

Criorhina ranunculi

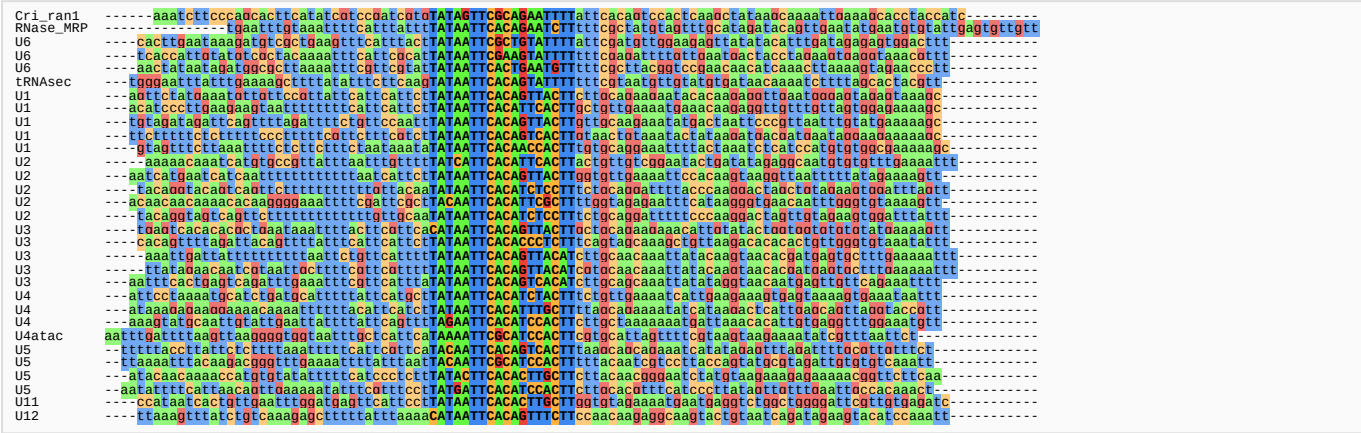
Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Criorhina

Assembly: GCA\_951813785.1\_idCriRanu1.1\_genomic

Cri\_ran1 | OX68385.1:33132367-33132668 (+) | 302 nt | lncRNA: noe consensus e-value: 4.1e-10

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

GGGCGGTTGGATGCTTCACAGTGTGACGGTGGGTACATTCCGTTCCGCCAATTTGTAGCAATCCAAATATATCGTATGCTTTGACATCCATACCTATATAAAACTGCAAAAAGTGTGTTTGA AAAAGTTTACCACAAATAAAAAAAACAAATCGCAAAAACAAATATTTCTTCTATCTATAAATCAACTTCGTATATAGATTAGGAACATATAGAAATATAAGCAATCAATAAAATGAGAAAAAAAAGTTTCATCAAAAACGAATTCGTGAGGTAGATGCGATCGCCTTTT



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.