GTP cyclohydrolase I (E.C. 3.5.4.16)

**ALIGNMENTS:**

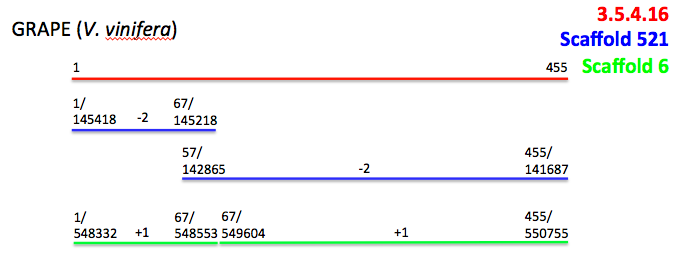


Fig. 1: Alignment results for a tblastn comparing the blueberry scaffolds to the amino acid sequence for GTP cyclohydrolase I (E.C. 3.5.4.16) from the grape genome. Numbers at either end of the lines represent the location (top = location in 3.5.4.16 sequence; bottom = location in scaffold sequence). Numbers in the middle of scaffolds indicate reading frame values.

Query = 455 aa sequence for enzyme 3.5.4.16 (GTP cyclohydrolase I) in *Vitis vinifera*

Subject = *V. corymbosum* 454-Scaffolds

Results: Significant hits on scaffolds 6 and 521

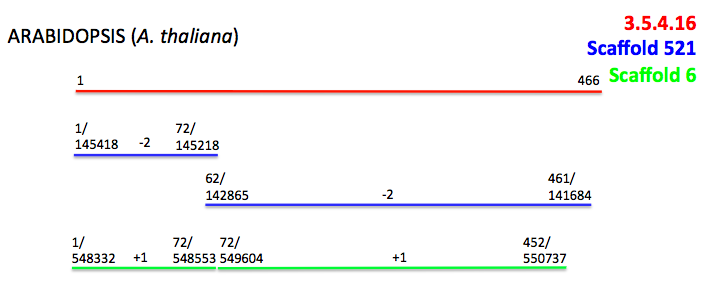


Fig. 2: Alignment results for a tblastn comparing the blueberry scaffolds to the amino acid sequence for GTP cyclohydrolase I (E.C. 3.5.4.16) from the *Arabidopsis thaliana* genome. Numbers at either end of the lines represent the location (top = location in 3.5.4.16 sequence; bottom = location in scaffold sequence). Numbers in the middle of scaffolds indicate reading frame values.

Query = 466 aa sequence for enzyme 3.5.4.16 (GTP cyclohydrase I) in *Arabidopsis thalian*

Subject = *V. corymbosum* 454-Scaffolds

Results: Significant hits for scaffolds 6 and 521

**PRIMERS:**

E.C. 3.5.4.16 in Scaffold 6 (query sequence starts at base 548332 on the scaffold)

1)

For Primer: AGCGCTCCAGATTCTTTAGTTG

Rev Primer: GATTGTAGCAGTGCCTCTACCC

Repeats (tc) x 30 PCR product = 279 bp & start at base 490223

2)

For Primer: TAGAAGAGAACGGAGTGAAGGG

Rev Primer: AGGAAAACCCATAAAGAGGAGG

Repeats (tc) x 24 PCR product = 297 bp & start at base 548595

3)

For Primer: GATGGTTTCTTGAACGTGATGA

Rev Primer: GCGCCTCCTGCTTCTTATAGTA

Repeats (ag) x 13 PCR product = 160 bp & start at base 471712

E.C. 3.5.4.16 in Scaffold 521 (query sequence starts at base 145418 on the scaffold)

1)

For Primer: CTCTTCCTGATCCAGAAGCTGT

Rev Primer: GTTTTTCTTGCGTCTTTCTGCT

Repeats (ag) x 16 PCR product = 267 bp & start at base 155555

2)

For Primer: TCGAATATAGGTCCACCTCAGC

Rev Primer: TGAGTTTACCTTCAGACCAGCA

Repeats (ct) x 12 PCR product = 210 bp & start at base 103449

3)

For Primer: TTGTTGTACGGTTGTACCAAGG

Rev Primer: GTTAAGACTTGCGAGAGGAGGA

Repeats (ag) x 11 PCR product = 139 bp & start at base 135665

5-formyltetrahydrofolate cycloligase (E.C. 6.3.3.2)

**ALIGNMENT:**

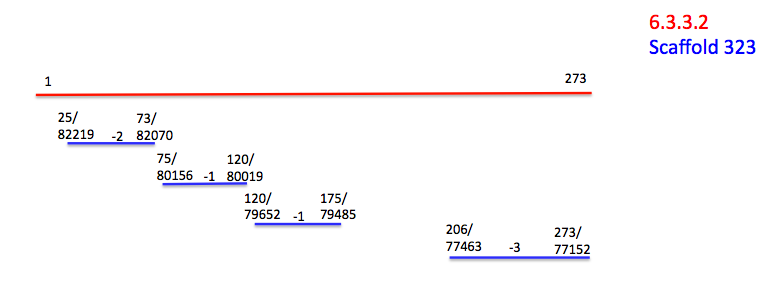


Fig. 3: Alignment results for a tblastn comparing the blueberry scaffolds to the amino acid sequence for 5-formyltetrahydrofolate cycloligase (E.C. 6.3.3.2) from the grape (*Vitis vinifera*) genome. Numbers at either end of the lines represent the location (top = location in 6.3.3.2 sequence; bottom = location in scaffold sequence). Numbers in the middle of scaffolds indicate reading frame values.

Query = 273 aa sequence for enzyme 6.3.3.2 (5-formyltetrahydrofolate cycloligase) in *Vitis vinifera*

Subject = *V. corymbosum* 454-Scaffolds

Results: Significant hits on scaffold 323

**PRIMERS:**

E.C. 6.3.3.2 in Scaffold 323 (query sequence starts at base 82219 on the scaffold)

1)

For Primer: TACTCGATCAATGTGGGCTATG

Rev Primer: TGGACTAGGTTCACAGATGCAG

Repeats (ct) x 16 PCR product = 271 bp & start at base 78798

2)

For Primer: CTCCTCCGGTATGAATATCGTC

Rev Primer: GAGAGAGAGAGCACAATCAGCA

Repeats (tc) x 15 PCR product = 168 bp & start at base 101841

3)

For Primer: TATTGCCACGTTACCTGAGTTG

Rev Primer: CAATTGGCAATGAGTGAAGAGA

Repeats (tg) x 13 PCR product = 292 bp & start at base 71649