Katie Gwathmey

**Dihydroneopterin aldolase [EC: 4.1.2.25]- *Vitis vinifera***

* 142 amino acids
* Involved in Folate biosynthesis and metabolic pathways
* Link to protein overview: <http://www.genome.jp/dbget-bin/www_bget?vvi:100263553>

Amino Acid Sequence: METSLGGAMVDSGEIMKGDKLILRGLRFHGFHGVKPEERKLGQKFLVDVDAWMDLRAAGRSDCLSDTISYTDIYRIVKEIVEGPPQNLLESVAQLIASTTLTKHSRISAIRVKVGKPHVAVQGPVDYLGVEILRYRSVDAQI

Hit on Scaffold 269

* E-value: 4e-29
* Length: 240267



**Legend:** Figure diagrams the results of tBLASTn of the sequence above on *V. corymbosum* 454 scaffolds. Query sequence is represented by the blue line and scaffold 269 by the red. The black box highlights the overlapping region of two sections of the scaffold. The box points to the scaffold’s amino acid sequences of the two sections.

SSR Repeats for Scaffold 269

1)

For Primer CAAAAAGGCCTTATACACCACC

Rev Primer CGGTGAGTGATGACTGTAGCTC

Repeats (ca) x16 PCR product = 224 bp & start at base 221,808

2)

For Primer CAAAAAGGCCTTATACACCACC

Rev Primer CGGTGAGTGATGACTGTAGCTC

Repeats (tc) x12 PCR product =224 bp & start at base 221,767

3)

For Primer GATTGGGACTTGGGATCAATAA

Rev Primer GATGAGTCGAACGGGTTTTTAG

Repeats (ct) x11 PCR product = 193bp & start at base 218,295

*Note:* Took amino acid sequence from *Vitis vinifera* and performed a NCBI Blast to find amino acid sequence of the protein in the *Arabidopsis thaliana* genome. Found the information below:

LOCUS NP\_187781 146 aa linear PLN 22-JAN-2014 DEFINITION Dihydroneopterin aldolase [Arabidopsis thaliana]. ACCESSION NP\_187781 VERSION NP\_187781.1 GI:15229838 DBSOURCE REFSEQ: accession [NM\_112008.1](http://www.ncbi.nlm.nih.gov/nuccore/18399344)

Amino Acid sequence of protein from *Arabidopsis Thaliana*:

MHSSLETTAPATLERRESNLGDKLILKGLKFYGFHGAIAEERTLGQMFLVDIDAWVSLKKAGESDNLEDTISYVDIFSLAKEIVEGSPRNLLETVAELIASKTLEKFHQINAVRVKLSKPNVALIKSTIDYLGVDIFRQR NTSSKN

BLAST of this amino acid sequence in *V. corybosum* resulted in same scaffold hits with similar E-values as those of *V. vinifera.*

**Methionyl-tRNA formyltransferase [EC: 2.1.2.9] –  *Vitis vinifera***

* 365 amino acid
* Involved in metabolism; Metabolism of cofactors and vitamins; genetic Information Processing; translation
* Link to protein overview: <http://www.genome.jp/dbget-bin/www_bget?vvi:100265562>

Amino Acid Sequence: MNSSLMLRRFFTLNATSSSSSSCSASLKPPSKRKQLVFLGSPQVSAAVLDDLFNASTAPDSMFEVAAIVTQPPSGRNRGRKVMPSPVAQHALDRGFPSDLIFTPEKAGEEIFLSSLRALQPELCITAAYGNILPRKFLEIPPMGTVNIHPSLLPLYRGAAPVQRALQDGVKETGVSLAFTVRALDAGPVIACERFEVDDQIKATDLLALLFSQGSKLLIHELPSIFDGSANLKAQPQDDSKATLAPKITPEESWLSFDQEASVLHNKVRAFAGWPGTRAKVVVIDDKNGEHNVLDLKIITTRVCGQSNIQVNEADDVRFIKDALVFPCSGSSALEVLEVQLPGKKVVNAAAFWNGLRGQRLKILG

Hit on Scaffold 330

* E-value: 7e-22
* Length: 245678

Hit on Scaffold 642

* E-value: 2e-16
* Length: 195069



**Legend:** Figure diagrams the results of tBLASTn of the sequence above on *V. corymbosum* 454 scaffolds. Query sequence is represented by the blue line, scaffold 330 by the red, and scaffold 642 by the green. Reading frames and subject location are included.

SSR for Scaffold 330

1)

For Primer GTCAACGTTTTGAGGGTGAAG

Rev Primer AGCTCCGTAAACATATTGCTGC

Repeats (ct) x23 PCR product = 298 bp & start at base 3998

2)

For Primer CAAGGAGCTATTTTCGCTGAAT

Rev Primer GCCTTTTGAGACTGGGTAAATG

Repeats (ct) x21 PCR product =291 bp & start at base 49904

3)

For Primer GTCAACGTTTTGAGGGTGAAG

Rev Primer AGCTCCGTAAACATATTGCTGC

Repeats (cg) x8 PCR product =298 bp & start at base 4044

SSR for Scaffold 642

1)

For Primer GACCAGAGAGAGAGCGAGAGAG

Rev Primer AGGAATGATATCACGAAATCCG

Repeats (ag) x14 PCR product = 284 bp & start at base 42409

2)

For Primer GACAGCGATTGGATTGATGATA

Rev Primer TTAACGAAATAATGCGTACCCC

Repeats (ag) x13 PCR product = 168 bp & start at base 131808

3)

For Primer TGTGTTTAAGGTCAGGATGCAG

Rev Primer AGGCTTATGCTAGATGGGTCAA

Repeats (tc) x10 PCR product = 270 bp & start at base 46746