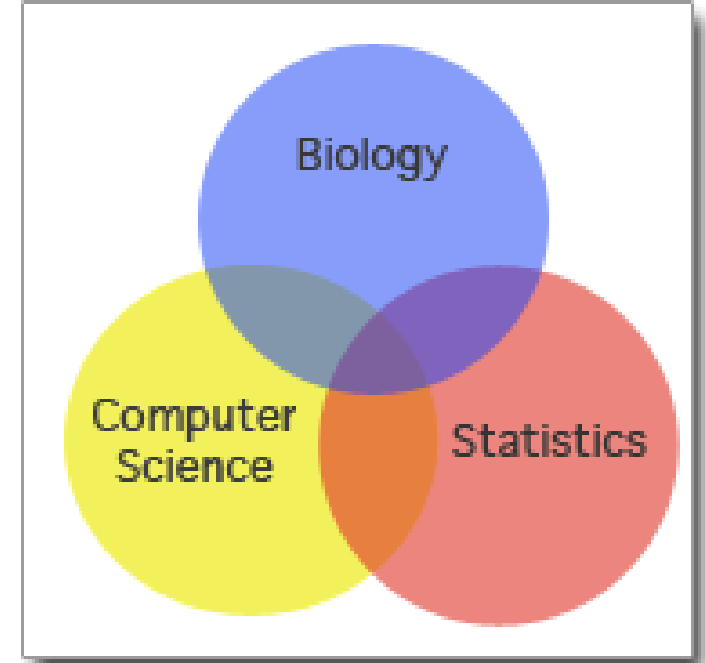


# Biyoinformatik

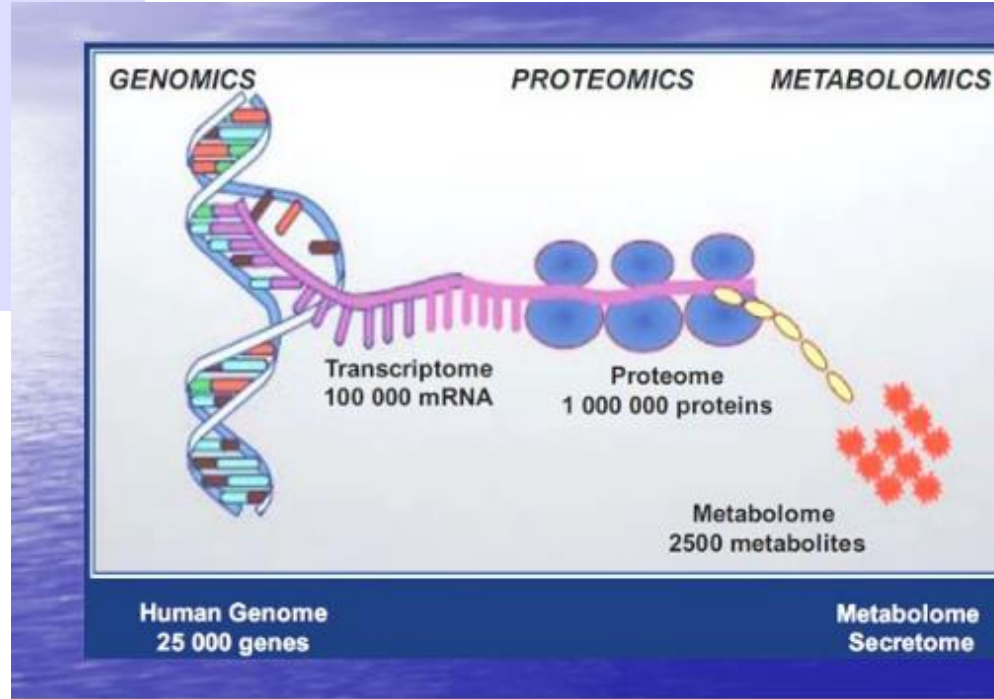
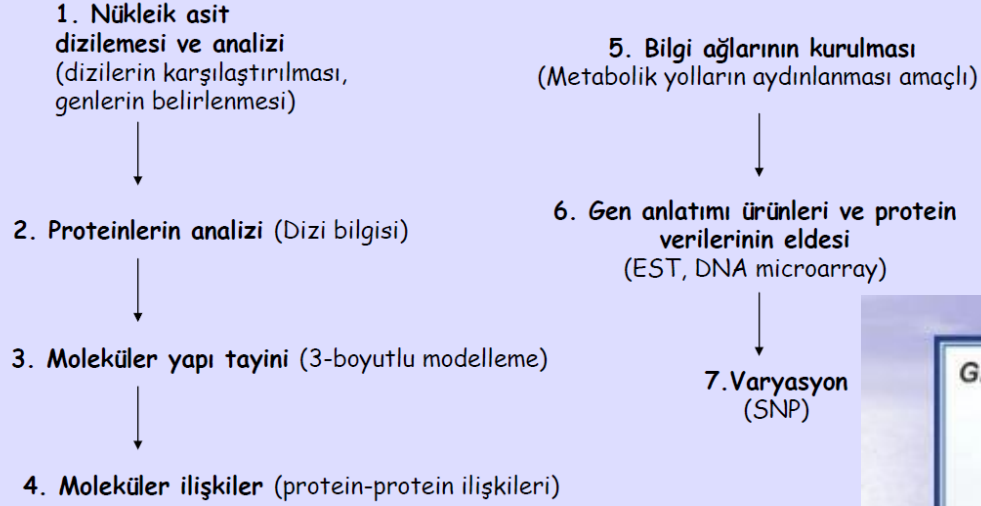
- Biyolojik bilginin bilgisayar yardımı ile incelenmesi ve işlenmesidir.
- Biyoinformatik biliminin işlediği veri tipi çoğunlukla genetik veri ve buna bağlı gen ifadesidir.

- Molecular biology
- Genomics
- Functional genomics
- Systems biology
- Protein design and engineering
- Pharmaceutical development
- Medicine
- Ecology / population genetic



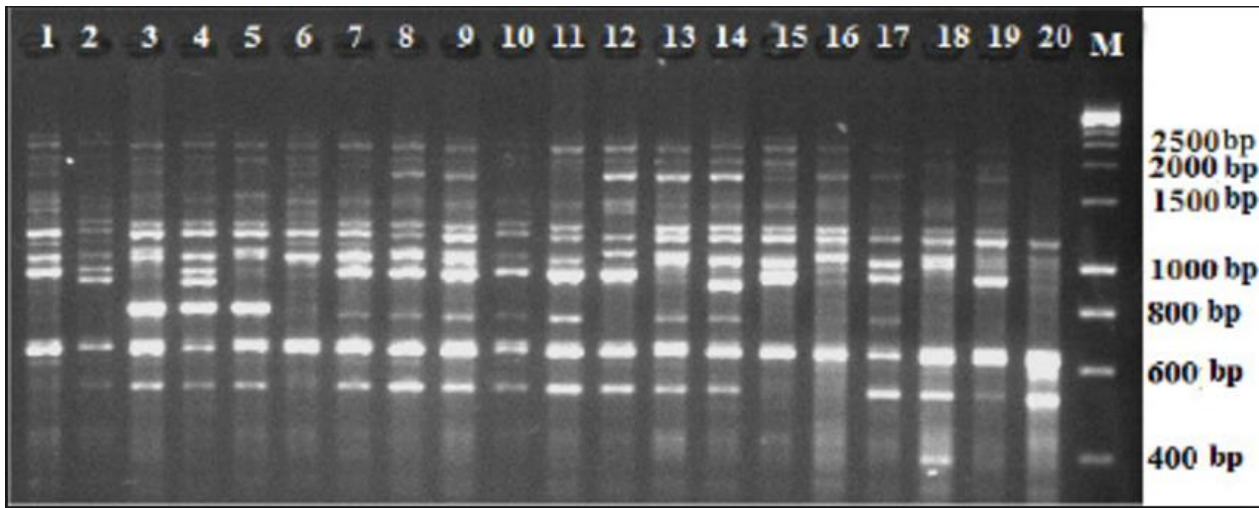
- Morfolojik, fenotipik ve genotipik özelliklerinin belirlenmesi,
- Popülasyon biyolojilerinin araştırılması,
- Dayanıklılık kaynaklarının belirlenmesi
- Konukçu-etmen ilişkilerinin belirlenmesi
- Bunlara bağılı olarak korunma ve mücadele yöntemlerinin geliştirilmesi

# Biyoinformatik (Bilgi Akışı)



Genomics → Transcriptomics → Proteomics  
→ Metabolomics → Functional Phenotype

- Metabolomik; Genomik ve Proteomik alanlarından gelişen bir daldır.
- Genomik; DNA zincirindeki bilgilerin analizi,
- Proteomik; proteinlerin analizi



**Parts of a phylogenetic tree**

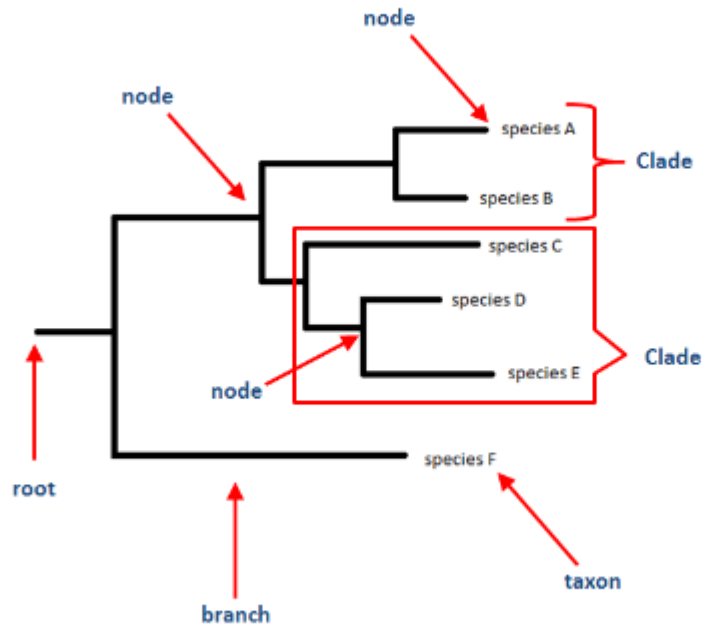
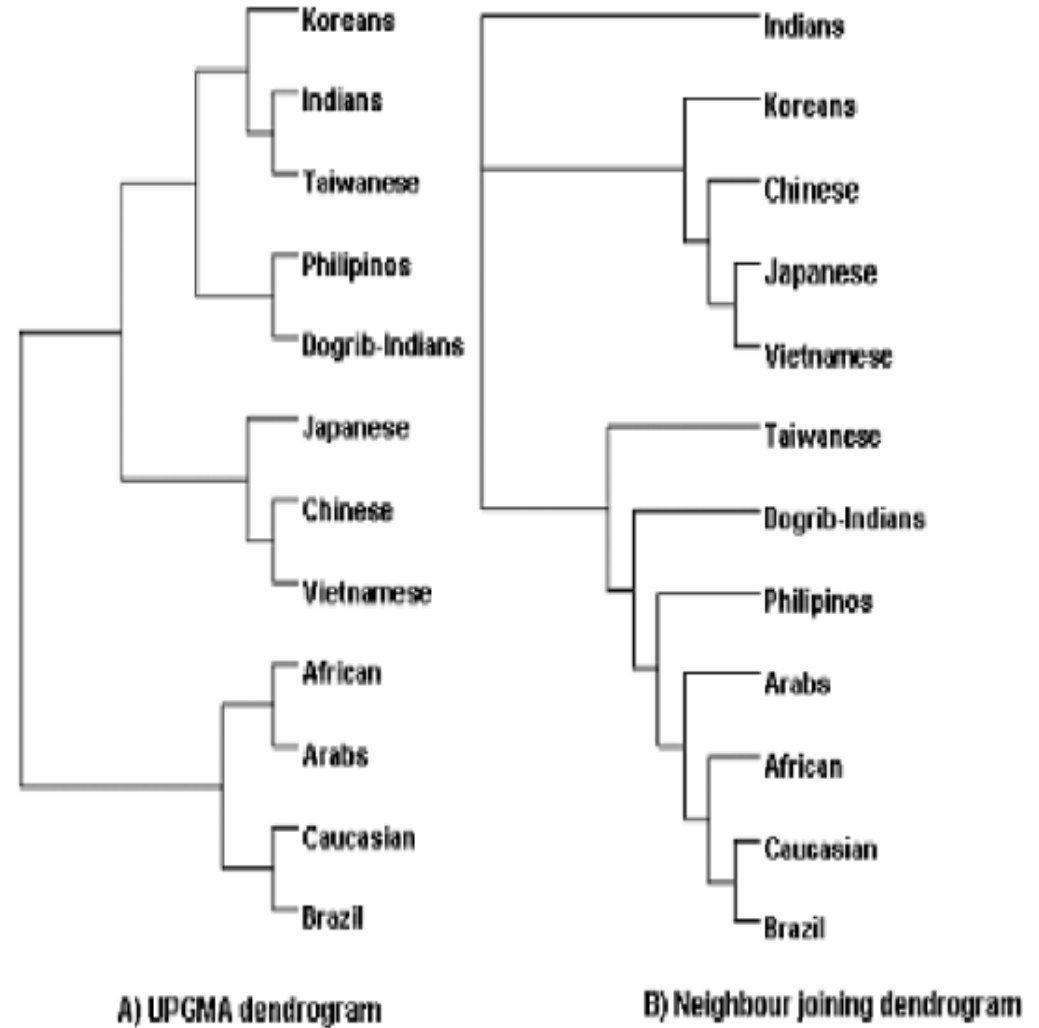


Figure 6.4: Parts of a phylogenetic tree



- NCBI ("The National Center for Biotechnology Information")
  - <http://www.ncbi.nlm.nih.gov/>
- SwissProt/ExPASy ("Swiss Bioinformatics Resource")
  - <http://expasy.cbr.nrc.ca/sprot/>
- EBI ("The European Bioinformatics Institute")
  - <http://www.ebi.ac.uk/>
- "The Canadian Bioinformatics Resource"
  - <http://www.cbr.nrc.ca/>
- PDB ("The Protein Databank")
  - <http://www.rcsb.org/PDB/>

Nucleotide

Nucleotide

Search

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## Nucleotide

The Nucleotide database is a collection of sequences from several sources, including GenBank, RefSeq, TPA and PDB. Genome, gene and transcript sequence data provide the foundation for biomedical research and discovery.

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[INSDC](#)

You are here: NCBI > DNA & RNA > Nucleotide Database

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- [PubChem](#)

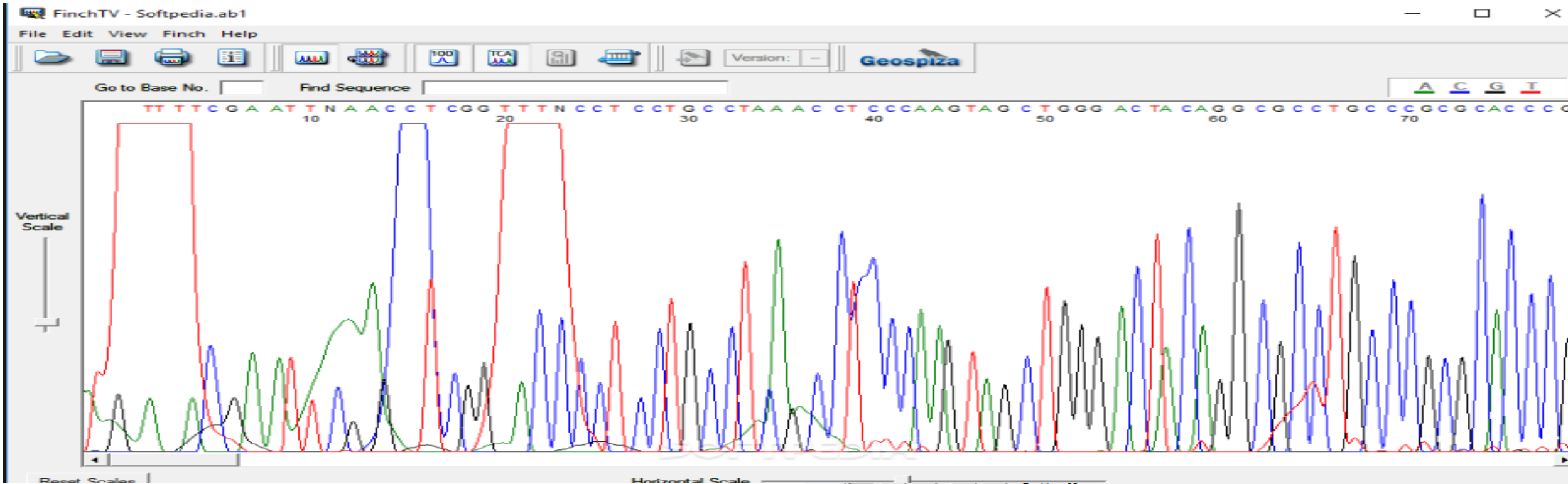
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Triplet Sequence Document Header Sequence Indicator

Document Header Sequence Indicator

Sequence Pane

Comments Pane

Features Pane

Pane Dividers

**tetris21.seq : SEQUENCE**

Position: 1 906 bp

```

aatttggttaattaagccccaatagataaataataaataa 40
attatccaatttaaaaaataaattatccaatcagaacgcag 80
aaaaagaagattatccaatcagatgcttttttaatagaag 120
atcacagataactggaagagatagaaaaaaagaaaaggata 160
atgcagaaaaaaatcataattttaatcaaaaaatataaatt 200

```

LOCUS	TETHIS21MA	906 bp	DNA
DEFINITION	T.thermophila macronuclear histone H2B-1		
ACCESSION	M31332		
VERSION	M31332.1 GI:161783		

source 1..906

/organism="Tetrahymena thermophila"

/mol\_type=genomic DNA

Unspecified Search

ATC

Position: 36 Working Pair "Pair 1" Forward: Length=23 bp, Tm=53.7°C, Reverse: Length=23 bp, Tm=46.1°C

5' ggggtaccctgactcttatacacaagtagcgtcctgaacggaaacctttcccggtttccaggatc

3' ccccatgggactgagaatagtgttccatcgcaggacttgccctggaaagggcaaaaggtcctag

1 G V P . L L Y T S S V L N G T F P V F Q D

2 P G P L Y T S S V

2 G Y P D S Y T Q V A S . T E P F P F S R I

3 R G T L T L I H K . R P E R N L S R F P G S

3 P A L I H K . R

S1 Pair 1 Forward

Nucleotide

Nucleotide

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GenBank

Send to:

Change region shown

Customize view

## Fusarium oxysporum strain Fo1502 beta-tubulin gene, partial cds

GenBank: AY714094.1

[FASTA](#) [Graphics](#) [PopSet](#)

Go to:

LOCUS AY714094 405 bp DNA linear PLN 26-JUL-2016  
 DEFINITION Fusarium oxysporum strain Fo1502 beta-tubulin gene, partial cds.  
 ACCESSION AY714094  
 VERSION AY714094.1  
 KEYWORDS .  
 SOURCE Fusarium oxysporum  
 ORGANISM *Fusarium oxysporum*  
 Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;  
 Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae;  
 Fusarium; Fusarium oxysporum species complex.

REFERENCE 1 (bases 1 to 405)  
 AUTHORS Kim,Y., Hutmacher,R.B. and Davis,R.M.  
 TITLE Characterization of California isolates of *Fusarium oxysporum* f.  
 sp. vasinfectum  
 JOURNAL Plant Dis. 89, 366-372 (2005)

REFERENCE 2 (bases 1 to 405)  
 AUTHORS Kim,Y., Hutmacher,R.B. and Davis,R.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-AUG-2004) Plant Pathology, UC Davis, One Shields  
 Ave., Davis, CA 95616, USA

FEATURES  
 source Location/Qualifiers  
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 /organism="Fusarium oxysporum"  
 /mol\_type="genomic DNA"  
 /strain="Fo1502"  
 /specimen\_voucher="RMD 1502 PP"  
 /db\_xref="taxon:5507"

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 /product="beta-tubulin"

CDS complement(join(<1..255,303..>405))  
 /codon\_start=2  
 /product="beta-tubulin"  
 /protein\_id="AAU15035.1"  
 /translation="FWQTIISGEHGLDSNGVYNGTSELQLERMSVYFNEASGNKYVPRP  
 VLVLDLEPGTMDAVRAGPFGQLFRPDNFVFGQSGAGNNWAKGHYTEGAELVDQVLDVVR  
 REAEGDCCLQGFIITHS"

ORIGIN

```

1 agagtgggtg atttgaaac cctggaggca atcgcagccc tcggcctcac ggccgacgac
61 gtcgaggacc tggtcgacaa gttcggcacc ctctgtgtag tgacccttgg cccagttggt
121 tccagcaccg gactgaccga aaacaaagt gtcgggacgg aagagctgac cgaagggacc
181 agcacggacg gcgtccatgg taccaggctc aagatcgacg aggacggctc gaggaacata
241 cttgttgcca gaggcctagt tgtgtgagct tgggtttctt gacattgact gtcaatacat
301 acctcgttga agtagacact catgcgctc agctggagct cggagggtacc gttgtagaca
361 ccattgctgt cgaggccgtg ctgccagag atggtctgcc agaaa

```

//

### Analyze this sequence

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Protein

Taxonomy

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-  Fusarium oxysporum strain Fo1502 beta-tubulin gene, partial cds Nucleotide
-  fusarium oxysporum (215268) Nucleotide
-  Fusarium proliferatum FDB2 gene cluster, complete sequence Nucleotide
-  fusarium (534428) Nucleotide
-  Acquisition of Resistance to Sterol Demethylation Inhibitors by Populatio PubMed

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**BLAST Results**

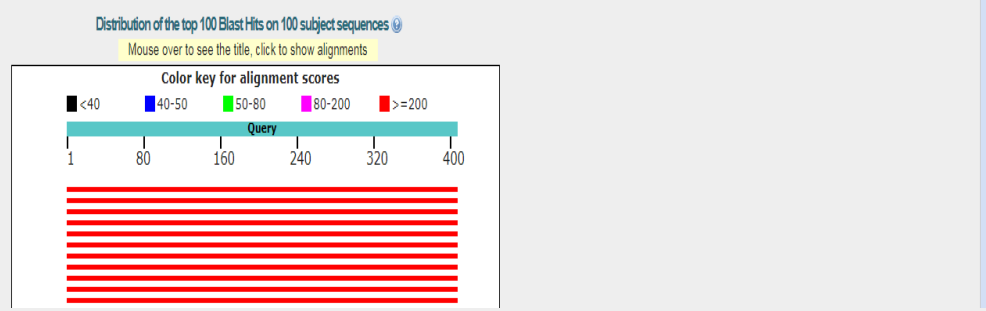
[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#) [YouTube](#) [How to read this page](#) [Blast report description](#)

**Job title: Nucleotide Sequence (405 letters)**

<b>RID</b> <a href="#">0V33JJNX015</a> (Expires on 11-17 20:02 pm)	<b>Database Name</b> nr
<b>Query ID</b> lc Query_53365	<b>Description</b> Nucleotide collection (nt)
<b>Description</b> None	<b>Program</b> BLASTN 2.7.1+ <a href="#">Citation</a>
<b>Molecule type</b> nucleic acid	
<b>Query Length</b> 405	

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [MSA viewer](#)

**Graphic Summary**



**Sequences producing significant alignments:**

Select: [All](#) [None](#) Selected: 0

Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> <a href="#">Fusarium oxysporum isolate Oe30 TUB gene, partial sequence; and beta-tubulin gene, partial cds</a>	749	749	100%	0.0	100%	<a href="#">KU863572.1</a>
<input type="checkbox"/> <a href="#">Fusarium redolens isolate NI-96 beta-tubulin gene, partial cds</a>	749	749	100%	0.0	100%	<a href="#">KP964925.1</a>
<input type="checkbox"/> <a href="#">Fusarium redolens isolate M119 beta-tubulin (TUB2) gene, partial cds</a>	749	749	100%	0.0	100%	<a href="#">KP710629.1</a>
<input checked="" type="checkbox"/> <a href="#">Fusarium redolens isolate M72 beta-tubulin (TUB2) gene, partial cds</a>	749	749	100%	0.0	100%	<a href="#">KP674300.1</a>
<input type="checkbox"/> <a href="#">Fusarium redolens isolate Ch45 beta-tubulin (TUB2) gene, partial cds</a>	749	749	100%	0.0	100%	<a href="#">KP674294.1</a>
<input type="checkbox"/> <a href="#">Fusarium redolens isolate Ch23 beta-tubulin (TUB2) gene, partial cds</a>	749	749	100%	0.0	100%	<a href="#">KP674290.1</a>
<input type="checkbox"/> <a href="#">Fusarium redolens isolate Z318 beta-tubulin (TUB2) gene, partial cds</a>	749	749	100%	0.0	100%	<a href="#">KP674235.1</a>
<input type="checkbox"/> <a href="#">Fusarium redolens strain FF-00411 beta-tubulin gene, partial cds</a>	749	749	100%	0.0	100%	<a href="#">KJ572783.1</a>
<input type="checkbox"/> <a href="#">Fusarium oxysporum strain Fo1502 beta-tubulin gene, partial cds</a>	749	749	100%	0.0	100%	<a href="#">AY714084.1</a>
<input type="checkbox"/> <a href="#">Fusarium hostae strain NRRL 29642 beta-tubulin (TUB2) gene, partial cds</a>	743	743	100%	0.0	99%	<a href="#">KF466440.1</a>
<input type="checkbox"/> <a href="#">Fusarium oxysporum f. sp. vasinfectum strain CN8 beta-tubulin gene, partial cds</a>	704	704	100%	0.0	98%	<a href="#">KP175330.1</a>
<input type="checkbox"/> <a href="#">Fusarium oxysporum f. sp. vasinfectum strain AUST19 beta-tubulin gene, partial cds</a>	704	704	100%	0.0	98%	<a href="#">AV714083.1</a>
<input type="checkbox"/> <a href="#">Fusarium cf. oxysporum AMP-2017a strain GL1802 beta-tubulin gene, partial cds</a>	699	699	100%	0.0	98%	<a href="#">KY563166.1</a>
<input type="checkbox"/> <a href="#">Fusarium cf. oxysporum AMP-2017a strain GL1314 beta-tubulin gene, partial cds</a>	699	699	100%	0.0	98%	<a href="#">KY508660.1</a>
<input type="checkbox"/> <a href="#">Fusarium cf. oxysporum AMP-2017a strain GL1313 beta-tubulin gene, partial cds</a>	699	699	100%	0.0	98%	<a href="#">KY508659.1</a>
<input type="checkbox"/> <a href="#">Fusarium cf. oxysporum AMP-2017a strain GL1312 beta-tubulin gene, partial cds</a>	699	699	100%	0.0	98%	<a href="#">KY508658.1</a>
<input type="checkbox"/> <a href="#">Fusarium cf. oxysporum AMP-2017a strain GL1518 beta-tubulin gene, partial cds</a>	699	699	100%	0.0	98%	<a href="#">KY508657.1</a>
<input type="checkbox"/> <a href="#">Fusarium cf. oxysporum AMP-2017a strain GL1516 beta-tubulin gene, partial cds</a>	699	699	100%	0.0	98%	<a href="#">KY508656.1</a>
<input type="checkbox"/> <a href="#">Fusarium cf. oxysporum AMP-2017a strain GL1300 beta-tubulin gene, partial cds</a>	699	699	100%	0.0	98%	<a href="#">KY508655.1</a>
<input type="checkbox"/> <a href="#">Fusarium cf. oxysporum AMP-2017a strain GL1311 beta-tubulin gene, partial cds</a>	699	699	100%	0.0	98%	<a href="#">KY498497.1</a>
<input type="checkbox"/> <a href="#">Fusarium cf. oxysporum AMP-2017a strain GL1787 beta-tubulin gene, partial cds</a>	699	699	100%	0.0	98%	<a href="#">KY498496.1</a>
<input type="checkbox"/> <a href="#">Fusarium cf. oxysporum AMP-2017a strain GL1704 beta-tubulin gene, partial cds</a>	699	699	100%	0.0	98%	<a href="#">KY498495.1</a>

**Fusarium oxysporum isolate Oe30 TUB gene, partial sequence; and beta-tubulin gene, partial cds**  
 Sequence ID: [KU863572.1](#) Length: 405 Number of Matches: 1

**Range 1: 1 to 405** [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
749 bits(405)	0.0	405/405(100%)	0/405(0%)	Plus/Minus
Query 1	AGAGTGGGTGATTTGGAAACCTTGGAGGCAATCGCAGCCCTCGGCCACGGCCGGACGAC	60		
Sbjct 405	AGAGTGGGTGATTTGGAAACCTTGGAGGCAATCGCAGCCCTCGGCCACGGCCGGACGAC	346		
Query 61	GTCGAGGACCTGGTCGACAAGTTGGGACCCTCTGTGTAGTGACCCTTGGCCAGTTGTT	120		
Sbjct 345	GTCGAGGACCTGGTCGACAAGTTGGGACCCTCTGTGTAGTGACCCTTGGCCAGTTGTT	286		
Query 121	TCCAGCACC GGACTGACCGAAAACAAAGTTGTCGGGACGGAAGAGCTGACCGAAGGGACC	180		
Sbjct 285	TCCAGCACC GGACTGACCGAAAACAAAGTTGTCGGGACGGAAGAGCTGACCGAAGGGACC	226		
Query 181	AGCACGGACGGCGTCCATGGTACCAGGCTCAAGATCGACGAGGACGGCTCGAGGAACATA	240		
Sbjct 225	AGCACGGACGGCGTCCATGGTACCAGGCTCAAGATCGACGAGGACGGCTCGAGGAACATA	166		
Query 241	CTTGTGGCCAGAGGCCCTAGTTGTGTGAGCTTGGGTTCTTGACATTGACTGTCAATACAT	300		
Sbjct 165	CTTGTGGCCAGAGGCCCTAGTTGTGTGAGCTTGGGTTCTTGACATTGACTGTCAATACAT	106		
Query 301	ACCTCGTTGAAGTAGACTCATGCGCTCGAGCTGGAGCTCGGAGGTACCGTTGTAGACA	360		
Sbjct 105	ACCTCGTTGAAGTAGACTCATGCGCTCGAGCTGGAGCTCGGAGGTACCGTTGTAGACA	46		
Query 361	CCATTGCTGTCGAGGCCGTGCTCGCCAGAGATGGTCTGCCAGAAA 405			
Sbjct 45	CCATTGCTGTCGAGGCCGTGCTCGCCAGAGATGGTCTGCCAGAAA 1			

[Reset Tree](#)

BLAST RID [OV3311NX015](#)

Query ID [Id|Query\\_53365](#)

Database [nr](#)

Tree method: Neighbor Joining  
Max Seq Difference: 0.75  
Sequence Label: Taxonomic Name (if av)

Mouse over an internal node for a subtree or alignment. Click on tree label to select sequence to download

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Find:  all

Tools Upload ?

Label color map

Query  
From type material

Blast names color map

Unknown  
Ascomycetes



Primer-Blast results

https://www.ncbi.nlm.nih.gov/tools/primer-blast/primerblast.cgi

Primer-BLAST

NCBI/Primer-BLAST : results: Job id=0dsOv3P0fXZZu5J4wPKUZKY22O0C8B-tQ

Input PCR template: X65215.1 B.taurus microsatellite DNA (624bp)  
Range: 1 - 624  
Specificity of primers: primer specificity was not determined as specificity checking option was not selected.  
Other reports: [Search Summary](#)

### Graphical view of primer pairs

### Detailed primer reports

**Primer pair 1**

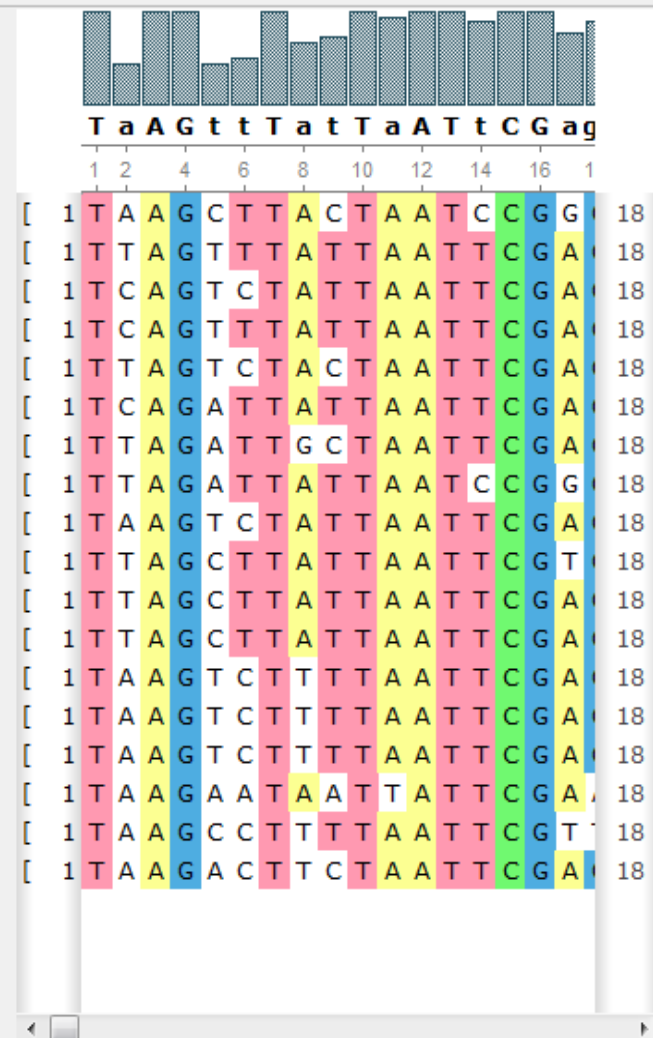
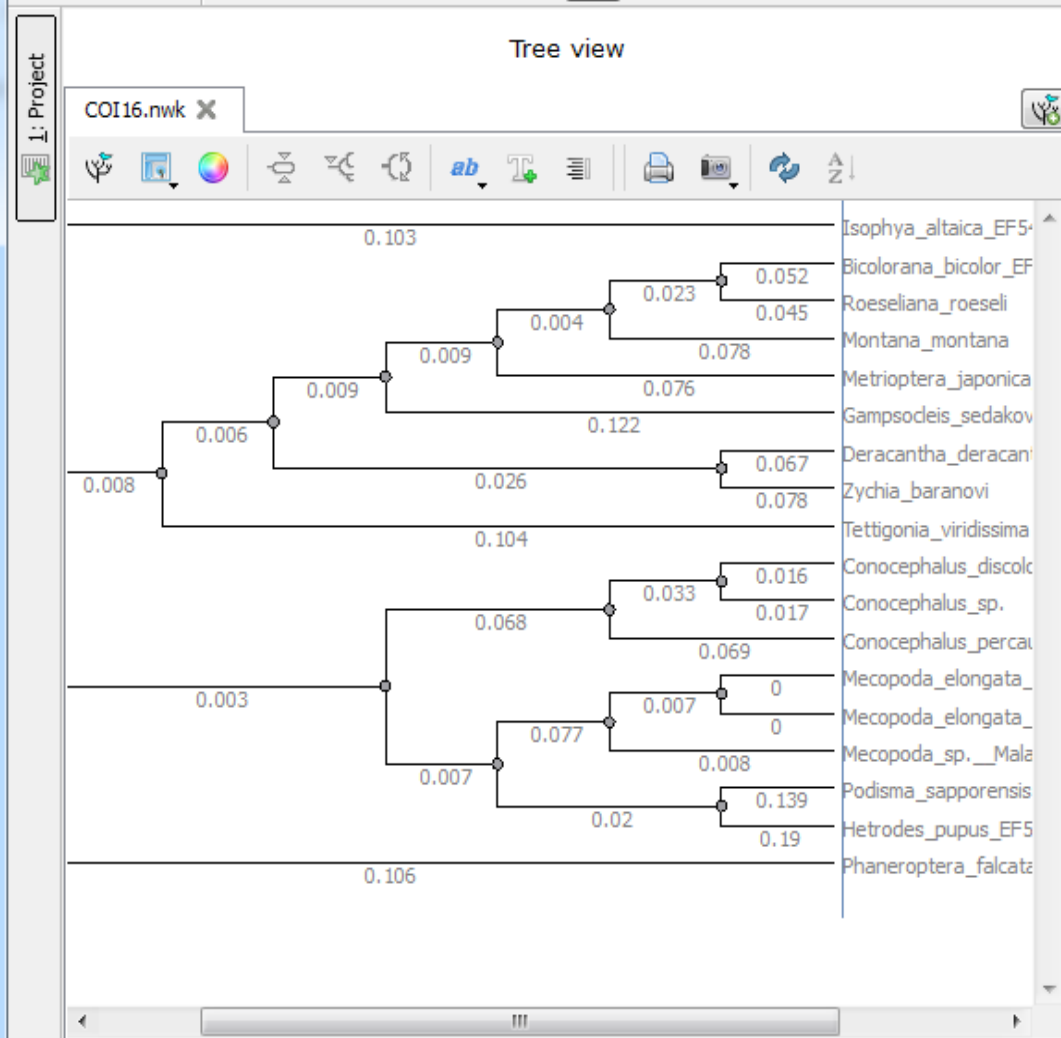
	Sequence (5'->3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	GCATTGGAAGGTGGCTAGGT	Plus	20	176	195	60.03	55.00	4.00	0.00
Reverse primer	AGCCCTACCAGGCTCTCATCA	Minus	20	337	318	60.03	55.00	7.00	2.00
Product length	162								

**Primer pair 2**

	Sequence (5'->3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	CGGACATGACTGAGCGACTT	Plus	20	362	381	60.11	55.00	4.00	0.00
Reverse primer	TCTCTGCGACCCCATAGACA	Minus	20	502	483	60.03	55.00	6.00	0.00
Product length	141								

**Primer pair 3**





Tree Settings

General

Tree layout: Rectangular

Tree view: Default

Labels

Show names

Show distances

Show node labels

Align labels

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Scale Bar

Scale range: 0.011

Font size: 8

Line width: 1

Branches

Width:

Height:

[Show pen settings](#)

Help

Find:  Ln 1 / 18 Col 1 / 604 Pos 1 / 601



**Views**

- Sequen
- Feature
- Comm
- Linear
- Circular
- Primer
- Primer
- Minima
- Site Sur
- Cloning
- Enzymes Displ
- Features Displ
- Ruler

**Position: 1**  
**Magnification: 0.9x**  
**7249 bp**

**M13mp18**  
**7249 bp**

**misc\_feature** 7249..7249  
 /note = 1. M13mp10 7244bp, MCS 2. oligo SphI-KpnI 12bp gcatcggtacc-> M13mp18 7249bp

**Choose the cloning region:**

**rfc.1 verB**  
 1714 bp

Left Cut: **None**

Right Cut: **None**

Choose the cloning region:

**None**

- BsrGI (1021) - TGTACIA
- BspHI (1299) - TCATGIA
- PacI (4136) - TTAATATA
- ApaLI (4743) - GTGCAIC
- NgoMIV (5613) - GTCGGIC
- BsrFI (5613) - RCGGIC
- NgoMIV (5613) - GTCGGIC

**General Description**

**Standard Fields**

**Author**  
 Sharon Wilhovsky  
 EMAIL: Sharon.Wilhovsky@imvirogen.com

**Comments**

**Annotations**

- Feature Map**
- CDS (2 total)**
- Cm(R)**  
 Start: 239 End: 919  
 Original Location Description: 239..919
- ccdB**  
 Start: 1239 End: 1544  
 Original Location Description: 1239..1544
- Primer (2 total)**
- Primer 1**  
 Start: 165 End: 187  
 Recommended reverse primer  
 Original Location Description: 165..187
- Primer 2**

```

1  ATCAAACAAG TTTGTACAAA AAAGCTGAAC GAGAAAAGTA AAATGATATA AATATCAATA TATTAATTA GATTTTGCAT AAAAAACAGA CTACATAATA
101 TAGTTTGTTC AAACATGTTT TTTCGACTGG CTCTTTGCAT TTACTATAT TTATAGTTAT ATAATTTAAAT CTA AAAACGTA TTTTGTCT GATGTATTAT
201 BspHI
AGGATCCGTC GAGATTTTCA GGAGCTAAGG AAGCTAAAT GGAGAAAAAA ATCACTGGAT ATACCACGT TGATATATCC CAATGGCATC GTAAGAACA
TCCTAGGCAG CTCTAAAGAT CCTCGATCC TTCGATTTA CCTTTTTT TAGTGACCTA TATGGTGGCA ACTATATAGG GTTACCGTAG CATTTCTTGT
AAAGACCG TAAGAAAAA TAAGACAAG
TTTCTGCG ATTCTTTTT ATTCTGTTTC
  
```

T7 promoter primer #69348-3

pET upstream primer #69214-3

**T7 promoter** → **lac operator** → **XbaI** → **rbs**

**NcoI** → **His\*Tag** → **NdeI** → **NheI** → **T7\*Tag**

AGATCTCGATCCCGCAAATAATACGACTCACATAGGGGAATTGTGAGCGGATAACAATTCCTCTAGAAAATAATTTGTTAACTTAAAGAAGGAGA

TATACCATGGGCAGCAGCCATCATCATCACAGCAGCGGCCCTGGTCCGCGCGCAGCCATATGGCTAGCATGACTGGTGGACAGCAA  
 MetGlySerSerHisHisHisHisHisHisSerSerGlyLeuValProArgGlySerHisMetAlaSerMetThrGlyGlyGlnGln

**thrombin**  
**His\*Tag**

ATGGGTCGGGATCCGAATTCGAGCTCCGTCGACAAGCTTGGCGCCGACTCGAGCACCACCACCACCAGCTGAGATCCGGTGCTAACAAAGCCC pET-28a (+)  
 MetGlyArgGlySerGluPheGluLeuArgArgGlnAlaIcysGlyArgThrArgAlaProProProProLeuArgSerGlyCysEnd

...GGTCGGGATCCGAATTCGAGCTCCGTCGACAAGCTTGGCGCCGACTCGAGCACCACCACCACCAGCTGAGATCCGGTGCTAACAAAGCCC pET-28b (+)  
 ...GlyArgAspProAsnSerSerSerValAspLysLeuAlaAlaAlaLeuGluHisHisHisHisHisHisEnd

...GGTCGGGATCCGAATTCGAGCTCCGTCGACAAGCTTGGCGCCGACTCGAGCACCACCACCACCAGCTGAGATCCGGTGCTAACAAAGCCC pET-28c (+)  
 ...GlyArgIleArgIleArgAlaProSerThrSerLeuArgProHisSerSerThrThrThrThrThrThrLeuIleArgLeuLeuThrLysPro...

**Bpu1102I** → **T7 terminator**

GAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGCGCTCTAACGGGTCTTGAGGGGTTTTTTTG

T7 terminator primer #69337-3

**pET-28a-c(+)** cloning/expression region

Software	Company	Cost (USD) <sup>a</sup>	Free trial (days)	Platform <sup>b</sup>	NGS analyses <sup>c</sup>	Evolut analys
Avadis NGS	Strand Scientific Intelligence	\$4500	20	M, W, L	✓	X
CLC Genomics Workbench	CLC bio, Qiagen	\$5500	30	M, W, L	✓	✓
CodonCode Aligner	CodonCode	\$720	30	M, W	✓	✓
Genamics Expression	Genamics	\$295	30	W	X	✓
Geneious	Biomatters	\$795	14	M, W, L	✓	✓
Full Lasergene Suite	DNASTAR	\$5950	30	M, W	✓	✓
MacVector & Assembler	MacVector	\$300	21	M	✓	✓
NextGENe	Softgenetics	\$4049	35	W	✓	X
Sequencher	Gene Codes	\$2500	30	M, W	✓	✓
VectorNTI Advance	Life Technologies	\$600	30	W	X	✓