

# Volucella pellucens

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

Assembly: GCA\_965234375.1\_idVolPell3.hap1.1\_genomic

Vol\_pel1 | OZ248633.1:119393033-119393318 (+) | 286 nt | lncRNA: noe consensus e-value: 4.0e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.83

666C66TTC6ATGCCTCACAGTGTTC666TGGTACATTCCGTTCCCCCAATTGTAGCTTCTAAATCGTATGCTTTGACATCCATACTATAAATAATAAATAAAATACTATATAAAAAAGTGTGTTTGAAGAAAGTTTACCAAAAACAAACGCAAAACAAAAATAAATTTTCTCTCTATCATAGATAAAATAAAATATAGAAATAAGCAATTCATCGAATCGAGAAAAAATGTTTGTCCAAAAAGGTTTCTGCTG666TATGCGATCGCCTTTTT

Vol_pel1	-----ttccaccdaadcaatfaccctacattttccaatcattTATACTTCACAGTATTTTaatcttctctctgacatctataadcaaattoaaadcatotaccatc-----
RNAse_MRP	-----caataggtaaatgttattttttattgctttATAATTCCGABAAATTTttttacagcgctttgaactaaacgcttggacagtaataaggaagggtgt
U6	-----ctcaccactaggtggcgtgtattttttgttcataatATAATTCCGABAAATTTttttcattactagttattacaaaaagcgtttttctttgcaacaatttt-----
U6atac	-----tataaaccatttaaaaaaagaatttcaatcacTATAATTCCGABAAATTTttttcactctataaacgctttgtttattaaaaaaaacaaatgttaattt-----
tRNAsec	-----ctgaatttcgaatgaagaaatattttattggcgataAAATTCGABAAATTTttttacgttcccttggatgggtataccgtgtcttttaaacacatgat-----
U1	-----ctaaggcgggtgaattccctctgttttaattcattactTATAATTTCACATCCCTCTTcacacagaaaaataacataaggagagatccactcgctgtgaaaggc-----
U1	-----acaaacaaaaatatacccccattttcattcaacodtTATAGTTTCACATCTTCTTcaagcdaaatttattaaaaaadaaataadtcotttccaaactaaadc-----
U2	-----cgttttaggtccacacagttttttctattcatattTATAATTTCACAGCCACTTgggtcaagtaccgttcatagtaactcggtatttgggtgagaaaagtt-----
U2	-----aatgtaccctggggttccctgggaatttttcactccctTATAATTTCACATCCGATGctgttaactattccacagttactcttatatgataaagtacagtt-----
U2	-----aaaaacaaaacacacagttacttatttcttttTATGATTCACATTCACATGaatgtacaaataacagttatgtatgtatgtatataacgaaaaaagtt-----
U2	-----aaacaacaaaaattgtgtgtgaaattcattttatcTATAATTTCACATTCCTTTtggtagagaattgtctaaagttagatcagtgaaatgggcaaacgtt-----
U3	-----cacaaaaatcatagcagaagttccactcacgttttTATAATTTCACAGTGACTTcaagcagtagtatccataagacactcgctatttgcagaatgacgtt-----
U3	-----cacaaaaatcatagcagaagttccactcacgttttTATAATTTCACAGTGACTTcaagcagtagtatccataagacactcgctatttgcagaatgacgtt-----
U3	-----cacaaaaatcatagcagaagttccactcacgttttTATAATTTCACAGTGACTTcaagcagtagtatccataagacactcgctatttgcagaatgacgtt-----
U3	-----gtgaatattgataacacatttttcactcgatattTATAATTTCACAGTTACTTtagagcaatagaacctcatgaataccacgggtcttgagatgaagaagtt-----
U4	-----cctaggaattttacttttttttttttcttctTATAATTTCACAGTCTCTTcgaggtagatattcttaactgttagtagaataattagaacagtt-----
U4	-----atccaataaataatggttttttttttttttcttctTATAATTTCACATCCACTTggtatgaaabaatttactaaacctgaacaaactgaatgtcatt-----
U4	-----ggttagaaaaacttggtttcttttttttctcattcagttTATAATTTCACAGTAACCTTgaaccacaaaaatatcataagtaggtgggaagtagatcaaccgtt-----
U4atac	tggtttaataactgtaacttattttggaaattgcattcactTATAATTTCACAGTTACTTgaacgtgaagttttcataagtaccacaaaaggtttatacctt-----
U5	-----tcatttatctattttcattatcttctcatttcattcattTATAATTTCACATCCACTTcaagcdaaadaattataaaoaattdcatatgaacaaattc-----
U5	-----atcaaaatttaaaagacgttgcatttttttttgatcattTATAATTTCACATCCACTTcaagcdaaadaattataaaoaattdcatatgaacaaattc-----
U5	-----gcagtcgttactcgtaccgtgagattttgttcacattctTATAATTTCACATTCAGTTctgcccacaaattcacatgaattctttacaaaaacactaaagaaa-----
U11	-----actattaccgaattaccatttaataaattcattccctTATAATTTCACATTAATTTatcaaaaaataaataaaoatctaatgaaatttcccttcgaatt-----
U12	-----ttgttaagtgcattttggaaagctttttcattcagttTACAATTTCACAGTTACTTataacatgtctactactgttaacggtttaatttagcagcaaacctc-----

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.