

# Solanum\_tuberosum \_Melatonin\_COF-R? Report

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## Melatonin\_COF-R\_Question\_PlantInvestigationInformationAnalyzeInterpretReport\_06072024.pdf

Plant of Interest for Investigation: *Solanum tuberosum* 'COF-R?'

### Results & Synopsis:

>A240605-017_E19_226EZA174:	Monilophthora perniciosa; cerato-platanin 12 <small>FA553, C BioType</small>	COF-R? Leaf from Stem 3, Forward 35S
>A240605-017_E19_226EZA175:	Monilophthora perniciosa; cerato-platanin 12 <small>FA553, C BioType</small>	COF-R? Leaf from Stem 3, Reverse 35S
>A240605-017_E19_226EZA176:	Monilophthora perniciosa; cerato-platanin 12 <small>FA553, C BioType</small>	COF-R? Leaf from Stem 5, Forward 35S
>A240605-017_E19_226EZA177:	Monilophthora perniciosa; cerato-platanin 12 <small>FA553, C BioType</small>	COF-R? Leaf from Stem 5, Reverse 35S
>A240605-017_E19_226EZA199:	Caffeic Acid 3-0-0 Methyltransferase <small>LOC 102590869</small>	COF-R? Leaves from Stems 2,7, & 8, Forward 35S

Excise & Recover from GE / UltraPure Combination of x3 Initial DNA Samples from Different Leaves on Varying Stems

**Monilophthora perniciosa; cerato-platanin 12** FA553 = *Mon.per* ... Causal Agent of 'Witch's Broom Disease' of Cocoa (*Theobroma cacao*), Potato (*Solanum tuberosum*) also a host; **C BioType**, Sequence Present in **x4** of these samples of extracted nucleic acid (DNA) from different individual leaves off of the varying stems  
= **CP12 ... Induced Systemic Defense Response** (Cell Necrosis & Phytoalexin (AntiMicrobial) Production)

**Caffeic Acid 3-0-0 Methyltransferase** LOC 102590869 = Roles & Regulations in **Melatonin & Lignin BioSynthesis**, among other **abiotic stress tolerance**;  
Sequence Present in **x1** sample of **combination** of nucleic acid samples extracted from, different leaves off of varying stems (2,7, & 8)

>A240605-017\_C19\_226EZA174\_premix.ab1 1011 (Source & CDS 1.. 471)

**Monilophthora perniciosa; cerato-platanin 12** FA553

**Original with Edit:**

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 TTCGAGCTCTCAATTGGTACCAATTCGCAATCATCAGCACTGAGCTGCT  
 CCGCCGTAACCGTAACGAAGCCCTTTTCGTACGCCTTTCCTGCTGTCAAC  
 TCATCCATAGCCTTCTGCGCGACATTGAAGCCCTTCTGAGCAGTGCAAC  
 GGCCACAACCTGAATCGTCCTGACAGTGCCATTGTCGTCTGAGTACTT  
 TCCAGCATGTGCCACACGAGTCGGAATCCATTCTTTGACAGGGAAGGCG  
 CCTCTGGATAGACATTGACACCGTCGACAGACTGTTTACATCTCCAAC  
 TGTGTTGATGCCCTTCGGGCTCAGGATGTTGAGCAAGAGCCATGGTCGG  
 ACAAAGTGAAGTCACTGTTGTCGTATTCGCTAATGTATCGCAGCTTGAGA  
 GTGCCGTCAGCGCTCTGACGTTTGTATGCTGAGTGCAGCGGAGAGGTAGC  
 GAGGATAGCGATAGCAGCGATGAACCTCATTCTAGAGTCCCCGTTTCT  
 CTCCAATGAAATGAACCTCCTTATATAGAGGAAGGGTCTTGCGAAGGAT  
 AGTGGGATTGTGCGTCNCCNCCNTTACNNCANCNGANNTNTGGATGGAT  
 TGGACGCAACTCCTTTGTTTATGTAGGGGTGACAAACCTGCGGTCATGA  
 TAACTGGCTTTTCTNTACCACCCTAAGNCAAAGAACATNACATTTNGA  
 NCNGGATATTGAAGATGAACANCCCTCACNCNTGANNNNGCNTATNAGNAG  
 GTGACTGGTTNGCNTGTNTGNCNAATGNGCCATGAANNCTTNAAGCAATT  
 GNATTGANCCGATTGGACCNTACNAGCATNGNTTGAAANNTTGTGTAT  
 AAATGCTTGAAAGCACTGTCTNNNNAAACGAGNTACNNGNCAAAAANGN  
 GGGAAANNNGAATNNNTTTCGGNAAAGNGNCCTNAANCNACCCNNNNNG  
 GNNCNCNNNN

**Edit & Reverse Compliment:**

ATGAAGTTCATCGCTGCTATCGCTATCCTCGCTACCTCTGCCGCTGCACTCAGCATCAAACGTCAGAGCGCTGACGGCACTCTCAAGCTGCGATACATTAGCGAATACGACAACAGTGACTTCA  
 CTTTGTCCGACCATGGCTCTTGTCTAAACATCCTGAGCCCGAAGGGCATCAACACAGTTGGAGATGTAACAAGTCTGTGCGACGGTGTCAATGTCTATCCAGGAGGCGCCTTCCCTGTCAAAG  
 AATGGAATCCGACTCGTGTGGACATGCTGGAAAGTCAGCTACGACGACAATGGCACTGTCAGGACGATTTCGAGTTGTGGCCGTTGACACTGCTCAAGAGGGCTTCAATGTGCGCGAGAA  
 GGCTATGGATGAGTTGACAGACGAAAGGCGTACGAAAAGGGCTTCGTTACGGTTACGGCGGAGCAGCTCAGTGCTGATGATTGCGAAATTGGTACCAATTGA

**Amino Acid Translation:**

MKFIAAIAILATSAAALSIKRQSDGTLKLRVISEYDNSDFTLSDHGSCSNILSPKGINTVGDVNSVDGVNVYPGGAFPVKWNSDSCGTCWKVSYDDNGTVRTRVAVDVAQEGFNVAQKAMD  
 ELTDGKAYEKGFVTVAEQLSADDCEIGTN







>A240605-017\_A19\_226EZA199\_premix.ab1 985 (Source & CDS 1.. 813)

**Caffeic Acid 3-O-Methyltransferase** LOC102590869


**Original with Edit:**

NNNTNNCTTNNANTTTATTGCCAATGTTTGAACGATCGGGGAAATTCGAG  
 CTCAATGGGGTCAACAAGCCACAGCCAGAGCAACAGCCTAACTCAAAACAGA  
 GGATGAAGCTTTCTTATTGCGTATGCAATTGGCCAGTGCCTCTGTACTAC  
 CCATGGTCCTAAAATCAGCTGTAGAAGTTGACCTTCTTAAATATAGCT  
 AAGGCTGGTCCAGGTGCATCAATTCGCCTTCTGAGCTAGCAGATCAACT  
 CCCTTCGAAGAACCAGATGCACCGTAATGCTCGATCGAATGCTTAGGC  
 TCCTTGCTACTTACTCTGTTCTCAATTGTACACTCAGGACACTCCCTGAT  
 GGACGTGTAGAGCGGCTGTATAGTCTTGCTCCGGTTTGAAGTTTTGAC  
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 GGTGGAATCCCAATCAACAAGGCATATGGGATGACAGCATTGAGTACCA  
 TGAACAGATCCAAGATTCAATAAGGTTTTCAACCGTGAATGCTGATC  
 ACACCCTTGTCCATCAAGAGGATTCTGGAAGACTATAAAGGATTGAA  
 GGACTCAACTCCATTGTTGATGTTGGTGGGAACAGGGGCTACTGTGAG  
 CATGATTGTCTCTAAGTATCCCTCCATTAAGGGCATTAACTTTGATTTGC  
 CACATGTTATTGAAGATGCTCCACCTTACCCAGGCGTCGAACACATTGGT  
 GGTGACATGTTTGTAGTGTGCCGAAAGCGGATGCCATTTTCATGAAGT  
 GATTTGTCATGATTGGNCGATGAACATTGCTTAAAGTTCTTNGNNAAT  
 GCTACNNCACTTCTGNAATGGNNNNNGATNANGCNGNANNNGCTTNNC  
 TTTNCAGAAGGNNCCNNAACNNNCATTNANNNTNN

**Amino Acid Translation:**

MGSTSHSQSNLTQTDEAFLFAMQLASASVLPMLVLSAVELDL  
 LEIIKAGPGASISPSELADQLPSKNPDAPVMLDRMLRLATYVLNCTLRTPDGRV  
 ERLYSLAPVCKFLTKNAYGVSAPLLLMNQDKVLMESWYHLKDAVLGGIPFNKAYGM  
 TAFEYHGTDPFRNKVFNRMDSHTTSLIKRILEDYKGFELNSIVDVGGGTGATVSMI  
 VSKYPSIKGINFDLPHVIEDAPPYPGVEHIGGDMFVSVPKADAIFMKWICHDW

226EZAA174 through 226EZAA177 (BLASTn)

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### Monilophthora perniciosa strain FA553 cerato-platanin 12 (CP12) mRNA, complete cds

GenBank: JX422027.1  
[FASTA](#) [Graphics](#)

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**LOCUS** JX422027 471 bp mRNA linear PLN 05-NOV-2014  
**DEFINITION** Monilophthora perniciosa strain FA553 cerato-platanin 12 (CP12) mRNA, complete cds.  
**ACCESSION** JX422027  
**VERSION** JX422027.1  
**KEYWORDS** .  
**SOURCE** Monilophthora perniciosa (Crinipellis perniciosa)  
**ORGANISM** [Monilophthora perniciosa](#)  
Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Marasmiineae; Marasmiaceae; Monilophthora.  
**REFERENCE** 1 (bases 1 to 471)  
**AUTHORS** de O Barsottini,M.R., de Oliveira,J.F., Adamoski,D., Teixeira,P.J., do Prado,P.F., Tiezzi,H.O., Sforca,M.L., Cassago,A., Portugal,R.V., de Oliveira,P.S., de M Zerl,A.C., Dias,S.M., Pereira,G.A. and Ambrosio,A.L.  
**TITLE** Functional diversification of cerato-platanins in Monilophthora perniciosa as seen by differential expression and protein function specialization  
**JOURNAL** Mol. Plant Microbe Interact. 26 (11), 1281-1293 (2013)  
**PUBMED** 23982259  
**REFERENCE** 2 (bases 1 to 471)  
**AUTHORS** Barsottini,M.R.O., Oliveira,J.F., Teixeira,P., Pereira,G.A.G., Ambrosio,A.L.B. and Dias,S.M.G.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (19-JUL-2012) Departamento de Genetica e Evolucao/IB, Universidade Estadual de Campinas, Cidade Universitaria Zeferino Vaz, Campinas, Sao Paulo 13083-970, Brazil


**FEATURES** Location/Qualifiers  
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421 gttacaggcg agcagctcag tctgatgat tgcaaaatg gtccaactg a

//

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**cerato-platanin 12 [Monilophthora perniciosa]**

GenBank: AGL40506.1

[Identical Proteins](#) [FASTA](#) [Graphics](#)

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**LOCUS** AGL40506 156 aa linear PLN 05-NOV-2014

**DEFINITION** cerato-platanin 12 [Monilophthora perniciosa].

**ACCESSION** AGL40506

**VERSION** AGL40506.1

**DBSOURCE** accession JX422827.1

**KEYWORDS** .

**SOURCE** Monilophthora perniciosa (Crinipellis perniciosa)

**ORGANISM** [Monilophthora perniciosa](#)  
Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;  
Agaricomycetes; Agaricomycetidae; Agaricales; Marasmiineae;  
Marasmiaceae; Monilophthora.

**REFERENCE** 1 (residues 1 to 156)  
**AUTHORS** de O Barsottini,M.R., de Oliveira,J.F., Adamoski,D., Teixeira,P.J., de Prado,P.F., Tiezzi,H.O., Sforca,M.L., Cassago,A., Portugal,R.V., de Oliveira,P.S., de M Zeri,A.C., Dias,S.M., Pereira,G.A. and Ambrosio,A.L.

**TITLE** Functional diversification of cerato-platanins in Monilophthora perniciosa as seen by differential expression and protein function specialization

**JOURNAL** Mol. Plant Microbe Interact. 26 (11), 1281-1293 (2013)

**PUBMED** 23982259

**REFERENCE** 2 (residues 1 to 156)  
**AUTHORS** Barsottini,M.R.O., Oliveira,J.F., Teixeira,P., Pereira,G.A.G., Ambrosio,A.L.B. and Dias,S.M.G.

**TITLE** Direct Submission

**JOURNAL** Submitted (19-JUL-2012) Departamento de Genetica e Evolucao/IB, Universidade Estadual de Campinas, Cidade Universitaria Zeferino Vaz, Campinas, Sao Paulo 13083-970, Brazil

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Conserved Domains (Concise)

Conserved Domains (Full)

Domain Relatives

Encoding mRNA

---

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- cerato-platanin 12 [Monilophthora perniciosa] Protein
- Monilophthora perniciosa strain FA553 cerato-platanin 12 (CP12) mRNA, C Nucleotide
- PREDICTED: caffeic acid 3-O-methyltransferase [Solanum tuberosum] Protein
- PREDICTED: Solanum tuberosum caffeic acid 3-O-methyltransferase Nucleotide

See more...

**FEATURES** Location/Qualifiers

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/organism="Monilophthora perniciosa"  
/strain="FA553"  
/isolate="CP02"  
/db\_xref="taxon:153609"  
/note="biotype: C"

**Protein** 1..156  
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**Region** 30..151  
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121 aqkandeldt gkayekgfvv tvaeqlsadd ckigtg
//
                
```

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**PREDICTED: Solanum tuberosum caffeic acid 3-O-methyltransferase (LOC102590869), mRNA**

NCBI Reference Sequence: XM\_015308845.1  
[FASTA](#) [Graphics](#)

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LOCUS XM\_015308845 1532 bp mRNA linear PLN 05-JAN-2016  
DEFINITION PREDICTED: Solanum tuberosum caffeic acid 3-O-methyltransferase (LOC102590869), mRNA.  
ACCESSION XM\_015308845  
VERSION XM\_015308845.1  
DBLINK BioProject: [PRJNA225997](#)  
KEYWORDS RefSeq.  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum  
Fikarynna; Vireidiplaneta; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; Gunnerales; Pentapetales; asterids; lamids; Solanales; Solanales; Solanoideae; Solanales; Solanales; Solanoideae; Solanales; Solanum.  
COMMENT MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from a genomic sequence ([HWI-085299181.1](#)) annotated using gene prediction method: Gnomon, supported by EST evidence.  
Also see: [Documentation of NCBI's Annotation Process](#)  
##Genome-Annotation-Data-START##  
Annotation Provider :: NCBI  
Annotation Status :: Full annotation  
Annotation Version :: Solanum tuberosum Annotation Release 103  
Annotation Pipeline :: NCBI eukaryotic genome annotation pipeline  
Annotation Software Version :: 5.5  
Annotation Method :: Best-placed RefSeq; Gnomon  
Features: Annotated  
:: Gene; mRNA; CDS; ncRNA  
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ORIGIN  
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1261 agattactt tttttctag tggatgaca tatgatgat tgatactt ttgaaataa  
1321 agaanatg cttttcatg gaagagatt atgtctaaa gggggaaa aagaatgaa  
1381 ataatgtt cagtgaaag ggaatgatt aatagaaq tttttgctt gattttgac  
1441 ttgatgtc taattctga atagatgt atgaaaga tcccaattc atcatatat  
1501 tctattgac ta

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**PREDICTED: caffeic acid 3-O-methyltransferase [Solanum tuberosum]**  
NCBI Reference Sequence: XP\_015164331.1  
[Identical Proteins](#) [FASTA](#) [Graphics](#)

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**LOCUS** XP\_015164331 363 aa linear PLN 05-JAN-2016  
**DEFINITION** PREDICTED: caffeic acid 3-O-methyltransferase [Solanum tuberosum].  
**ACCESSION** XP\_015164331  
**VERSION** XP\_015164331.1  
**DBLINK** BioProject: [PRJNA225997](#)  
**DBSOURCE** REFSEQ: accession [XM\\_015308845.1](#)  
**KEYWORDS** RefSeq.  
**SOURCE** Solanum tuberosum (potato)  
**ORGANISM** Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae; Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Solanoideae; Solaneae; Solanum.  
**COMMENT** **MODEL REFSEQ:** This record is predicted by automated computational analysis. This record is derived from a genomic sequence ([NW\\_006239018.1](#)) annotated using gene prediction method: Gnomon, supported by EST evidence.  
Also see: [Documentation of NCBI's Annotation Process](#)  
**##Genome-Annotation-Data-START##**  
Annotation Provider : NCBI  
Annotation Status : Full annotation  
Annotation Version : [Solanum tuberosum Annotation Release 101](#)  
Annotation Pipeline : NCBI eukaryotic genome annotation pipeline  
Annotation Software Version : [6.5](#)  
Annotation Method : Best-placed RefSeq; Gnomon  
Features Annotated : Gene; mRNA; CDS; ncRNA  
**##Genome-Annotation-Data-END##**  
**COMPLETES:** full length.

**FEATURES** Location/Qualifiers  
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/note="O-methyltransferase domain; pfam00891"  
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121 gvsvapllm ngdkvlmesv yhlkdvldg gipfkaygm tafeyhgtdp rfnkvfrngm  
181 sdhttslkk iledykgfeg lnsivdvvgg tigtvsmivs kypsikginf diphviedap  
241 pyppvehigg dmfvsvpkad aifmkwchd wsdehckflf kkyealpan gkvlieacll  
301 pevptstst kntvhdivm lahnpqgker tekefealak gagngfska ccayntwvme  
361 fsk  
//

**Articles about the LOC102590869 gene**  
TreeGrafter: phylogenetic tree-based annotation of proteins with Gene Onto [Bioinformatics, 2019]  
Manual GO annotation of predictive protein signatures: the InterPrc [Database (Oxford), 2012]  
[See all...](#)






**Reference sequence information**  
RefSeq mRNA  
See reference mRNA sequence for the LOC102590869 gene ([XM\\_015308845.1](#)).




**More about the gene LOC102590869**  
LOC102590869 gene

**Related information**  
[BioProject](#)  
[Nucleotide](#)  
[Taxonomy](#)  
[BioSystems](#)  
[CDD Search Results](#)  
[Conserved Domains \(Concise\)](#)  
[Conserved Domains \(Full\)](#)  
[Domain Relatives](#)  
[Encoding mRNA](#)  
[Full text in PMC](#)  
[Gene](#)  
[PubMed \(RefSeq\)](#)  
[PubMed \(Weighted\)](#)

**Recent activity**    
 PREDICTED: caffeic acid 3-O-methyltransferase [Solanum tuberosum] Protein  
 Monillophthora perniciosa strain FA553 cerato-platanin 12 (CP12) mRNA, c Nucleotide  
 cerato-platanin 12 [Monillophthora perniciosa] Protein  
 PREDICTED: Solanum tuberosum caffeic acid 3-O-methyltransferase Nucleotide  
[See more...](#)

**FOLLOW NCBI**

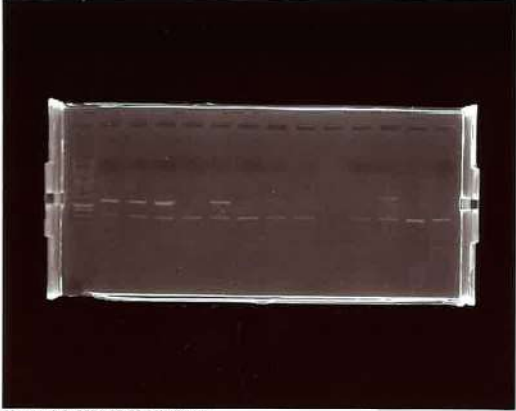
    

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### GE of tsPCR's

USDA-ARS-GIFVL      (Melatonin/COF-R?)      5/30-6/3/2024




Name: chris 2024-05-31 10h35m06s  
Acquired: 5/31/2024 10:35:06 AM  
Application: SYBR Safe

Friday, May 31<sup>st</sup>, 2024

1	2	3	4	5	6	7	8	9	10	11	12	13	14	
L	COF-R?							NC	PC	Pos				
1kb								Bint <sub>3e</sub>	COF-F					

COF-R? (✓)

---



Name: chris 2024-06-03 08h45m12s  
Acquired: 6/3/2024 8:45:12 AM  
Application: SYBR Safe

Monday, June 3<sup>rd</sup>, 2024

1	2	3	4	5	6	7	8	9	10	11	12	13	14	
L	COF-R?							PC	NC	Kanamycin				
1kb								COF-F	Bint <sub>3e</sub>					

COF-R? (✓)

**COF-R?**



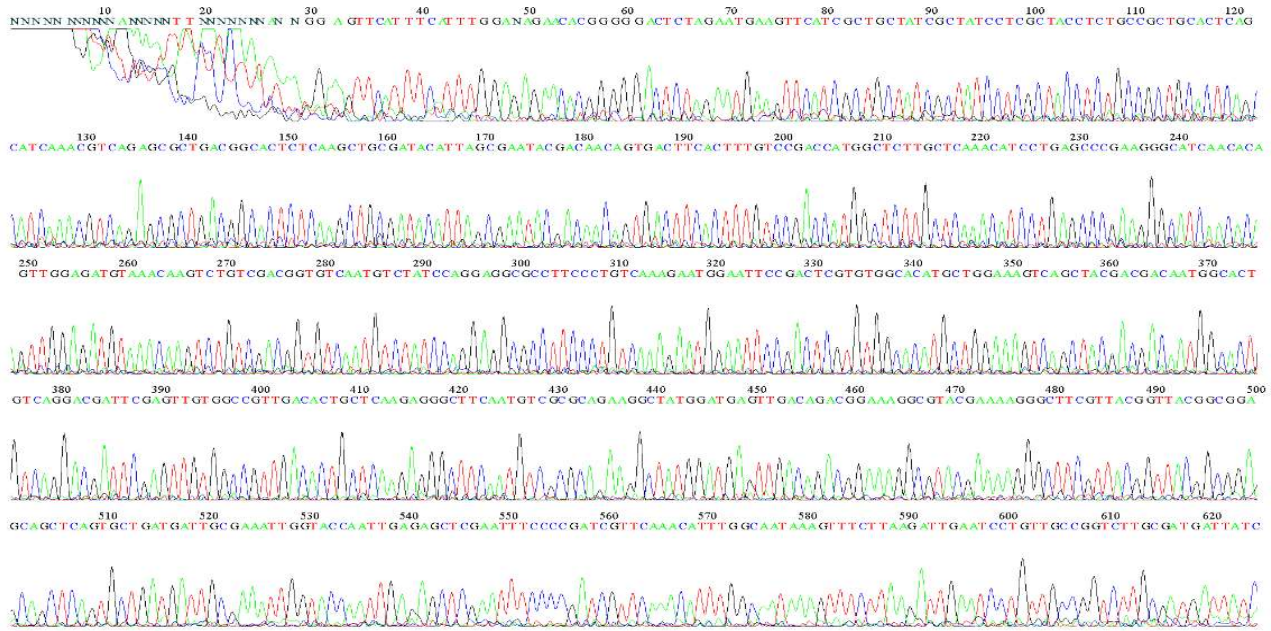
**COF-F**



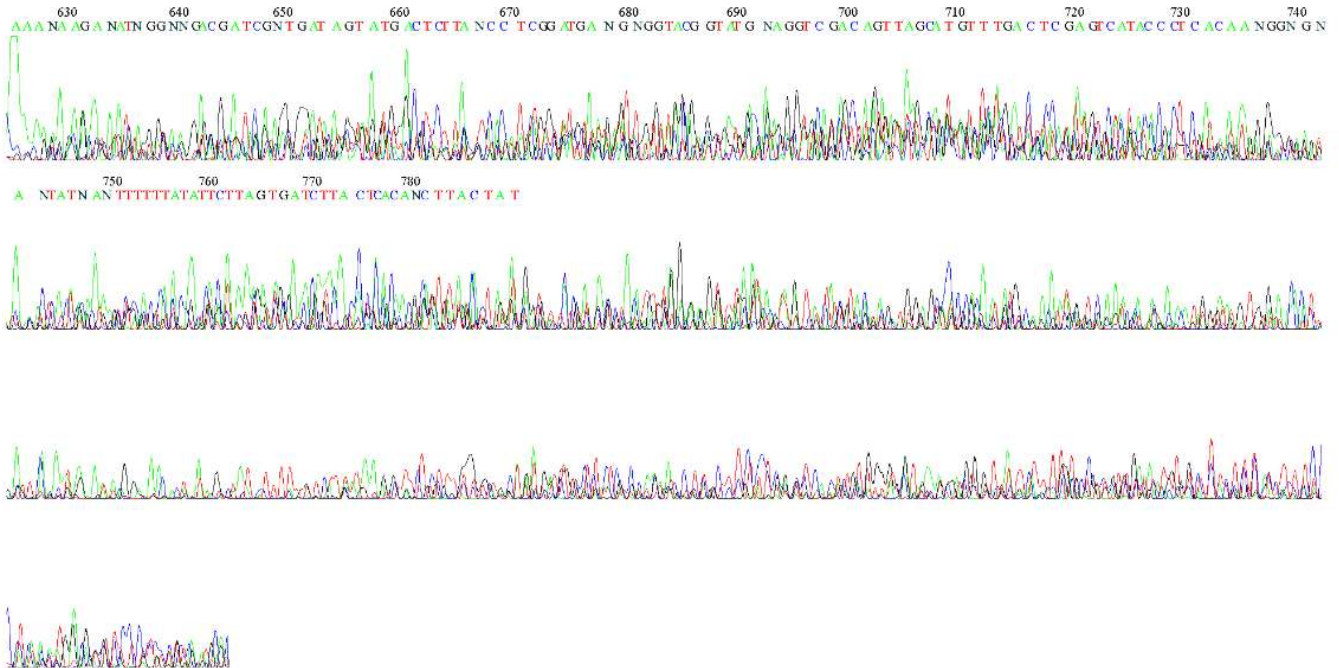


226EZA175\_Psomagen\_Sequencing

File: 226EZA175\_premix.ab1 Run Ended: 2024-06-06 03:54:08 Signal G:92 A:93 C:88 T:78  
Sample: 226EZA175\_premix Lane: 76 Base spacing: 15.4030695 789 bases in 12253 scans Page 1 of 2



File: 226EZA175\_premix.ab1 Run Ended: 2024-06-06 03:54:08 Signal G:92 A:93 C:88 T:78  
Sample: 226EZA175\_premix Lane: 76 Base spacing: 15.4030695 789 bases in 12253 scans Page 2 of 2





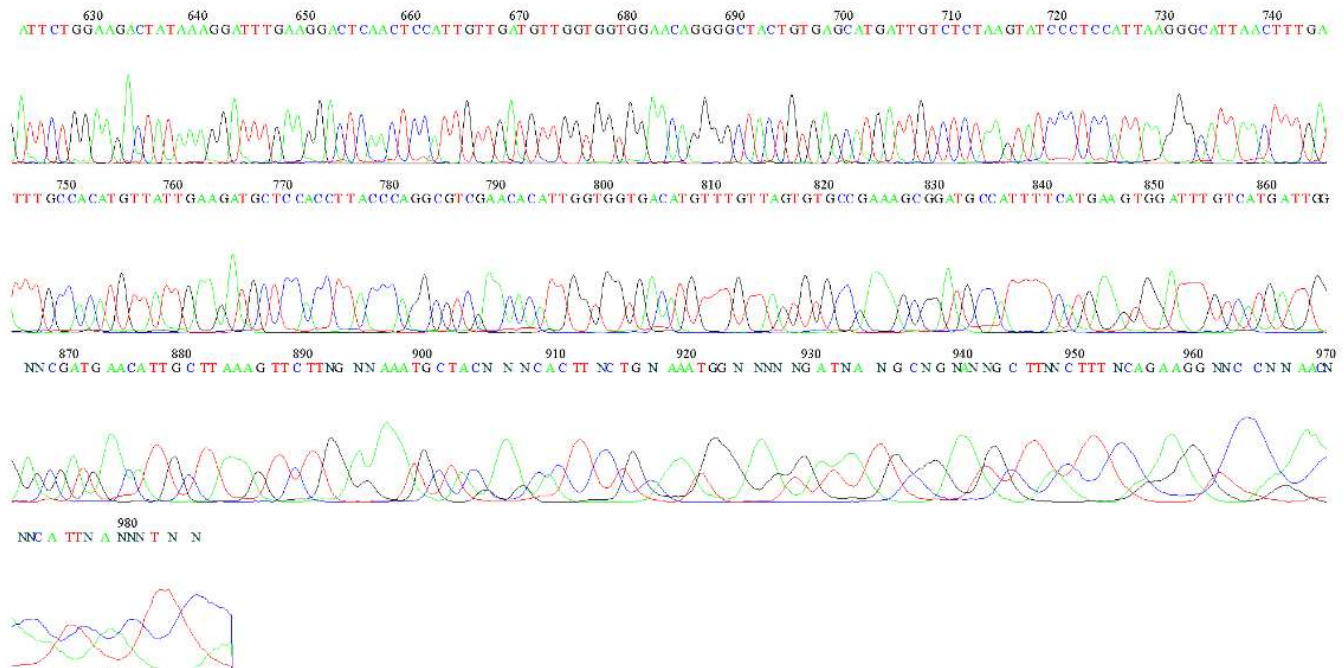


226EZAA199\_Psomagen Sequencing

File: 226EZAA199\_premitx.ab1 Run Ended: 2024-06-06 03:54:08 Signal G:3161 A:3024 C:2407 T:2677
Sample: 226EZAA199\_premitx Lane: 80 Base spacing: 15.673494 985 bases in 12252 scans Page 1 of 2



File: 226EZAA199\_premitx.ab1 Run Ended: 2024-06-06 03:54:08 Signal G:3161 A:3024 C:2407 T:2677
Sample: 226EZAA199\_premitx Lane: 80 Base spacing: 15.673494 985 bases in 12252 scans Page 2 of 2







226EZA176\_DNA5\_Analyze

USDA-ARS-GIFVL Melatonin\_COF-R?\_226EZA176 June 7th, 2024

Firefox

https://ccblimsdb.mgh.harvard.edu:8443/

Map created [here](#). Editor [here](#). Show/Hide:

Title Features Sequence > 3 Sites Edit Mode Diagram Data Encrypt

LOCUS % undefined 273 bp DNA linear SYN 07-JUN-2024

DEFINITION Linear element, undefined.

ACCESSION

VERSION

KEYWORDS

SOURCE Synthetic construct

ORGANISM synthetic construct

FEATURES

source Location/Qualifiers 637 ORF

1..273

CDS /note="open reading frame 1"

1..>273

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/data\_label="orf 1"

/translation="MKETAAEAILATSAAALSIRKQSDAGTLKLRVISEYDINSOFTLSMHGSCSNILSPRGINTVGDVNIKSDGVNVVYGGAFVPKENSDSCET"

ORIGIN

1 ATGAAGTTCATCGCTGCTATCGCTATCCTCGCTACCTCTCGCGCTGCACCTCAGCATCAAAGCTCAGAGCGCTGACGGCAGCTCTCAAGCTCGCATACATTA

61 CGTCAGAGCG CTGACGGCAC TCTCAAGCTG CGATACATTA GCGAATAGCA CAACAGTGAC

121 TTCACCTTGT CCGACCATGG CTCTTGCTCA AACATCTGGA GCCCGAAGGG CATCAACACA

181 GTTGGAGATG TAAACAAGTC TGTCGACGGT GTCAACTGCT ATCCAGGAGG CGCCTCCCT

241 GTCAAAGAAI GGMATTCGCA CTCGGTGGC ACA

ORF 1; ALL, RC

No In De Re Fr Sh Bu Dn M; Id

w/ In Sen To Nu AI

(BLASTn) = monilophthora perniciosa

Cerato-platonia

[BLASTP] = Cerato-platonia 12

MFICGT [monilophthora perniciosa]

sh in FASS

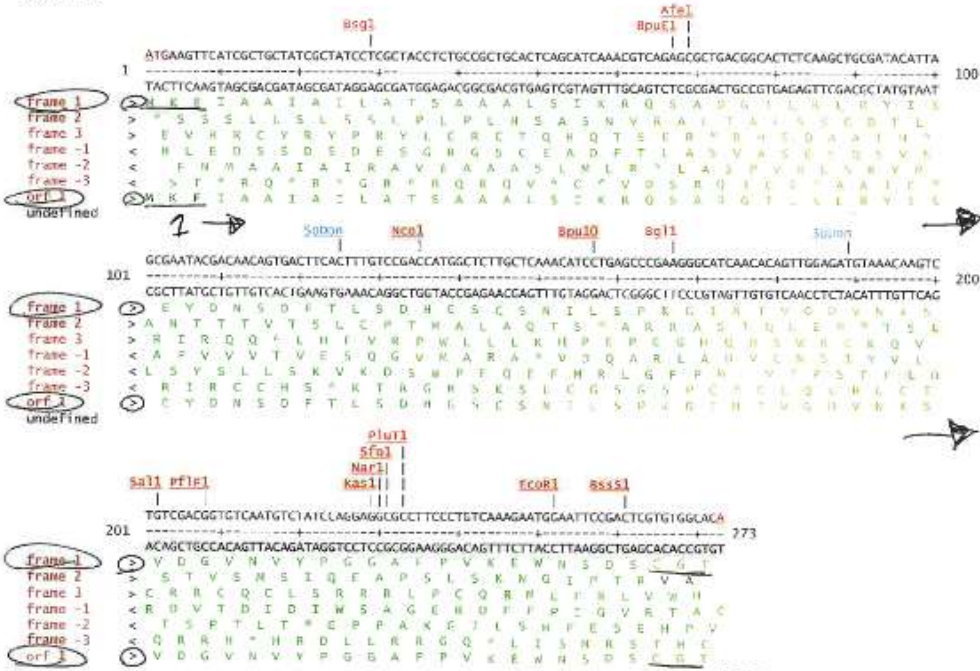
MEVA

Sy De Re Pr - Ca Ag Of Wi Br Pi

//

\*\*\* Sites protected by E. coli methylation are not shown in this map. \*\*\*

undefined



Found

AfeI BspI BpuE1 BpuE1 BspI BssS1 SmaI EcoR1 KasI NarI NcoI PflE1 PfuI Sall

SfiI SspI

Unique





**To Be  
Continued ...**