BioJotter :A Biological Notepad

Rahul.V.V.

Neetu Jabalia, Ashish Gupta, Jitendra Narayan

Background

Notepad : A simple text Editor

It helps to note the sequence& save them

Developed by Microsoft for windows

Cont..

Data Repositories are Increasing

Annotation of Sequence is demanding
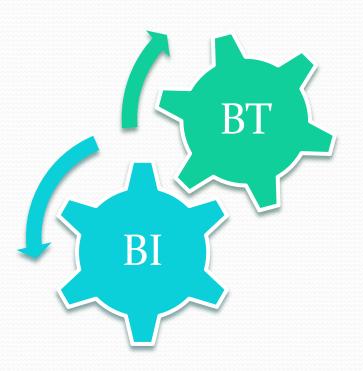
Information Retrieval is Necessary

Challenges

Non-availability of Features on a Common Platform
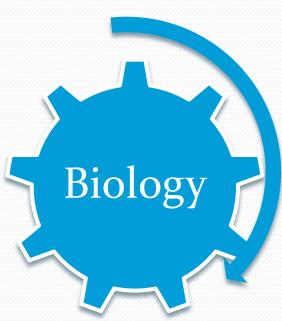
Absence of a Biological Notepad

Expensive Bioinformatics Tools

BioJotter: Intuitive Biotext Editor

Easy to use GUI	Features on a common platform	Replacement for Microsoft Notepad
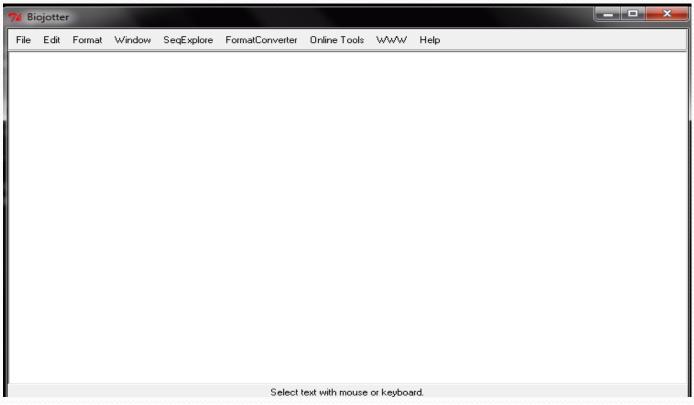
BioJotter

❑Written in Perl/Tk, which provides a graphical user interface.

❑Modules Used :
    *LWP::UserAgent
    *HTTP::Request::Common
    *Tk::Graph
    *Tk::NoteBook
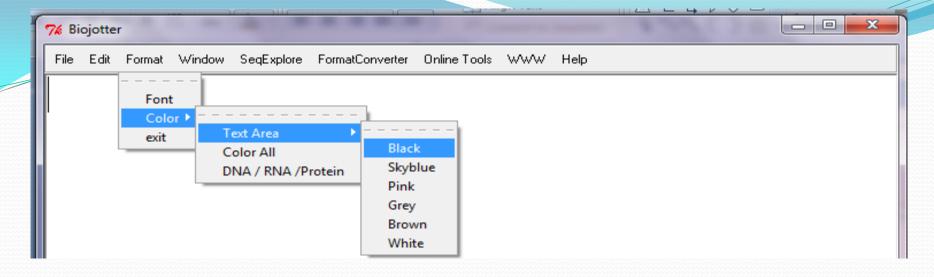   * Bio::AlignIO
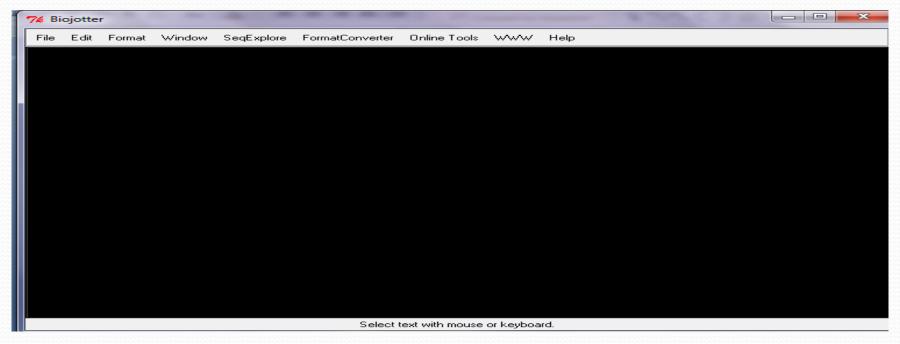   *Bio::SeqIO
    * Tk::BrowseEntry

❑PAR is used to make exe file

Biojotter

File   Edit   Format   Window   SeqExplore   FormatConverter   Online Tools   WWW   Help

Font
Color ▶   Text Area ▶
exit   Color All
                DNA / RNA /Protein

GCTAGC...CTACGTCGTACGTCGATCGATGCTAGCTAGCTAGCTCGTGACAGCCTGCATCGTACGCTGCTATTACGTCGTACGTCGATCGATGCTAGCTAGCTAGCTCGTGACAGCCTG
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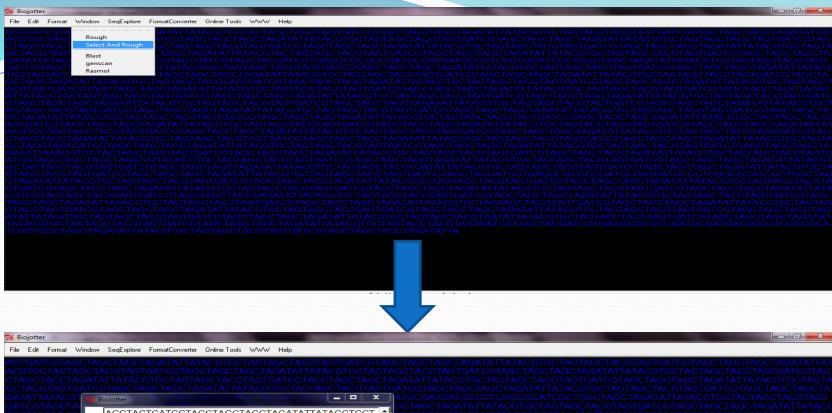CTCGTGACAGCCTGCATCGTACGCTGCTATTACGTCGTACGTCGATCACAGCCTGCATCGTACGCTGCTATTACGTCGTACGTCGATCGTACGTCGATCGATGCTAGCTAGCTAGCTCGTGAC
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CTATTACGTCGTACGTCGATCGTACGTCGATCGATGCTAGCTAGCTAGCTCGTG

- Biojotter allows Blast & Genscan.
- Requires only net connection; No need to go to the respective web pages.
- Biojotter will send the sequence directly to the webserver .
- The result will be displayed inside a text file.

Biojotter

File　Edit　Format　Window　SeqExplore　FormatConverter　Online Tools　WWW　Help

Window

Rough
Select And Rough

Blast
genscan
Rasmol

Biojotter

feature helps to read multiple DNA or Protein sequences(FASTA format) from a file and returns the blast result into a

Input file name -

Browse

Output file name -

Browse

Type of Blast -

Submit

Select text with mouse or keyboard

- Input Sequence :

gi|306483213|gb|CP002176.1| Streptococcus pneumoniae 670-6B, complete genome.

```
                              Score     E
Sequences producing significant alignments:              (Bits)  Value

pdb|3O5H|1  Chain 1, Yeast 80s Ribosome. This Entry Consists O...  28.3    4.8
pdb|3O58|1  Chain 1, Yeast 80s Ribosome. This Entry Consists O...  28.3    4.8
pdb|3IZF|A  Chain A, Model Of The Large Subunit Rna Based On A...  28.3    4.8
pdb|3IZ9|A  Chain A, Model Of The Large Subunit Rna Based On A...  28.3    4.8
pdb|3JYX|5  Chain 5, Structure Of The 60s Rrna For Eukaryotic ...  28.3    4.8
pdb|2ZKR|0  Chain 0, Structure Of A Mammalian Ribosomal 60s Su...  28.3    4.8


ALIGNMENTS
>pdb|3O5H|1 Chain 1, Yeast 80s Ribosome. This Entry Consists Of The 60s Subunit
Of The Second 80s In The Asymmetric Unit.
Length=3396

 Score = 28.3 bits (30),  Expect = 4.8
 Identities = 19/20 (95%), Gaps = 1/20 (5%)
 Strand=Plus/Plus


Query  1261  TAGCCAAATG-CTCGTCATC  1279
             |||||||||| |||||||||
Sbjct  2274  TAGCCAAATGCCTCGTCATC  2293



>pdb|3O58|1 Chain 1, Yeast 80s Ribosome. This Entry Consists Of The 60s Subunit
Of The First 80s In The Asymmetric Unit.
Length=3396

 Score = 28.3 bits (30),  Expect = 4.8
 Identities = 19/20 (95%), Gaps = 1/20 (5%)
 Strand=Plus/Plus


Query  1261  TAGCCAAATG-CTCGTCATC  1279
             |||||||||| |||||||||
Sbjct  2274  TAGCCAAATGCCTCGTCATC  2293
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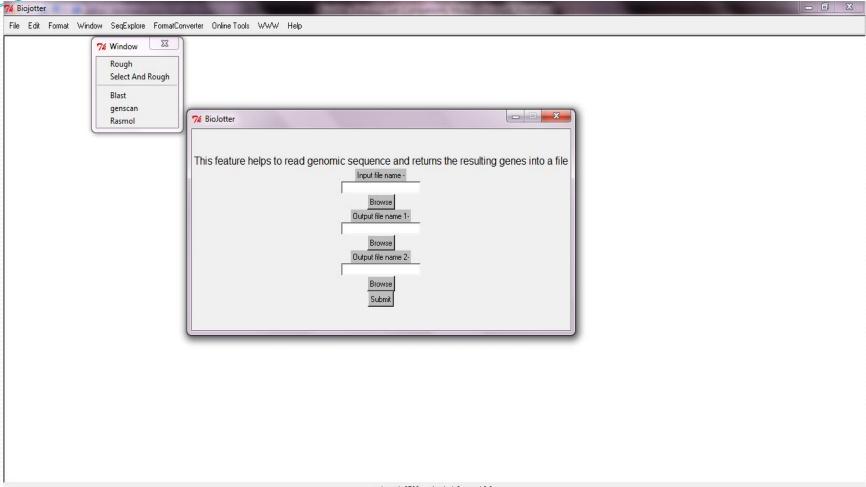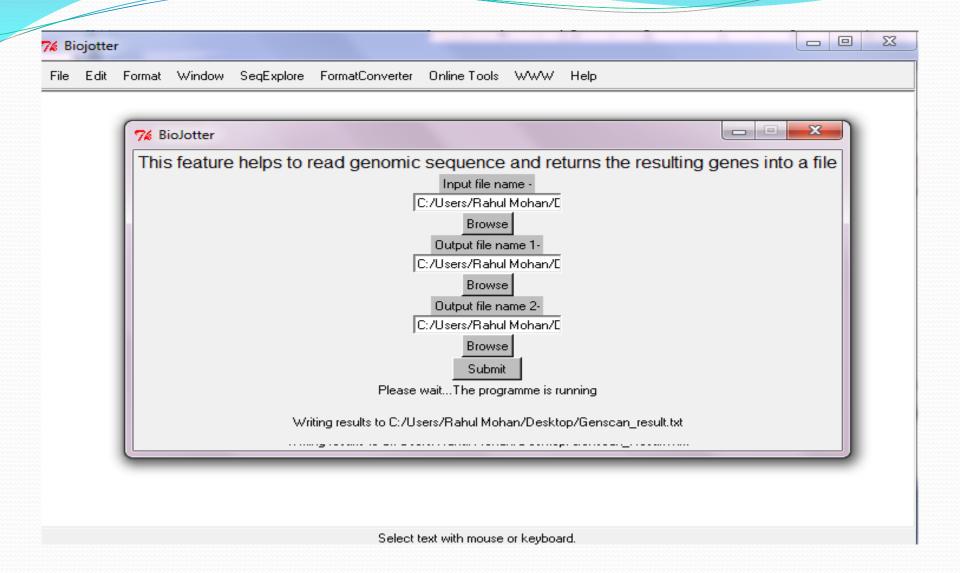
- gi|1500688|gb|L77119.1|MII1CG Methanocaldococcus jannaschii DSM 2661 small extra-chromosomal element, complete sequence
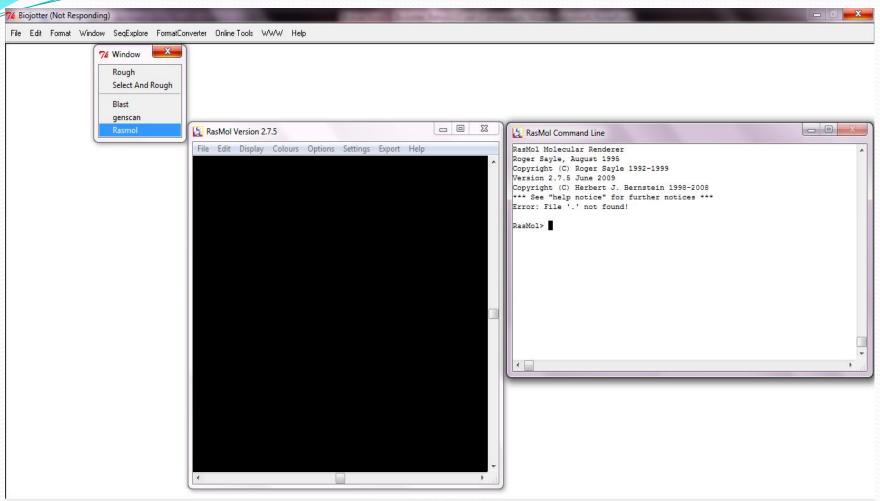
Genscan results for "gi|1500688|gb|L77119.1|MJI1CG Methanocaldococcus jannaschii DSM 2661 small extra-chromosomal element, complete sequence".
Length = 16909 bp.
Genscan returned 2 translations:
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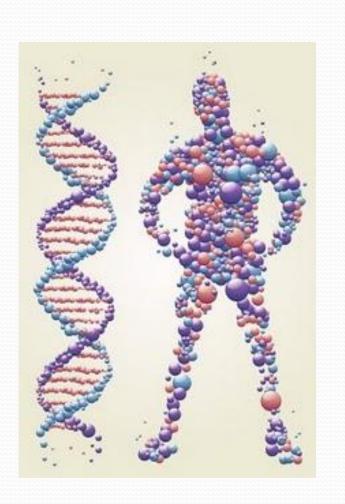
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RVDMPNIENLIGLVISRDNIKFYKKGIIPMNHNRPIFIEEMMDFILRVGNDLDLLKSGKT

SeqExp helps in :

*Finding Composition
*Translating sequence
*Calculating Length
*Reversing the sequence
*Identification of ORF region,
*Translating the ORF
*Graph Drawing
*Pattern Matching,
*Replacing,Mutating
*Inserting Gap

Biojotter

File Edit Format Window SeqExplore FormatConverter Online Tools WWW Help

Composition ▶   DNA/RNA
Translate ▶   Protein

Length
Reverse
orf region
Translated ORF
Graph ▶

Finder
Mutate
InsertGap

MFNFEKFWQHFNDE...WEKNTKPISYNQKTHELKIQVQNPVAKGYWEKNLSSQLIQSAYGYAGVELLPVFQISEDSDTPERIVTPEPQHNLQTTPTRAPQREFAKDLKLNEKYTFDNFV
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EIPDLSERLVSRFTWO...AEGLTIDDDTLDYIASQVDTNIRELEGALVKVQAYATIEKADIDINLAREALVDLKLVQKNRGLQIPKIQEVVANYFQTSTAELKGKKRVRQIVIPRQI
AMYLSRELTDASLPKI...KQMKTDADIKTAVFDLKQMLEHMDENQTQDHRIRNVDLTGMMRSSFLDYAMSVIVARALPDVRDGLKPVQRRILYGMSELGVTPDKPYKKSA
RIVGEVMGKFHPHGD...IDFSYRYMLVDGHGNFGSVDGDEPAAMRYTEARMSKIAVEMLRDINKNTIDWQRNYDDTESEPVVLPARIPNLLVNGANGIAVGMTTNIPPHNLSEVISGLHM
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VNIPEGADDNYLFFVT...EFANIRNSGLIALTLRDGDELSNVLTTDGNQNILIGTHLGYAVTFNESDVRAMGRTAAGVRGINLRPEDYVVGSGVLGANDQVLVISEKGYGKRTPASEYPVKG
RGGKGIKTANITEKNG...DIMVITTDGIMIRFKTADVSQTSRSTIGVRLIKVNDDSRVASLTIVPTEAEQDEIGDEDSEKMSSTRIELDQDFIDQVKHEIKPHWGELGWVTYKRTYARWLPEK
NRSENWDETVKRVIE...TPSEEVINELTNEAKQLFRLTYGLSATPSGRNLWISGTDYQKRTGDSLNNCWFIAIRPQEYGDSHIVPTYIDKREKAVSMPFSFLFDQLMKGGGVGFSVVNSNI
KQIPKVDNKIDLTVVIN...GAVDKDEWEKQNPDHDDIIYYRLPDTREGWVLANARLIDMHFNNTNPDQKTKLVLDISDIRPYGAKIHGFGGTASGPMPLVEMFIDINNVINARVGKNLTAVD
ATDICNLIGKTVVAGNVRRSAELALGSNDDQDFIKMKQDKEKLYHHRWASNNSVAINSKFNNYGPIADGILHNGEPGIVNLDLSRNYGRIVDGYQPGIDDDVEGTNPCGEISLANGEPCNLFEVFPYTAEK
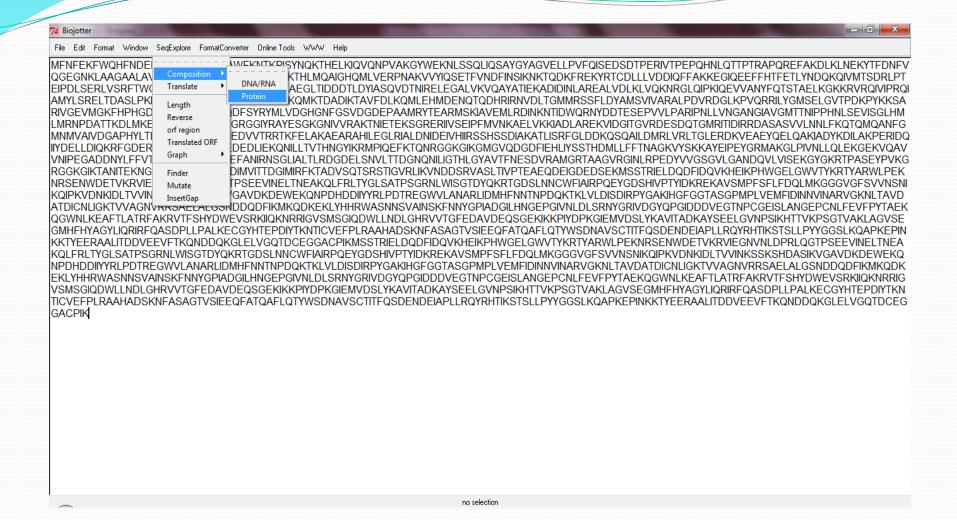QGWNLKEAFTLATRFAKRVTFSHYDWEVSRKIIQKNRRIGVSMSGIQDWLLNDLGHRVVTGFEDAVDEQSGEKIKKPIYDPKGIEMVDSLYKAVITADKAYSEELGVNPSIKHTTVKPSGTVAKLAGVSE
GMHFHYAGYLIQRIRFQASDPLLPALKECGYHTEPDIYTKNTICVEFPLRAAHADSKNFASAGTVSIEEQFATQAFLQTYWSDNAVSCTITFQSDENDEIAPLLRQYRHTIKSTSLLPYYGGSLKQAPKEPIN
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KQLFRLTYGLSATPSGRNLWISGTDYQKRTGDSLNNCWFIAIRPQEYGDSHIVPTYIDKREKAVSMPFSFLFDQLMKGGGVGFSVVNSNIKQIPKVDNKIDLTVVINKSSKSHDASIKVGAVDKDEWEKQ
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EKLYHHRWASNNSVAINSKFNNYGPIADGILHNGEPGIVNLDLSRNYGRIVDGYQPGIDDDVEGTNPCGEISLANGEPCNLFEVFPYTAEKQGWNLKEAFTLATRFAKRVTFSHYDWEVSRKIIQKNRRIG
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GACPIK

no selection

Biojotter

File　Edit　Format　Window　SeqExplore　FormatConverter　Online Tools　WWW　Help

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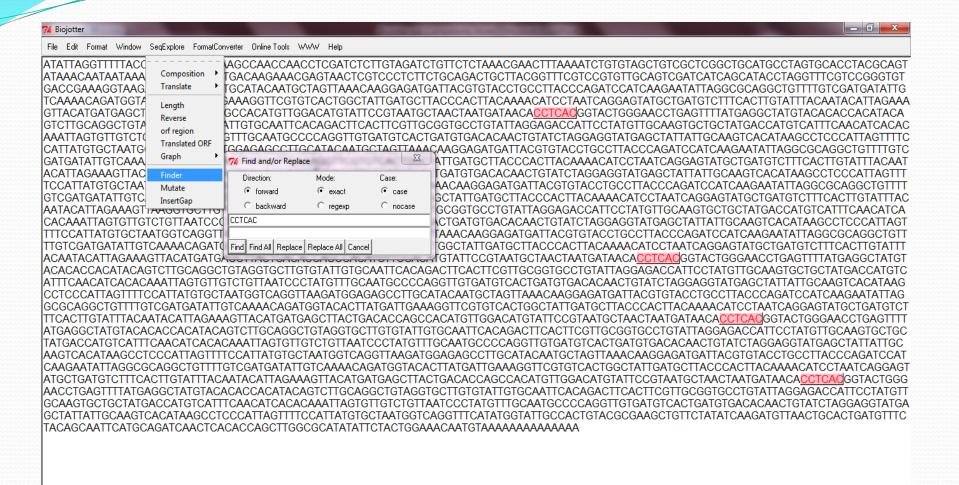

Biojotter

Reading frame +1 265 to 294, Length: 30.
Reading frame +1 703 to 723, Length: 21.
Reading frame +1 877 to 885, Length: 9.
Reading frame +1 916 to 930, Length: 15.
Reading frame +1 961 to 966, Length: 6.
Reading frame +2 104 to 136, Length: 33.
Reading frame +2 284 to 1210, Length: 927.
Reading frame +3 303 to 347, Length: 45.
Reading frame +3 366 to 398, Length: 33.
Reading frame +3 426 to 548, Length: 123.
Reading frame +3 558 to 635, Length: 78.
Reading frame +3 720 to 752, Length: 33.
Reading frame +3 771 to 809, Length: 39.
Reading frame +3 885 to 923, Length: 39.
Reading frame +3 933 to 956, Length: 24.
Reading frame +3 975 to 1199, Length: 225.

Biojotter

Translated ORFs for , length = 1211 bp.,minimum ORF size kept = 10
2 bases.

>ORF rf +2, from 284 to 1210, 927 bases.
MLVKQGDDYVYLPYPDPSRILGAGCFVDDIVKTDGTLMIERFVSLA
IDAYPLTKHPNQEYADVFHLYLQYIRKLHDELTGHMLDMYSVMLTN
DNTSRYWEPEFYEAMYTPHTVLQAVGACVLCNSQTSLRCGACIR
RPFLCCKCCYDHVISTSHKLVLSVNPYVCNAPGCDVTDVTQLYLG
GMSYYCKSHKPPISFPLCANGQVFGLYKNTCVGSDNVTDFNAIAT
CDWTNAGDYILANTCTERLKLFAAETLKATEETFKLSYGIATVREA
VLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVKKKK

>ORF rf +3, from 426 to 548, 123 bases.
MLTHLQNILIRSMLMSFTCIYNTLESYMMSLLATCWTCIP*

>ORF rf +3, from 975 to 1199, 225 bases.
MLAITYLPTLVLRDSSFSQQKRSKPLRKHLSCHMVLPLYAKLFYIK
MLTALMFLQQFMQINSHQLGAYILLETM*

>ORF rf -2, from 143 to 280, 138 bases.
MQGSPSYLSVTPGRNLGMLMIDCNTDETVSSLQKRDELLVSCQR
Q*

no selection

Future Adins

❑Multiple Sequence Allignment of sequences.

❑Phylogenetic tree construction.

❑Gene Pattern Identifier(Chaos Game representation of sequence).

❑S2AS(Sequence to Audio Signal) Conversion.

Availability

http://bioinformaticsonline.com/BioJotter.php

REFERENCES

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THANK YOU !!!