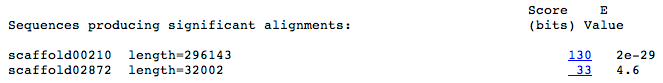
Nisha Crouser

**Gamma-glutamyl hydrolase EC 3.4.19.9**

I performed a blastp of the aa sequence for 3.4.19.9 from *Vitis vinifera* and found the sequence for the enzyme in *Arabidopsis thaliana,* which is evolutionary more closely related to the blueberry. I then used this aa sequence (347 aa) for 3.4.19.9 to do a tblastn against *V. corymbosum* 454- Scaffolds. Reliable hits were only found in Scaffold 00210.



3.4.19.9 found in Scaffold 00210 (query sequence starts at base 243033 on scaffold)

1)

For Primer TTTTCCTCAAAGACTGCTCTCTC

Rev Primer AGCAGTCACCATCTTTTTAGGG

Repeats (tc) × 27 PCR product = 236 bp & start at base 256014

2)

For Primer ATTCACCCCGTGTAAGTAATGG

Rev Primer CGACAACACTAAGAGACACCCA

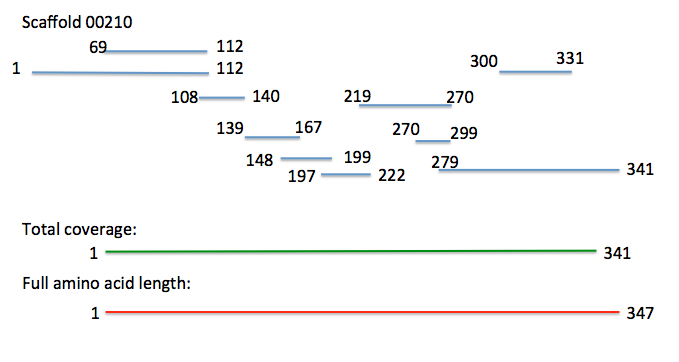
Repeats (ga) × 15 PCR product = 201 bp & start at base 176902

3)

For Primer GTCGGTTTACCAAAAACTGCTC

Rev Primer CAGGATCTATGAGATGTGGACG

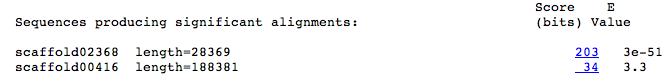
Repeats (ac) × 10 PCR product = 263 bp & start at base 285048



**Figure 1.** Alignment of 3.4.19.9 on Scaffold 00210 in V. corymbosum. Many different fragments found based on different reading frames, but overall coverage of amino acid sequence was very high.

**Bifunctional purine biosynthesis protein EC 2.1.2.3**

I performed a blastp of the aa sequence for 2.1.2.3 from *Vitis vinifera* and found the sequence for the enzyme in *Arabidopsis thaliana,* which is evolutionary more closely related to the blueberry. I then used this aa sequence (596 aa) for 2.1.2.3 to do a tblastn against *V. corymbosum* 454- Scaffolds. Reliable hits were found only in Scaffold 02368.



2.1.2.3 found in Scaffold 02368 (query sequence starts at base 19669 on scaffold)

1)

For Primer TTAAAGGGCACCATTCATATCC

Rev primer TGAGGCAGTACTTCTCCAGTCA

Repeats (ag) × 12 PCR product = 253 bp & start at base 9455

2)

For Primer AAATTGGTGTAGTGGGTTTTGG

Rev Primer TTCACAGTTTGACGGTTTATGC

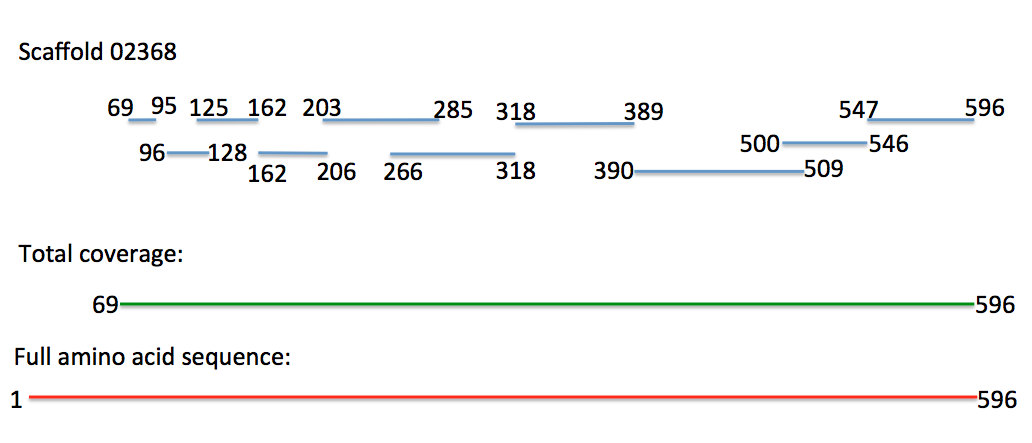
Repeats (ga) × 13 PCR product = 239 bp & start at base 72

3)

For Primer TCAGTGCAAATCATAAAGTGGG

Rev Primer TACTCGTAGGAAGGATGTGGGT

Repeats (ct) × 11 PCR product = 293 bp & start at base 13762



**Figure 2.** Alignment of 2.1.3.2 in *Arabidopsis thaliana* against Scaffold 02368 in *V. corymbosum.* Many different fragments found based on different reading frames, but overall coverage of amino acid sequence was very high.