGAATctctdaataaaatgaataaagccactctgtgcdaatgaaaaatt--
U3	-----cacagcaacgaatggattgtcttgattcgaatctTATAGTTACAGTCTGTATctgcaaaaataaattataaatacaaaacctgcagacggaagaatt--
U4	---aagggaagaacctgttgaatttttgaactgaatataTATAAATTCACAGTTACTTaaagcagaaaaagattgaaatgaaaaactttttgatgaaacctt--
U4	---tatgcaatcatttagtagcatgaaatttcacTgggcaTAGAATTCAGAGTTGGATgttgtgaaaaagtgttaaaagtgattagttggtgaaattgtt--
U4atac	tttttcaattcaactttttaatttaatttcatacaaccaTATAAATTCACATGTACTTaaatgaacatcttgaataatdcaaaaaagatactttcatc--
U5	-gagaaaaacaacaaaaaaatcaaaaatttcactcgctTATAAATTCACATTTATGACTactgcagaatatttatgaatgttgcctccgaagggtgcaaaat----
U5	-aagcattcgcttctacttcatttcatttctgttttTATAATTCACAGTTACTTactgcagaaaaaccataagagattcgagttggtgtgtgaaaaa----
U5	---ttcTaaaacaaTctctcatatttttttttatccctTATAAATTCACATCAGTCTcctacaaaatattagtaaatataaoccaaattgoottcnaaa--
U5	---gccaatggaataatcgtgtcataaatttttgcgtgtTATAAATTCACATCC6TTGcgagcagaaaaagtgtatgaataggagtgaaattgctgtgaaaaa----
U11	-----cttattcacttgtgttcagtgacgagtttatctgtTATAAATTCACATTTAGTTgtgcagatgtgaagtcaggtatagcgtcggaattcgttgggtattc--

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.