

# Volucella inanis

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

Assembly: GCA\_907269105.1\_idVollnan1.1\_genomic

Vol\_ina1 | OU026156.1:93699678-93699961 (+) | 284 nt | lncRNA:noe consensus e-value: 5.6e-09

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

GGGCGGTTGGATGCTCACAGTGTGTTGGGTTGGTGCATTCGGTCCGCCAATTGTAGCTTCTAAATCGTATGCTTGACATCCATACATAAATAATAAAAACTATATAAAAAAGTGTGTTGAAAAAGTTTACCAAAAACAAACGCAAAACAAAAATAATCTTCTCTCTATCATAGATAAAAATAAATATAGAAATAAGCAATTCAATTGAATCGAGAAAAAAGTTTGTCCAAAACGGTTTCTGCTGGGGTAGATGCGATCGCCTTTTT

Vol_ina1	-----TtctaccdaadcaotacctaacttttttctatccttTATACTTCACAGTATTTTaatttctctcaotdtdatctataadcaaaatttaaadcacctaccatc-----
RNAse_MRP	-----GaaagaggtatactatttttctattgccttTATAATTGCGAGAAATTTTTggacaatgtttgaactaataacattatccagcattttagagtggaagtgt-----
U6	-----gtcagcattaggtgacaccataatttttattcataaATAAGTTCACAGAAATTTTTcatctcagatacttacaaaatactctttttatacaaccctt-----
U6	----CatadattcactaaaaacttctcttttcttcttTACAATTCAAGATTTTtataatgctctcgaactgtaaaatactataacdaaatacaattattt-----
U6atac	-----ttgtaaagtcttgagaagaaaatttcaatcgctTATAATTGCGAGATTTTTtctgaattgaaggattattattttgaagcaagaaattcgtaaagg-----
tRNAsec	-----TaaactgttttaattgggaaaatttttctattggtatGTAATTGCGAGATTTTTtcttcttcttggatgattttttcttttaatacatgct-----
snoRNAme18SA1806	-----nattaaatttttctaatcccttttatttctctTATAATTGCGAGAAATTTTTtctaatcccaacataccaaactattctcaaatcaccttgaagct-----
U1	-----acaaacaaaaatttatgatgaaatttcttcaacgctTATAAGTTCACATCTTCTTctgtcttaatctattacaagaactaagccatttgcggaagaaagc-----
U1	----cttatttttattttaatttagatttcttcaacgctTATAAGTTCACATCTTCTTctgtcaaaattgattaaaagaagtaagccatttgcggaagaaagc-----
U2	----aaacacacacaaatgattgdaaatttcatattataCTAATTCAAGTTCCTTTttdadadaatttctaaagtaaaccaataaaattacaaacttt-----
U2	----gtcaccgtccagaaaatttttttctattcttataTATAATTCAATCCACTTtagcgaagtatctttcataagtaattcacatttggcacaaaacttt-----
U2	-----aaaaacaaagcacacagattttttctgattgattTATGATTACATTGCACTTggtgtaacagatacagttatgtagtggttaacatacaaggaagatt-----
U2	----agtaacctggggttccttgggaattttcactcactTATAATTCAATCCAGTTgctgtaagtattcttagaagtactaccctatgtgataaagcatattt-----
U3	----gdtadtdaatadacaaaatttttcaactcgaattttGTAATTACAGATTGCTTgaaacaaaaaaactcatdaataccaaadoodttaacttodaadaatt-----
U4	----tatgcaacattatataaatttttttcttcttTATAATTCAATCCACTTtggtaacagagatttactaaagtgtgtacagagtggaatttgtt-----
U4	----atagaaaacttgggtctcttttttttcttcttTATAATTGCGAGTTACTTgataccaaaaatacataagatacaatgggaatcgtggcaatagtc-----
U4	----cataaadtccatttttttttttttcttctTATAATTACAGTCTCTTcaadtdaataattcttaactctatdaaadaaaattaaatcagtt-----
U4atac	tggtttaaacttaagtctattttgaaaattgcattcactTATAATTCAACTTACTTcgagcaaaagatttcaatgataccaaaagatttatcgctct-----
U5	----tacaattttttattgttttttttttttcttctcgttctataTATAATTGCGATCCACTTcgaacagaaaaatgtataagcgagttgaaatcacctacattcg-----
U5	----ccaacattttaaagacttctcatttttttttttataTATAATTCAATCCACTTgaaacaaaaatcttadtaaaattttaaacaatacctadtaaaa-----
U5	----gtctcagaattttaggtatgcattttttcttctTATAAGTTCACATTCAGTTacggcacaaagtatctttagtaaaagtaccaaccatgcaatag-----
U5	----ccacggcaatccttacttgagatttttccacatcctTATAATTCAATCCACTTtaggcacaaattcacttgaatacttcacaaaaacaaaggacaaa-----
U11	----aaacataactattcccttgaataaattcattcctTATAATTCAATCCACTTgatttatacaaaaaataatgaagatcgaatgaatcgaattcgaatt-----
U12	----ttctgggtgaatttttgaagcttttcttctgattTATAATTACAGTTACTTataacattctacaactactgtaacagtttaattcagcagtaaaattt-----

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.