

# Volucella zonaria

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

Assembly: GCA\_963966105.1\_idVolZona1.1\_genomic

Vol\_zon1 | OZ014532.1:123019874-123020159 (-) | 286 nt | lncRNA: noe consensus e-value: 1.8e-09

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.84

666c66tTC6ATGCTCACA6T6TTTT6C66TTGGCTACATTCC6TTCCCTCAATT6TAGCTTCTAAATCGTATGCTTTGACATCCATACTATAAATAATAAATAAAATACTATATAAAAAAGT6T6TTTGA AAAAGTTTTACCAAAAAACAAACGCAACAAAAATAAATCTTTTCTCTCTATCATAGATAAAATAAAATAGAAATAAGCAATTCAATCGAATCGAGAAAAAATGTTTGTCCAAAAAGGTTTCTGCTG666T6ATGCGATCGCCTTTTT

Vol\_zon1

RNase\_MRP

U6

U6atac

tRNAsec

U1

U1

U2

U2

U3

U3

U4

U4

U4

U4atac

U5

U5

U5

U11

U12

-----ttctacadaadcaatfaccctactttttccaatcctttTATACTTCACAGTATTTTaatctctcaatccaatctataadcaaaatttgaagcacctaccatc-----

-----aataggtaaatgtttatTTTTtattgctttTATAGTTCGCAGAAATTTTTtagacatgcgtttgaactaataccgttagacagtactaaagtgaaggtgt-----

-----ttcaccactagggtggcgctataatTTTTtattcataatTATAATTCGCAGAAATTTTTtaccitggggttattacaaaaatgctttttctttgcaacaatttt-----

-----tataaataatttaaaaaaaatttcaatcactTATAGTTCGCAGAAATTTTTtaccacacaaacgttttatattgaadaaaaaacaacactttggc-----

-----ttgaagttcttttgaaggagcgttttcattggcaataAAATTCGCAGAAATTTTTtcttattccctttggaatggatagctgtcttttaagcacacggt-----

-----acaaacaaaaattacgacgagatttcattcaacgctTATAGTTCACATCTTCTTcgtgcgaattgggttaaaagaagtgaagccgaattcggaatgaaggt-----

-----tataattctdaattttccdaatttttaacctttacaTATAATTCACATCTCTTTacgcagaaaaaacaataaoodaotccactccctotaataatc-----

-----acaaacaaaaattacgacgagatttcatttaacgctTATAGTTCACATCTTCTTcgtgcgaattgggttaaaagaagtgaagccgaattcgcaaatgaagc-----

-----aatgtaccctgggggttcccttggaaataatcactccctTATAATTCACATCCAGTTgctgtacaattccagaagtactacttatatgaagaattcagtt-----

-----aacacaacaaaaatttgaataaaatttcattttacTATAATTCACATCTCTTTtgaataaaatttcaaatgaacgaatgaataaodcaaacott-----

-----cgttttagtgcacacagttttttcttattcattttTATAATTCACATCCACTTggtgcaagtatctttcataaagtgttcggaatttggcatggaagtt-----

-----cacaaaattcacaggcagaagttccactcacgttttTATAATTCACAGTCAITTcaagcagtagtatccataagatactcgcgtattcgcaagtacagtt-----

-----gtgaatcagtagatcacacatttttccactcgatattTATAATTCACAGTCAITTgagcagtagaactcatagaataccaagcttgcgaatgggaagtt-----

-----ccataaatttatctcttttttttttttcatctctctTATAATTCACAGTCTCTTctgtaaatattcttaaacctotaadtaaaaaatttgaadacatt-----

-----atgcaatagatatgggatttttttttcatctcgtttctTATAATTCACATCCACTTggtatagaagaatttactaaaccgtgtacagagcggagattcgtt-----

-----tggtagaanaacacttgggttcccttttttcatctgggtTATAATTCACAGTAACTTgaagcaaaaaattatcataagtaggtgggaatgaagtagcaaccgtt-----

-----tctttaataactotaacttatttttgaatttcacattcacTATAATTCACAGTTACTTcgaacataaattttcacaaotaccaaaaaatttatccctt-----

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-----tggtaagtgcatttttggaaagcttttcatcttgattTCAATTCACAGTTACTTataacatgctactactctgttaacgatttgaatttagcagcaagttc-----

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.