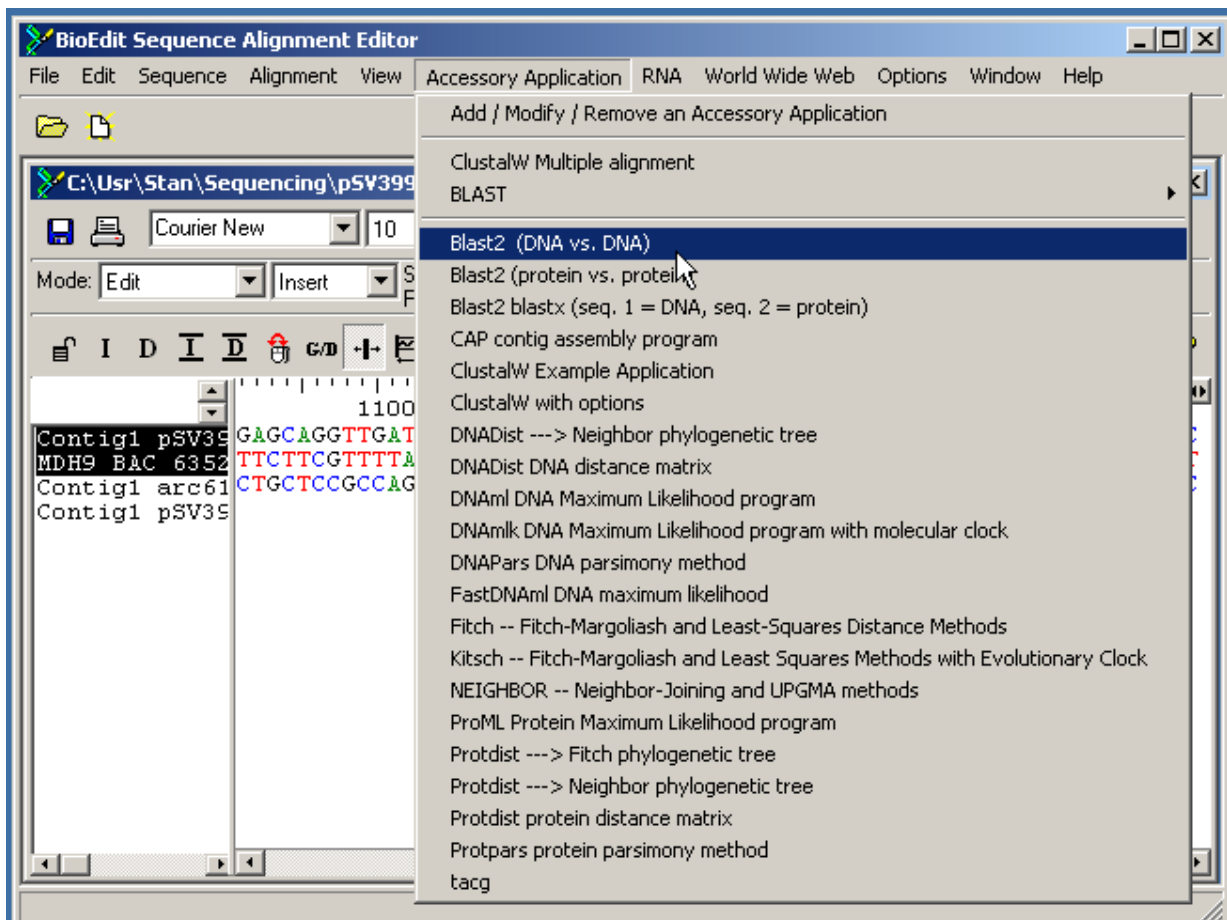


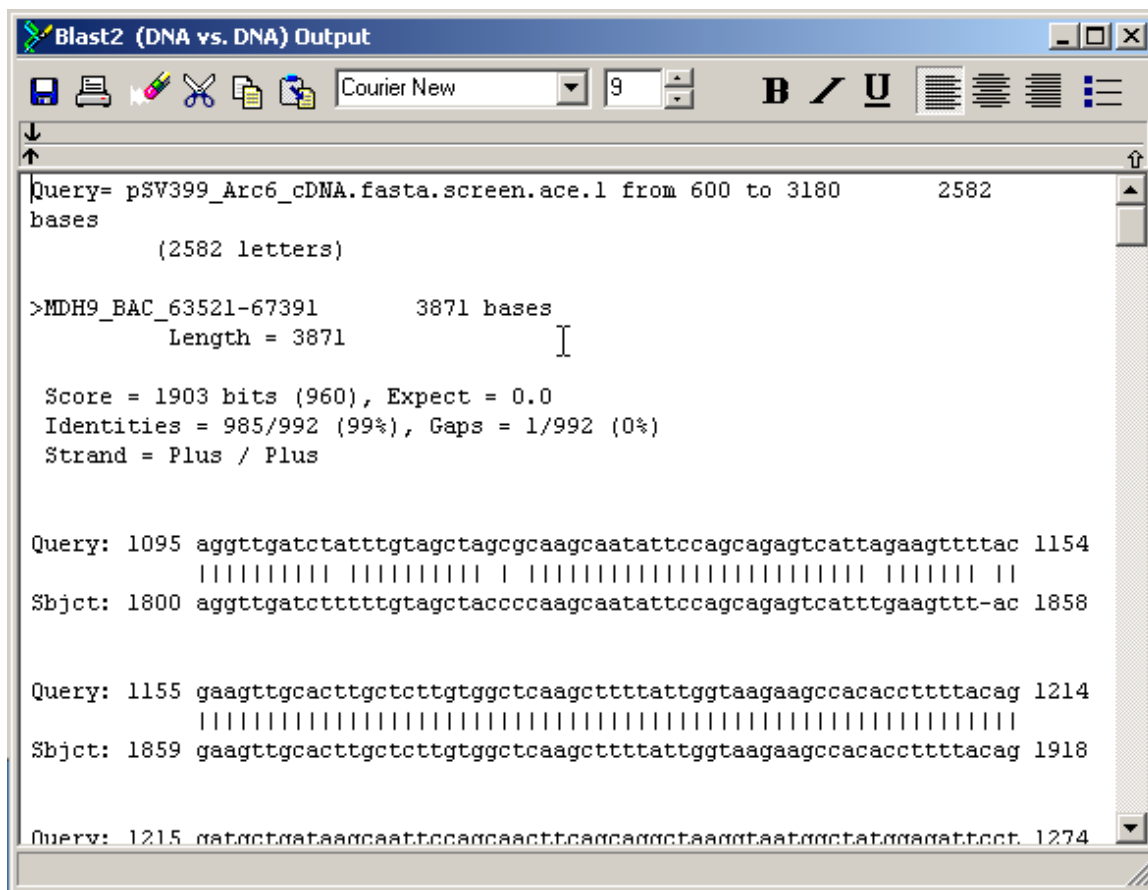
Setting up BLAST2 as an accessory application in Bioedit

To be able to blast two sequences against each other in Bioedit, proceed as follows:

1. Download the latest bl2seq.exe executable from NCBI, extract the compressed file into the "apps" folder in the Bioedit installation.
2. Edit the "Apps.ini" file in the "apps" folder, by adding the text shown below (Appendix 1) to the end of the file.
3. Start Bioedit, load your alignment file with multiple sequences and select the two sequences to be compared (both sequences must be from the same set).
4. Select the desired blast2 program from the "Accessory Applications" menu: (DNA vs. DNA; protein vs. protein; protein vs DNA):



5. Your results will open in a new window:



Appendix 1

Text to be added to the Apps.ini file

```
[Blast2 (protein vs. protein)]
Program=<Bioedit>\apps\bl2seq.exe
Don't use interface=1
Don't create menu item=0
Auto-Feed=1
Degap Sequences=1
Separate Files=1
Auto-Feed File Format=1
Auto-Feed File Name Required=1
Remove redundancies=0
Truncate titles=0
Change spaces in titles=0
Specific File Name=inseq
Prompt for Input File=0
Prompt for Output File=0
Open Output as Alignment=0
Open Output as Text=1
```

Open Output with External Program=0
 External Program Name=
 Open Output with Accessory Application=0
 Accessory Application to open with=
 Input File Prefix=
 Output File Prefix=
 Specify Input File Name=0
 Specify Output File Name=0
 Input File Name=
 Output File Name=out.txt
 Input File Prefix Required=0
 Space after input prefix=0
 Output File Prefix Required=0
 Space after output prefix=0
 Input File Name Arbitrary=0
 Output File Name Arbitrary=0
 Redirect input from stdin=0
 Redirect output from stdout=0
 Default Command Line=-i inseq -j inseq1 -p blastp -F F
 View Documentation Option=0
 Documentation File=
 Description=
 Include Additional Options Box=0
 Redirect General stdout=1
 Stdout Redirected Filename=out.txt
 Redirect General stdin=0
 Stdin Redirected Filename=
 Add input file to command line=0
 Add output file to command line=0
 output command at beginning=0
 input command at beginning=0
 output command at end=0
 input command at end=0
 Additional Output 0 Open with Accessory Application=0
 Additional Output 0 Accessory Application=
 Additional Output 0 Rename File=0
 Additional Output 0 New File Name=

[Blast2 blastx (seq. 1 = DNA, seq. 2 = protein)]
 Program=<Bioedit>\apps\bl2seq.exe
 Don't use interface=1
 Don't create menu item=0
 Auto-Feed=1
 Degap Sequences=1
 Separate Files=1
 Auto-Feed File Format=1
 Auto-Feed File Name Required=1
 Remove redundancies=0
 Truncate titles=0
 Change spaces in titles=0
 Specific File Name=inseq
 Prompt for Input File=0
 Prompt for Output File=0
 Open Output as Alignment=0

Open Output as Text=1
 Open Output with External Program=0
 External Program Name=
 Open Output with Accessory Application=0
 Accessory Application to open with=
 Input File Prefix=
 Output File Prefix=
 Specify Input File Name=0
 Specify Output File Name=0
 Input File Name=
 Output File Name=out.txt
 Input File Prefix Required=0
 Space after input prefix=0
 Output File Prefix Required=0
 Space after output prefix=0
 Input File Name Arbitrary=0
 Output File Name Arbitrary=0
 Redirect input from stdin=0
 Redirect output from stdout=0
 Default Command Line=-i inseq -j inseq1 -p blastx -F F
 View Documentation Option=0
 Documentation File=
 Description=
 Include Additional Options Box=0
 Redirect General stdout=1
 Stdout Redirected Filename=out.txt
 Redirect General stdin=0
 Stdin Redirected Filename=
 Add input file to command line=0
 Add output file to command line=0
 output command at beginning=0
 input command at beginning=0
 output command at end=0
 input command at end=0
 Additional Output 0 Open with Accessory Application=0
 Additional Output 0 Accessory Application=
 Additional Output 0 Rename File=0
 Additional Output 0 New File Name=

[Blast2 (DNA vs. DNA)]
 Program=<Bioedit>\apps\bl2seq.exe
 Don't use interface=1
 Don't create menu item=0
 Auto-Feed=1
 Degap Sequences=1
 Separate Files=1
 Auto-Feed File Format=1
 Auto-Feed File Name Required=1
 Remove redundancies=0
 Truncate titles=0
 Change spaces in titles=0
 Specific File Name=inseq
 Prompt for Input File=0
 Prompt for Output File=0

Open Output as Alignment=0
Open Output as Text=1
Open Output with External Program=0
External Program Name=
Open Output with Accessory Application=0
Accessory Application to open with=
Input File Prefix=
Output File Prefix=
Specify Input File Name=0
Specify Output File Name=0
Input File Name=
Output File Name=out.txt
Input File Prefix Required=0
Space after input prefix=0
Output File Prefix Required=0
Space after output prefix=0
Input File Name Arbitrary=0
Output File Name Arbitrary=0
Redirect input from stdin=0
Redirect output from stdout=0
Default Command Line--i inseq -j inseq1 -p blastn -F F
View Documentation Option=0
Documentation File=
Description=
Include Additional Options Box=0
Redirect General stdout=1
Stdout Redirected Filename=out.txt
Redirect General stdin=0
Stdin Redirected Filename=
Add input file to command line=0
Add output file to command line=0
output command at beginning=0
input command at beginning=0
output command at end=0
input command at end=0
Additional Output 0 Open with Accessory Application=0
Additional Output 0 Accessory Application=
Additional Output 0 Rename File=0
Additional Output 0 New File Name=