

Topic 2. Free BLAST to your hands
with customized databases and
well result viewer.

主題二：高效率平行BLAST之個人
化序列搜尋平台、客製化比對資
料庫及搜尋結果管理系統

2010.10.07.

by Linda Lu

MyBLAST

Myblast is the web-application of the customized biological sequence alignment tool.

Motivation of MyBlast

- In most public BLAST service, users can only search a pre-existing public database and find their interesting targets from massive blast results
- Here we construct **a web-accessible service, myBLAST, for running blast on customized databases and managing these databases as well as the blast results**
- **With the versatile BLAST result parser, users can browse the output filtered by options on strand-match and top n ranked hits**
- **A blast service can be shared for small group / personal use**

	myBLAST Web	myBLAST (standalone)	NCBI Web BLAST	NCBI BLAST (standalone)
Graphic Interface	✓	✓	✓	✗
Personalize Database	✓	✓	✗	✓
Parallel Computing	✓	✓	✓	✓
Batch Query	✓	✓	✓	✓
Database manager	✓	✓	✗	✗
Result Parser and manager	✓	✓	✗	✗
User manager	✓	✗	✓	✗

From Similarity Search and Phylogentic Analysis PDF file page15 ,2009,Dec.

MyBlast is **Multi-Thread Processing.**

-More efficiency.

-Faster then before.

The screenshot shows a Windows Internet Explorer browser window with the address bar displaying `http://140.109.16.56:8080/myblast_standalone/BlastFollow`. The browser content area shows a loading screen with the text "Now is working, the BLAST results" and "The BLAST result will be shown on BLAST". A Windows Task Manager window is overlaid on the browser, showing system performance metrics.

Windows 工作管理員

檔案(F) 選項(O) 檢視(V) 關機(U) 說明(H)

應用程式 | 處理程序 | 效能 | 網路功能 | 使用者

CPU 使用率: 100 %

CPU 使用率記錄

PF 使用量: 1.11 GB

分頁檔使用量記錄

總計			實體記憶體 (K)	
控制碼	52870		總共	1555696
執行緒	973		可用	974016
處理程序	66		系統快取記憶體	338988

確認負載 (K)			核心記憶體 (K)	
總共	1164924		總共	137008
限制	5592796		已分頁	94616
尖峰	2439476		未分頁	42392

處理程序: 66 CPU 使用率: 100% 認可可用: 1137K / 5461K

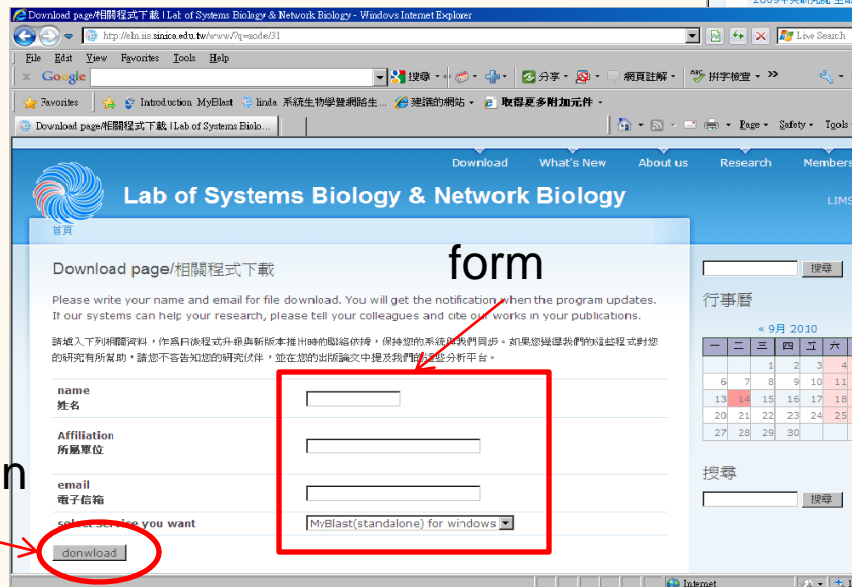
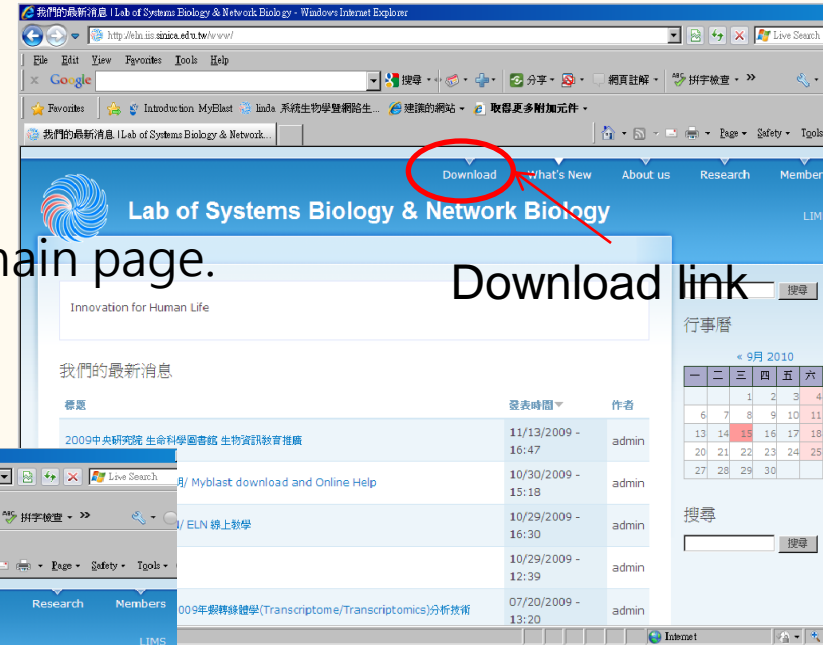
MyBLAST standalone installation

Lab of Systems Biology & Network Biology website

<http://eln.iis.sinica.edu.tw>

Download link.

1. Click the Download link on the top of the main page.
 2. Fill in the form, then submit it.
- The download process starts immediately.



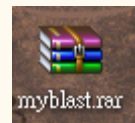
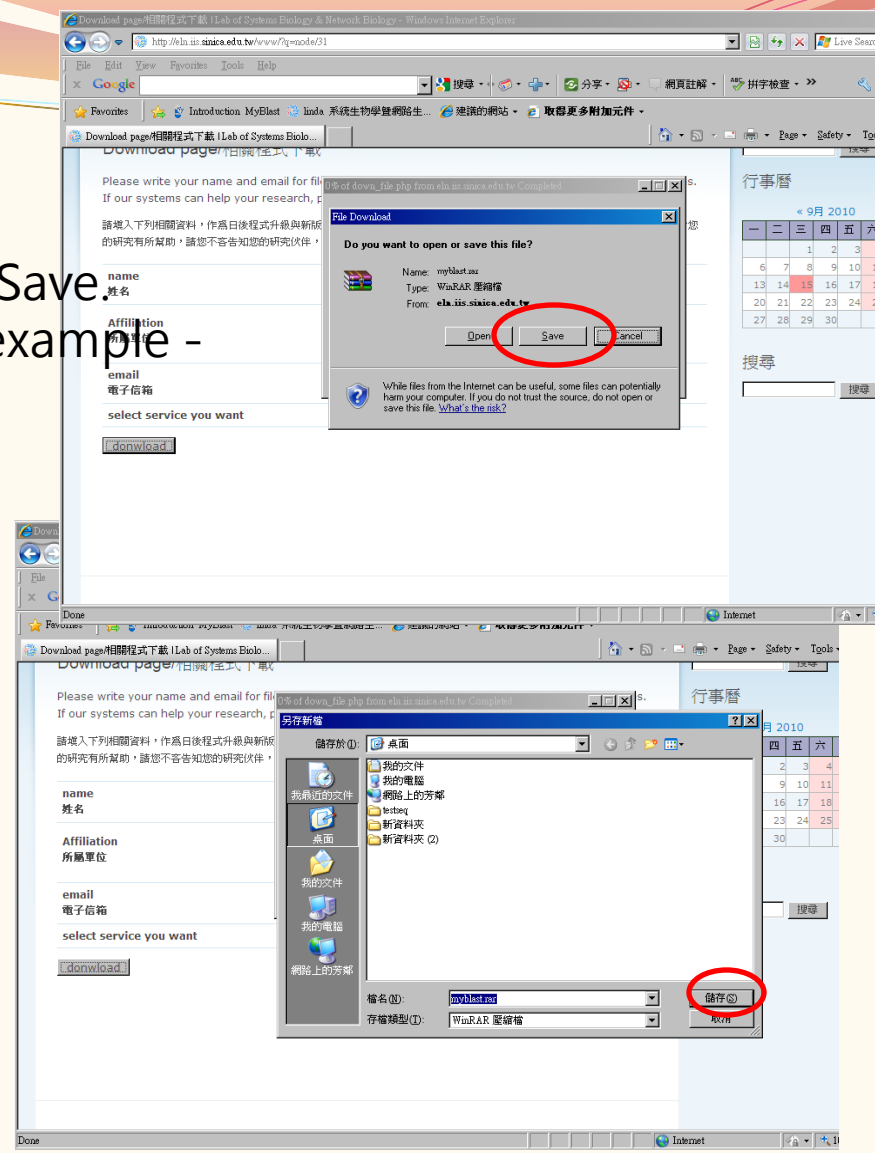
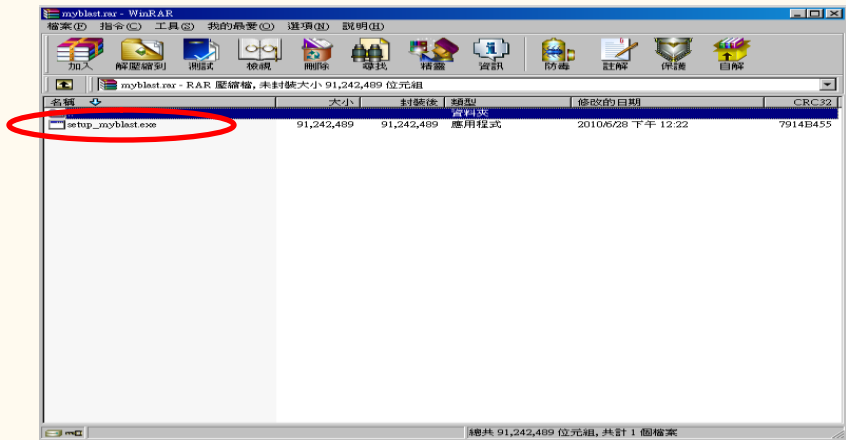
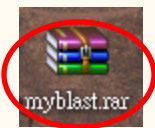
Download button

- **Download process**

- 1.The browser pop up the question. Click Save
- 2.Select the location to place the file.(for example - desktop)
- 3.Wait until the process done.

- **Execute setup_myblast.exe**

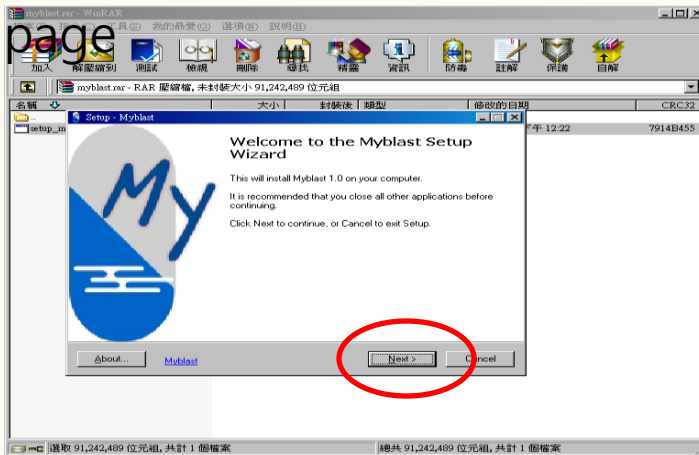
- 1.The setup_myblast.exe is inside the myblast.rar
Double click the myblast.rar
- 2.Execute this setup_myblast.exe



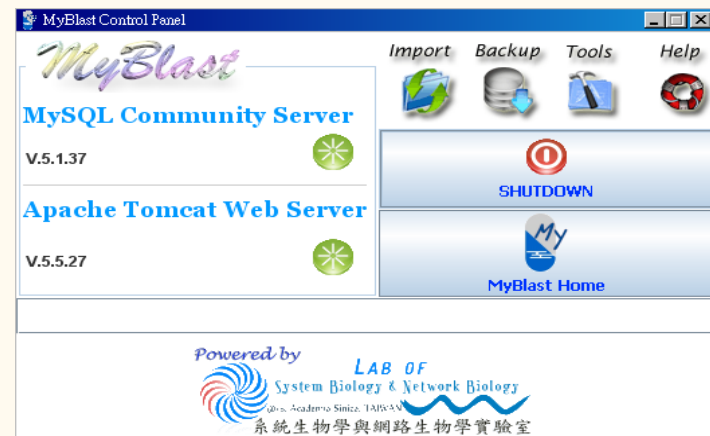
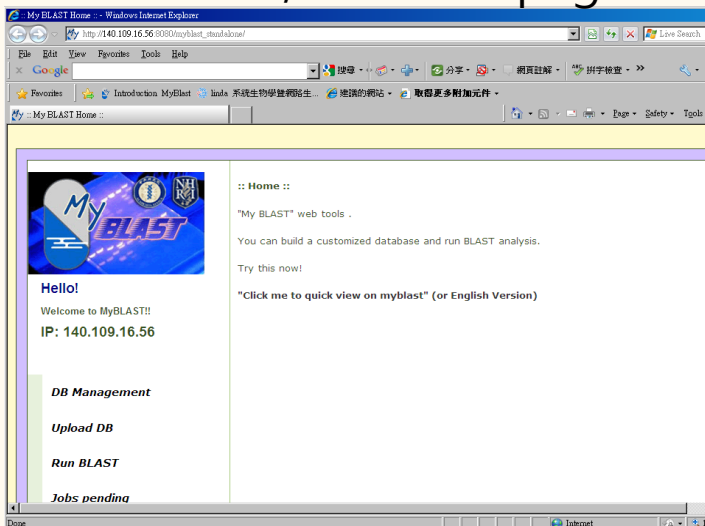
Myblast.rar shows on the desktop

● Follow the setup wizard

1. Start from the welcome



2. At the end, the main page and the control panel start automatically.



Information of web link

- Online website: (use MyBLAST online)

<http://mybioweb.nhri.org.tw/myblast>

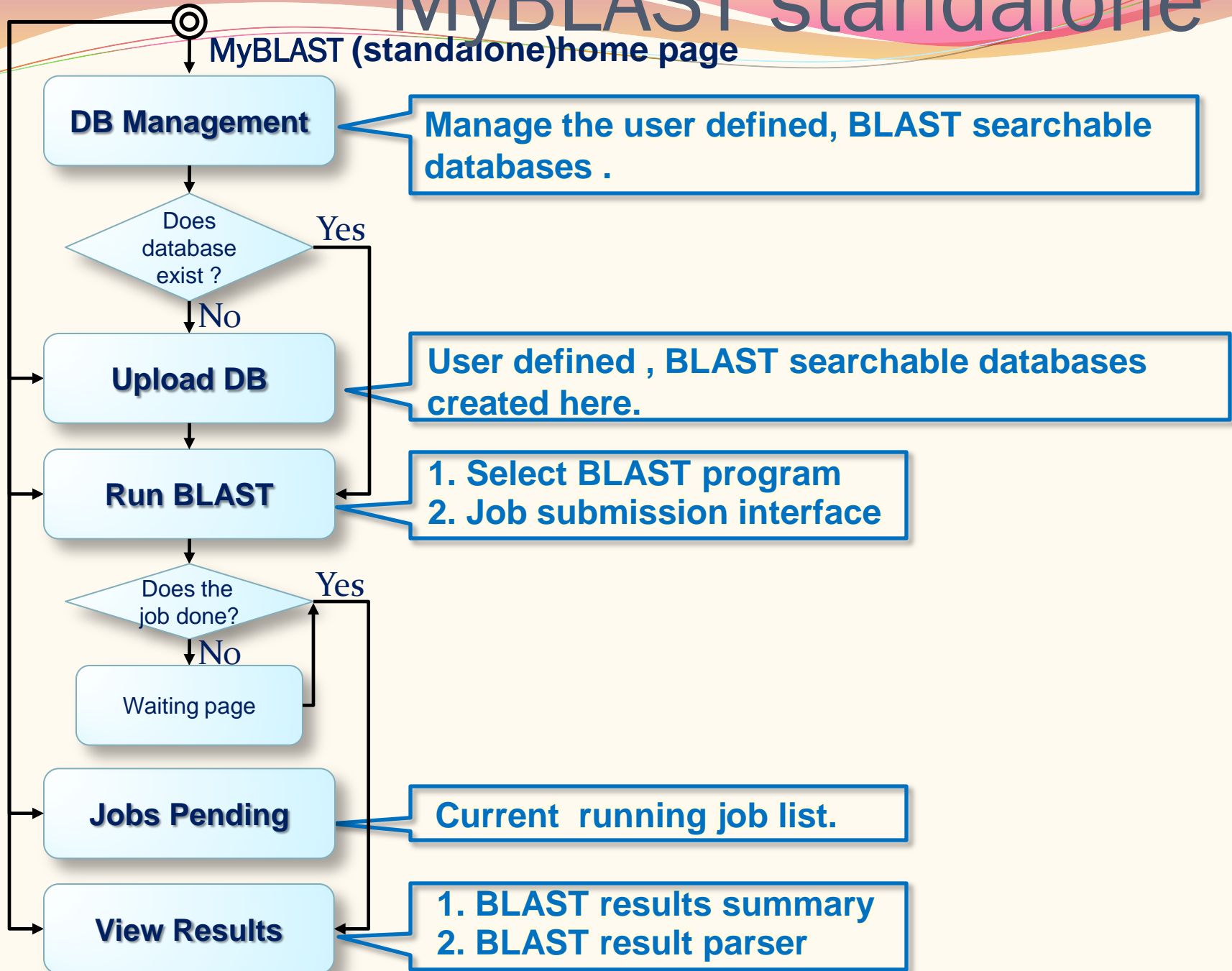
- Standalone version: (need to install MyBLAST in your computer)

<http://eln.iis.sinica.edu.tw>

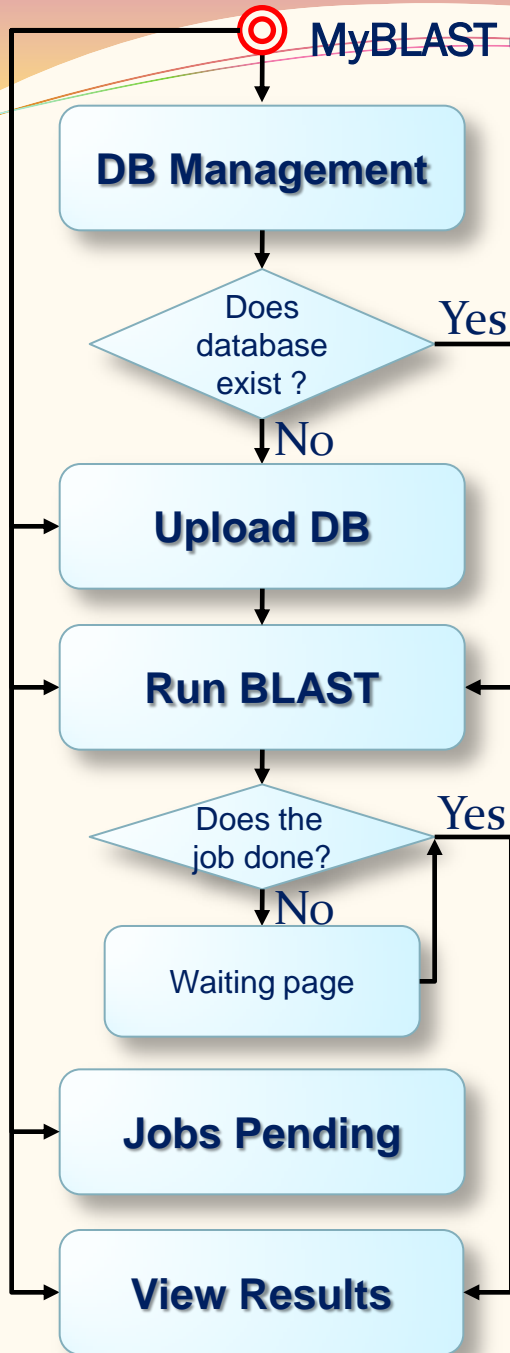
- MyBLAST video demo : (watch online)

<http://eln.iis.sinica.edu.tw>

MyBLAST standalone

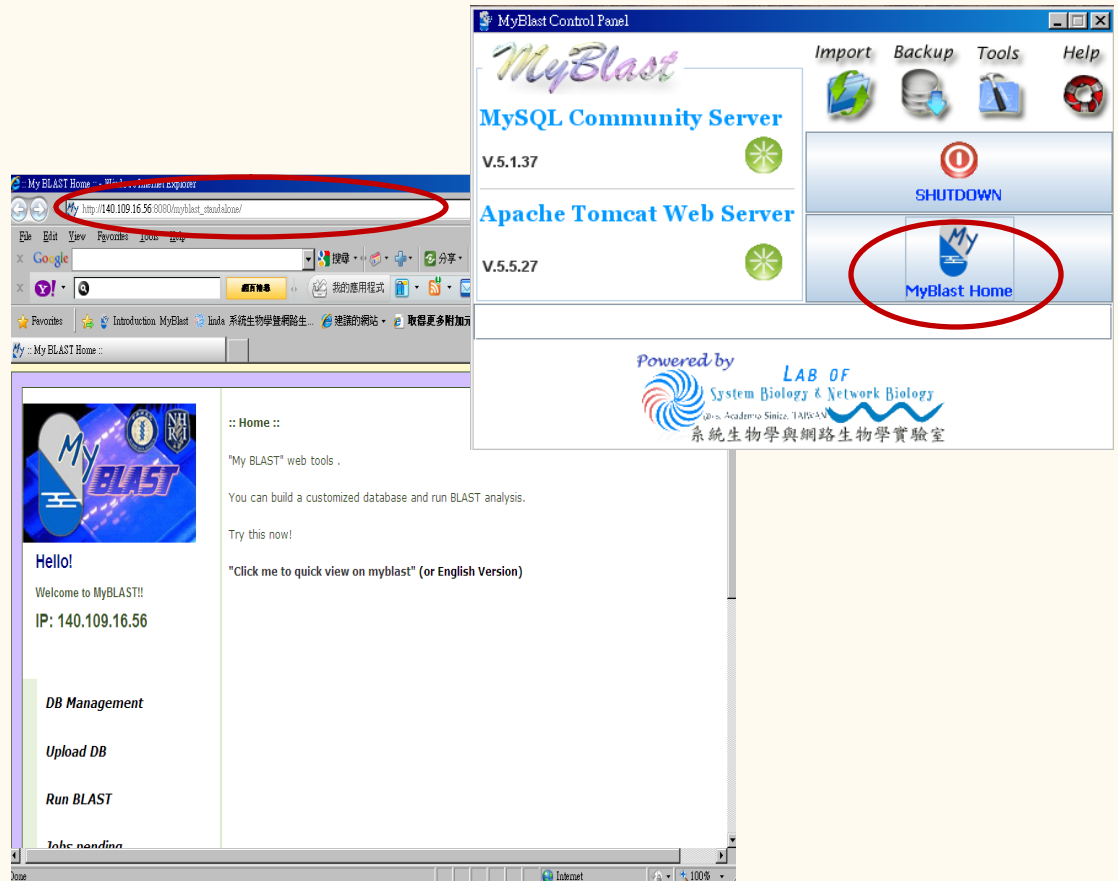


MyBLAST (standalone) home page



Start point : Go to MyBLAST home page.

1. Typing URL
http://localhost:8080/myblast_standalone/
2. Or by clicking the **MyBlast Home** button in the MyBlastControlPanel.





① MyBLAST (standalone)home page

Start point : Go to MyBLAST home page.

1. Typing URL

http://localhost:8080/myblast_standalone/

2. Or by clicking the **MyBlast Home** button in the MyBlastControlPanel.

My BLAST Home :: - Windows Internet Explorer

http://localhost:8080/myblast_standalone/

File Edit View Favorites Tools Help

Google 搜尋 分享 自動填入 登入

My BLAST Home ::

My BLAST

Hello!
Welcome to MyBLAST!!
IP: 140.109.16.56

DB Management

Upload DB

Run BLAST

:: Home ::

"My BLAST" web tools .

You can build a customized database and run BLAST analysis.

Try this now!

"Click me to quick view on myblast" (or English Version)

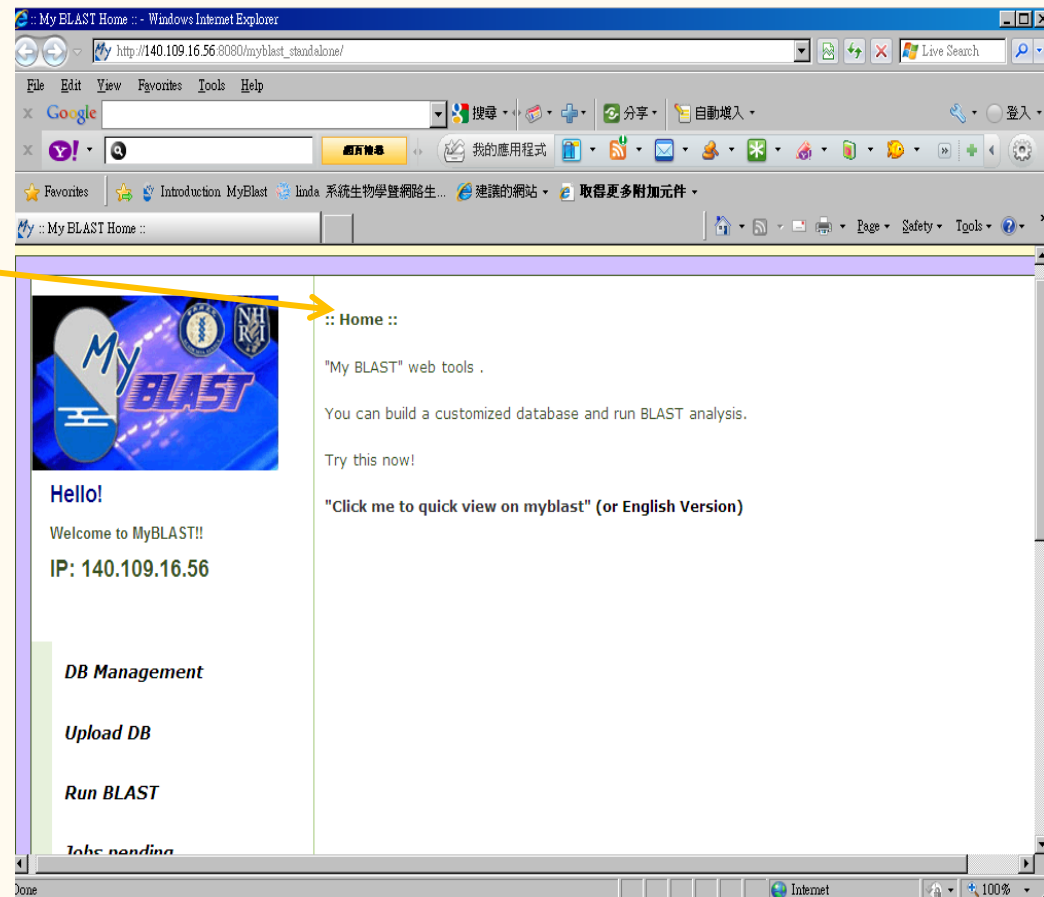
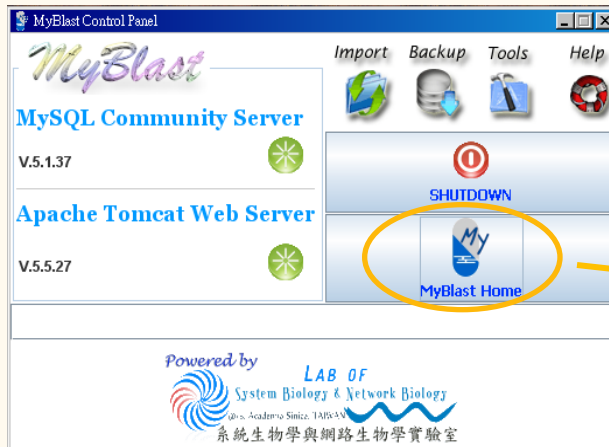
Local intranet 100%



◎ MyBLAST (standalone)home page

Start point : Go to MyBLAST home page.

1. Typing URL http://localhost:8080/myblast_standalone/
2. Or by clicking the **MyBlast Home** button in the MyBlastControlPanel.
(Don't need to type URL.)



MyBLAST (standalone) home page



①

Hello!

Welcome to MyBLAST!!

IP: 140.109.16.56

DB Management ②

Upload DB ③

Run BLAST ④

Jobs pending ⑤

View Results ⑥

User Guide ⑦

Contact Us ⑧

:: Home ::

"My BLAST" web tools .

You can build a customized database and run BLAST analysis.

Try this now!

"Click me to quick view on myblast" (or English Version) ⑨

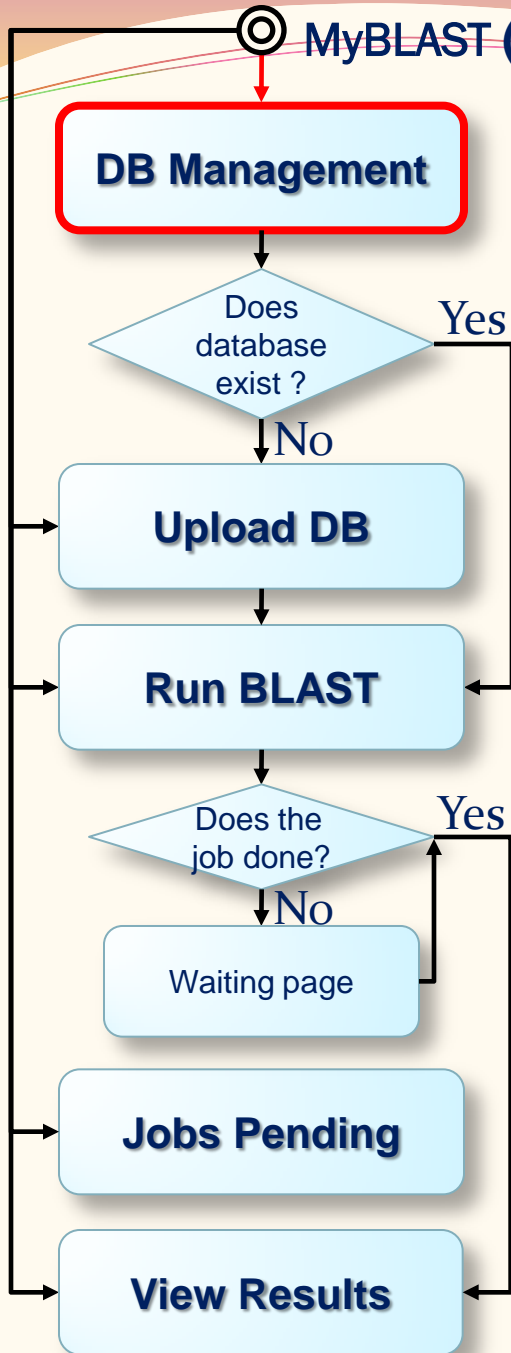
- ① MyBLAST home link
- ② DB Management link
- ③ Upload DB link
- ④ Run BLAST link
- ⑤ Jobs pending link
- ⑥ View Results link
- ⑦ User Guide link
- ⑧ Contact Us link
- ⑨ Flash Demo link
- ⑩ Websites link
- ⑪ Lab of System Biology & Network Biology website link

⑩

⑪

MyBLAST (standalone) home page

Manage the user defined, BLAST searchable databases .



The screenshot shows the MyBLAST web interface. On the left, there is a navigation menu with a 'DB Management' link highlighted in a red box. Below it are links for 'Upload DB', 'Run BLAST', 'Jobs Pending', and 'View Results'. The main content area is titled ':: Database Management ::' and contains a table of database lists. A message box states 'Your sequences was converted to database.' Below this are three icons: a green plus sign labeled 'Add', a red X labeled 'Delete', and a green magnifying glass labeled 'BLAST'. The table has columns for DB_id, type, description, date, Edit, Download, Detail, and Delete. The first row shows a database with ID 1, type N, description hp26695, and date 2010-09-20 16:35.

DB_id	type	description	date	Edit	Download	Detail	Delete
1	N	hp26695	2010-09-20 16:35				

DB Management

Manage the user defined, BLAST searchable databases.

- ① Edit icon: Modify the particular uploaded DB data.
- ② Download icon: Download the particular uploaded DB FASTA format file.
- ③ Detail icon: view the BLAST command and database log.
- ④ Delete checkbox: Check to delete the particular uploaded DB. Click the "Delete" button to start to do the DB deletion.
- ⑤ Link to Upload DB: Add a database.
- ⑥ Link to Run BLAST: Run a BLAST program

MyBLAST

Hello!

Welcome to MyBLAST!!

IP: 140.109.16.56

DB Management

Upload DB

Run BLAST

Jobs pending

Your sequences was converted to database.

:: Database Management ::

Here's your database lists:

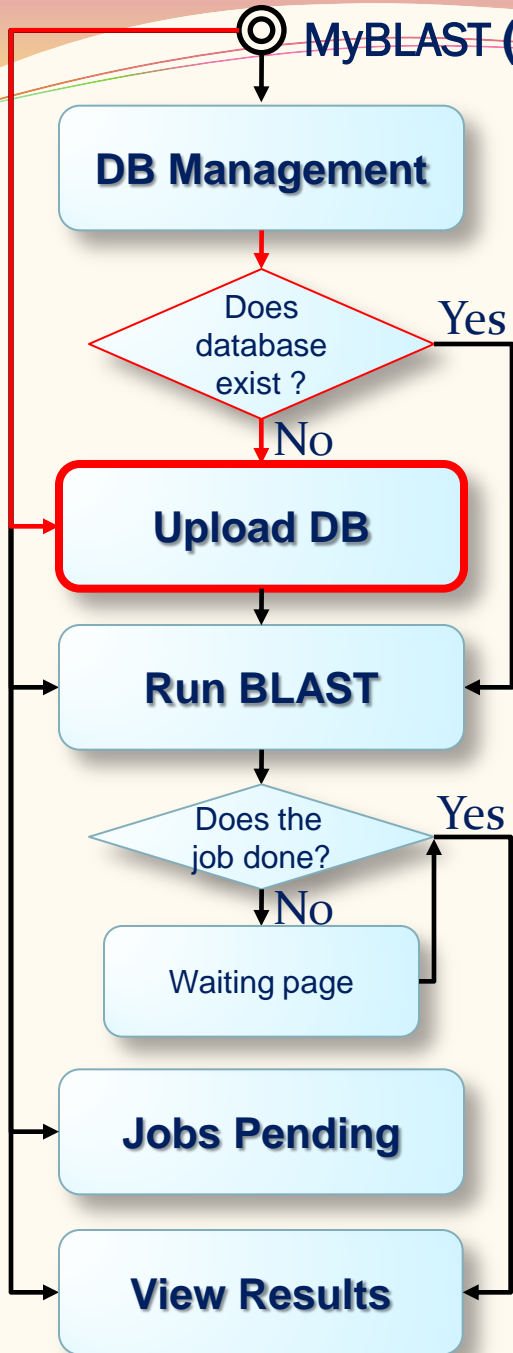
DB_id	type	description	date	Edit	Download	Detail	Delete
1	N	hp26695	2010-09-20 16:35	①	②	③	④

⑤ Add

④ Delete

⑥ BLAST

MyBLAST (standalone) home page



User defined , BLAST searchable databases created here.



Hello!

Welcome to MyBLAST!!

IP: 140.109.16.56

DB Management

Upload DB

Run BLAST

Jobs pending

View Results

User Guide

Contact Us

:: Upload Database ::

Upload your sequences to build a mini database.

Your Sequence Type:

Nucleotide

Protein

Select the sequences type.

Enter sequences below in **FASTA** format:

Or load from disk

Input your sequences in this area.

Database Description (optional) :

Upload DB

User defined, BLAST searchable databases created here.

① Sequence Type: Nucleotide or protein.

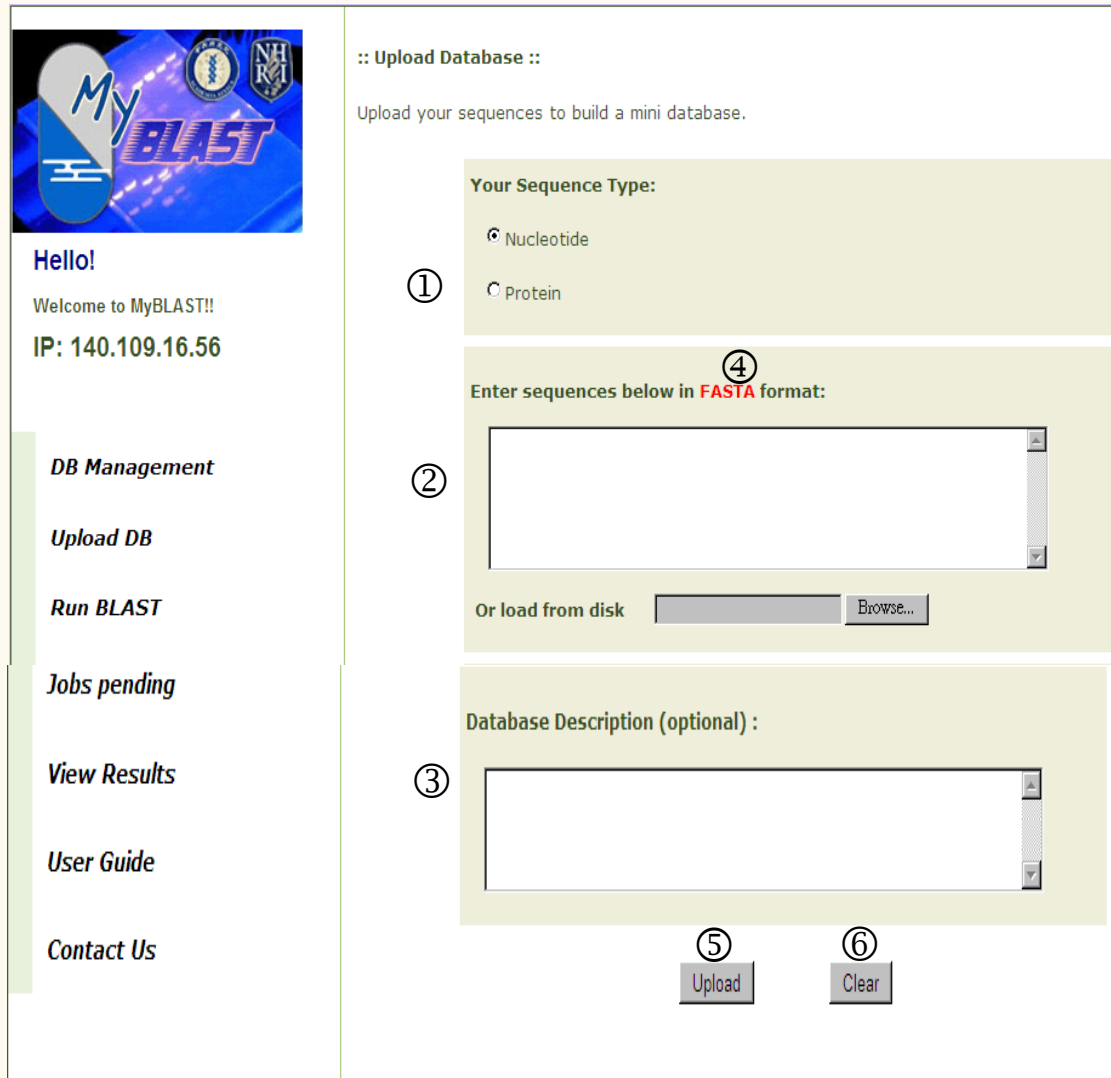
② Enter sequences:
Copy and paste the FASTA
format to the text area.
Or enter the full file path
and file name.

③ Description: simple notes
to this database.

④ FASTA format description
link

⑤ Upload button: Click to
send out the form.

⑥ Clear button: clean up the
form data.



The screenshot displays the MyBLAST web interface. On the left is a navigation menu with links: [DB Management](#), [Upload DB](#), [Run BLAST](#), [Jobs pending](#), [View Results](#), [User Guide](#), and [Contact Us](#). The main content area is titled "Upload Database ::" and includes a welcome message: "Hello! Welcome to MyBLAST!! IP: 140.109.16.56". Below this is a section for "Your Sequence Type:" with radio buttons for "Nucleotide" (selected) and "Protein". A text area for entering sequences is labeled "Enter sequences below in FASTA format:" and is marked with a circled 4. Below the text area is a "Browse..." button. At the bottom of the form are "Upload" (marked with a circled 5) and "Clear" (marked with a circled 6) buttons. A "Description (optional)" text area is also present, marked with a circled 3.

Upload DB

User defined, BLAST searchable databases created here.



Step1. Fill in the form, then submit it.
Step2. Wait until the process is done.

Your Sequence Type:

Nucleotide

Protein

Enter sequences below in FASTA format:

Or load from disk

Database Description (optional) :

Waiting page

Your sequence is now converting, the results will be shown later....

A result will be shown on DATABASE RESULT PAGE after finishing.

Note: The job is running in batch mode, and it's ok to close this window.

Show the DB_id

[Back Home] [DB Management] [Upload DB] [Run BLAST] [View Results]

Database Conversion Finished !!

Your sequences was building a mini database now.
And here is the DB_id: 3


You can go here to see database result.
<http://localhost/MainMenu>

Or Run BLAST directly!
<http://localhost/MainMenu>

Click the Upload button



You may want to go to DB Management to view the database.



Hello!
Welcome to MyBLAST!!
IP: 140.109.16.56

DB Management

Upload DB




Run BLAST

Jobs pending

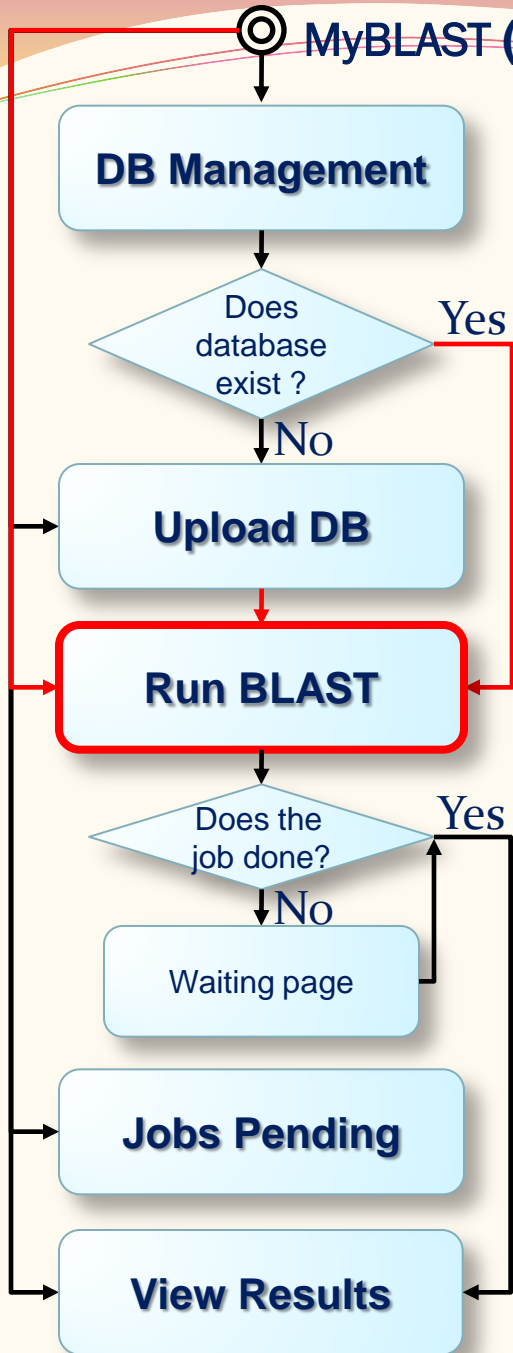
:: Database Management ::

Here's your database lists:

DB_id	type	description	date	Edit	Download	Detail	Delete
1	N	hp26695	2010-09-20 16:35				

 *Add*  *Delete*  *BLAST*

MyBLAST (standalone) home page



1. Select BLAST program
2. Job submission interface



Hello!
Welcome to MyBLAST!!
IP: 140.109.16.56

DB Management

:: Choose a BLAST program to run ::

Nucleotide BLAST	blastn megablast
Protein BLAST	blastp
Translated BLAST	blastx tblastn



Hello!
Welcome to MyBLAST!!
IP: 140.109.16.56

DB Management

Upload DB

Run BLAST

Jobs pending

View Results

:: Run blastp with your DB ::

Program: blastp (search protein databases using a protein query)

Job Note

Enter sequence below in FASTA format

```
>Acon2  
GSSELGAACALLGRIPTKEEYMNLVSEKLESQKDKIYR  
>O25294  
GVKEDDVHL
```

Input your seqs

Or load it from disk

Select Database:

Select a database

Advanced Options:

Max target:

Adjust proper parameters

Run BLAST

1. Select BLAST program
2. Job submission interface

- ① blastn link
- ② megablast link
- ③ blastp link
- ④ blastx link
- ⑤ tblastn link
- ⑥ tblastx link



Hello!

Welcome to MyBLAST!!

IP: 140.109.16.56

DB Management

Upload DB

Run BLAST

Jobs pending

View Results

:: Choose a BLAST program to run ::

Nucleotide BLAST

- ① blastn
- ② megablast

Protein BLAST

- ③ blastp

Translated BLAST

- ④ blastx
- ⑤ tblastn
- ⑥ tblastx

Run BLAST

1. Select BLAST program

2. Job submission interface

- ① Job note
- ② Copy and paste the FASTA format to the text area.
Or enter the full file path and file name.
- ③ Select Database
- ④ Advanced Options: Max target
- ⑤ Advanced Options: E-Value
- ⑥ Advanced Options: Matrix
- ⑦ Advanced Options: Gap Creation
- ⑧ Advanced Options: Word size
- ⑨ Advanced Options: Turn off the low complexity filter
- ⑩ question icon: link to the description of the particular parameter.

:: Run blastp with your DB ::

Program: blastp (search protein databases using a protein query)

Job Note ^①

Enter sequence below in **FASTA** format

^②

Or load it from disk

^③ Select Database:

Advanced Options:

^④ Max target: ^⑩
E-value: ^⑩
Matrix: ^⑥
Gap creation: ^⑦
Word size: ^⑧
 ^⑨ Turn off the low complexity filter ^⑩



Run BLAST

1. Select BLAST program
2. Job submission interface

Step1. Fill in the form, then submit it.
Step2. Wait until the process is done.

Select BLAST program

MyBLAST

Hello!
Welcome to MyBLAST!!
IP: 140.109.16.56

DB Management

Upload DB

Run BLAST

Jobs pending

View Results

:: Choose a BLAST program to run ::

Nucleotide BLAST	blastn megablast
Protein BLAST	blastp
Translated BLAST	blastx tblastn tblastx

:: Run blastp with your DB ::

Job submission interface

Program: blastp (search protein databases using a protein query)

Job Note

Enter sequence below in **FASTA** format

```
>acon2
GSAELGAACALLGRIPPTKEEYMNLVSEKLESQKDKIYR
>O25294
GVKEDDVHL
```

Or load it from disk

Select Database:

Advanced Options:

Max target:

E-value: ↻

Matrix: ↻

Gap creation: ↻

Word size: ↻

Turn off the low complexity filter ↻

Click the Submit button




Run BLAST



Waiting page

Now is working, the BLAST results will be shown later....



The BLAST result will be shown on BLAST RESULT PAGE after finishing.

Note: The job is running in batch mode, and it's ok to close this window.

Show result

[Back Home] [Upload D

:: MyBLAST Results ::

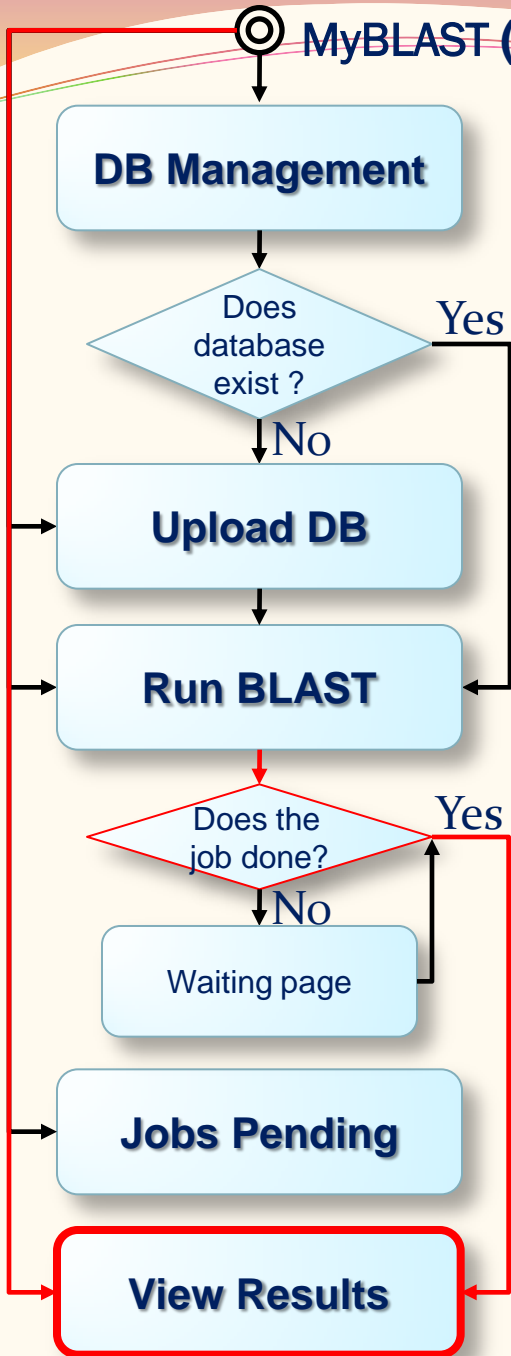
DB description: (4) hp26695 Matche Sequences

Submit description: (3) hp26695

Download Output Files (**text file**) or (**csv file**)

Seq.	Rank	Hits	E-value	Score	Bits	Match Length	Identities
Acon2	1	37_D:myblast_01astbase_01astdb4 Aconitate hydratase 2 - Helicobacter pylori	5.0E-17	77.8	190	852	38/38 (100%), Positives = 38/38 (100%)
Acon2	2	484_D:myblast_01astbase_01astdb4 UvrABC system protein C - Helicobacter pylori	3.1	21.9	45	594	9/19 (47%), Positives = 13/19 (68%)
Acon2	3	37_D:myblast_01astbase_01astdb4 CAG pathogenicity island protein 23 - Helicobacter pylori	3.1	21.9	45	983	8/18 (44%), Positives = 13/18 (72%)

MyBLAST (standalone) home page



1. BLAST results summary
2. BLAST result parser

MyBLAST logo and welcome message: Hello! Welcome to MyBLAST!! IP: 140.109.16.56

DB Management

Upload DB

Run BLAST

Does database exist? (Yes/No)

Does the job done? (Yes/No)

Waiting page

Jobs Pending

View Results

BLAST Results Summary:

All the BLAST results were saved in this page

Here's BLAST result lists:

Database Description	Submit Description	Date	Result	Detail	delete
(1)hp26695	(1)hp26695	2010-09-20 16:36 ~ 2010-09-20 16:38 (0.02hr. Size:28.57MB)			<input type="checkbox"/>

Click to see this result

View this result's BLAST command

Delete this result

Navigation: [Back Home] [Upload DB] [Run BLAST] [View Results]

MyBLAST Results

DB description: (1) hp26695

Submit description: (1) blastp 26695

Matche Sequences: Top 3 [Go] [Download]

Download Output Files (text file) or (csv file)

Select the amount of seqs that you want to show

Download the "text" or "csv" file

Seq.	Rank	Hits	E-value	Score	Bits	Match Length	Identities
Acon2	1	3_c:myblast@astbase@astdb1 Aconitate hydratase 2 - Helicobacter pylori	8.0E-18	77.8	190	852	38/38 (100%), Positives = 38/38 (100%)
Acon2	2	166_c:myblast@astbase@astdb1 2,3-bisphosphoglycerate-independent phosphoglycerate mutase - Helicobacter pylori	0.5	21.9	45	491	12/36 (33%), Positives = 19/36 (52%), Gaps = 4/36 (11%)
Acon2	3	37_c:myblast@astbase@astdb1 CAG pathogenicity island protein 23 - Helicobacter pylori	0.5	21.9	45	983	8/18 (44%), Positives = 13/18 (72%)
O25294	1	12_c:myblast@astbase@astdb1 Cytosol aminopeptidase - Helicobacter pylori	0.08	23.1	48	496	9/9 (100%), Positives = 9/9 (100%)

View Results

1. BLAST results summary
2. BLAST result parser

- ① Result parser link
- ② Log link.
- ③ Delete checkbox:
Check to delete the particular result.
Click the “Delete” button to start to do the result deletion.



Hello!

Welcome to MyBLAST!!

IP: 140.109.16.56

DB Management

Upload DB

Run BLAST

Jobs pending

All the BLAST results were saved in this page

:: BLAST Results ::

Here's BLAST result lists:

Database Description	Submit Description	Date	Result	Detail	delete
(1)hp26695	(1)hp26695	2010-09-20 16:36 ~ 2010-09-20 16:38 (0.02hr. Size:28.57MB)	① 	② 	③ <input type="checkbox"/>
(1)hp26695	(2)	2010-09-21 14:29 ~ 2010-09-21 14:31 (0.03hr. Size:28.57MB)			<input type="checkbox"/>
(4)hp26695	(3)hp26695	2010-09-23 17:23 ~ 2010-09-23 17:24 (0.01hr. Size:0.01MB)			<input type="checkbox"/>

Delete

③

Click to see this result

View this BLAST command

Delete this result

View Results

1. BLAST results summary
2. BLAST result parser

- ① Home link
- ② Upload DB link
- ③ Run BLAST link
- ④ Result Summary link
- ⑤ Filter
- ⑥ Filtered Result download
- ⑦ Output text file download
- ⑧ Output csv file download

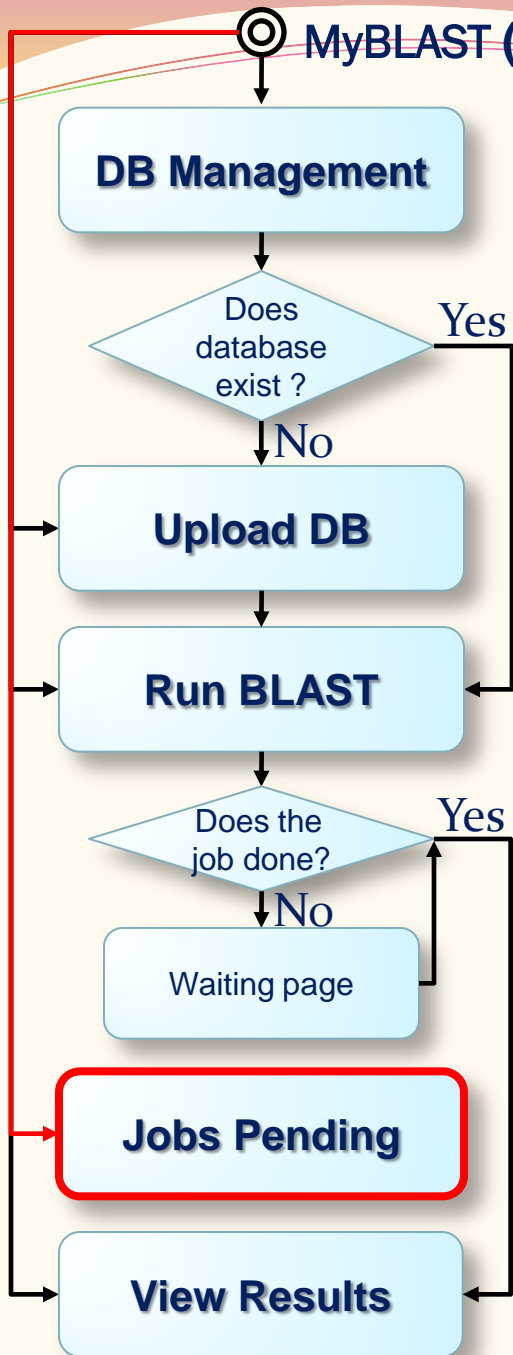
The screenshot shows a web interface for viewing BLAST results. At the top, there are four navigation links: [Back Home] (1), [Upload DB] (2), [Run BLAST] (3), and [View Results] (4). Below these is a section titled "MyBLAST Results" with the following details:

- DB description: (1) hp26695
- Submit description: (1) hp26695
- Matche Sequences: All matches (5) (Strand = Plus (6) / Plus (6))
- Download Output Files (7) (text file) or (8) (csv file)
- A button labeled "Download this 'txt' result file" points to the "text file" option.
- Buttons for "Go" (5) and "Download" (6) are also present.

The main content is a table of search results:

Seq.	Rank	Hits	E-value	Score	Bits	Match Length	Identities	strand
HP0001 hypothetical protein {Helicobacter pylori 26695}	1	HP0001 hypothetical protein {Helicobacter pylori 26695}	0.0	725.0	792	417	403/417 (96%)	Plus / Plus
HP0001 hypothetical protein {Helicobacter pylori 26695}	2	HP1470 DNA polymerase I (polA) {Helicobacter pylori 26695}	0.0040	36.9	39	2679	21/22 (95%)	Plus / Plus
HP0001 hypothetical protein {Helicobacter pylori 26695}	3	HP0266 dihydroorotase (pyrC) {Helicobacter pylori 26695}	0.016	35.1	37	1137	20/21 (95%)	Plus / Plus
HP0002 6,7-dimethyl-8-ribityllumazine		HP0002 6,7-dimethyl-8-ribityllumazine					471/471	Plus /

MyBLAST (standalone) home page



Current running job list.

MyBLAST home page interface. The page includes a navigation menu with 'DB Management', 'Upload DB', 'Run BLAST', and 'Jobs pending' (circled in red). The main content area shows a search management interface with a table of running jobs.

#	DB_id	Program	Description	ProcessID	Start	Status	Detail	Delete
2	1	blastn		4952	2010-09-21 14:29	Running!		<input type="checkbox"/>

Below the table are icons for 'Add', 'Delete', 'BLAST', and 'Job Restart'. The 'Jobs pending' link in the navigation menu is circled in red.

To get the newest running status , you'll need to click the browser's refresh button.

The same MyBLAST home page interface after a browser refresh. The 'CurrentTime' has updated from 14:30:07 to 15:47:31 CST 2010, and the 'current running' status is now 0. A red box highlights the updated 'CurrentTime' and 'current running:0' text. A red arrow points from this box to the 'Jobs pending' link in the navigation menu, which is also circled in red.

Jobs Pending

Current running job list.



Hello!

Welcome to MyBLAST!!

IP: 140.109.16.56

DB Management

Upload DB

Run BLAST



Jobs pending

View Results

:: Search Management ::

CurrentTime: Mon Sep 27 17:29:10 CST 2010 , current running:1

Here's your search lists:

#	DB_id	Program	Description	ProcessID	Start	Status	Detail	Delete
6	1	blastn		5712	2010-09-27 17:28	<input type="checkbox"/> Restart?		<input type="checkbox"/>
7	1	blastn		1872	2010-09-27 17:29	Running!		<input type="checkbox"/>



Add



Delete



BLAST



Job Restart

① Restart checkbox:
Check to restart the particular job. Click the “Job Restart” button to start to do the BLAST again.

② Log link

③ Delete checkbox:
Check to delete the particular job. Click the “Delete” button to start to stop the job and delete the search job.

④ Run BLAST link

⑤ View Results link

MyBLAST Control Panel

- ① Link to import Mysql database data and BLAST data page
- ② Link to backup Mysql database data and BLAST data page
- ③ Link to change port page
- ④ Link to help page
- ⑤ Shutdown or Restart button
- ⑥ MyBLAST Home page button
- ⑦ Link to lab home page
- ⑧ MySQL Community Server running status
- ⑨ Apache Tomcat Web Server running status
- ⑩ Message text area





- Try to restart or shutdown Servers

MyBlast Control Panel

MyBlast

MySQL Community Server V.5.1.37

Apache Tomcat Web Server V.5.5.27

SHUTDOWN

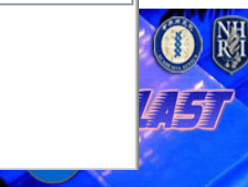
MyBlast Home

Powered by LAB OF System Biology & Network Biology
Academia Sinica, TAIWAN
系統生物學與網路生物學實驗室

Internet Explorer

9.16.56:8080/myblast_standalone/

Home Tools Help



Hello!
Welcome to MyBLAST!!
IP: 140.109.16.56

DB Management

Upload DB

Run BLAST

Jobs pending

View Results

:: Home ::

"My BLAST" web tools .

You can build a customized database and run BLAST analysis.

Try this now!

"Click me to quick view on myblast" (or English Version)




- Try to restart or shutdown Servers

MyBlast Control Panel


MyBlast

MySQL Community Server V.5.1.37 

Apache Tomcat Web Server V.5.5.27 

Import Backup Tools Help





Shutdown tomcat and mysql.....2010/09/30 11:53:13



display the webpage - Windows Internet Explorer

09.16.56.0080/myblast_standalone

File Edit View Favorites Tools Help

Introduction MyBlast linda 系統生物學暨網路生... 建議的網站 取得更多附加元件

display the webpage

Home Stop Back Forward Page Safety Tools

Explorer cannot display the webpage

an try:

Connection Problems

Information



- **Close MyBLAST Control Panel**

MyBlast Control Panel

MyBlast

MySQL Community Server
V.5.1.37

Apache Tomcat Web Server
V.5.5.27

Import Backup Tools Help

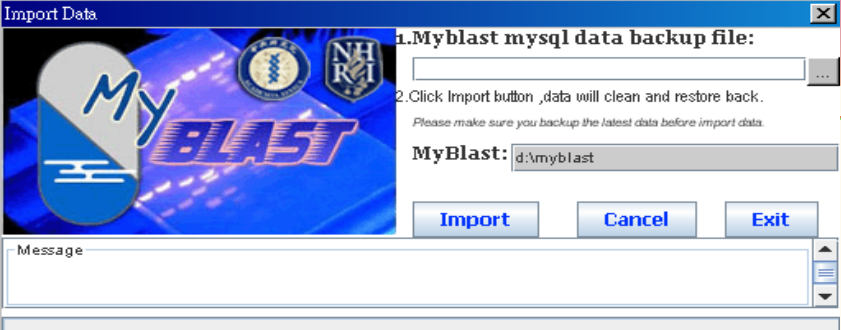
SHUTDOWN

MyBlast Home

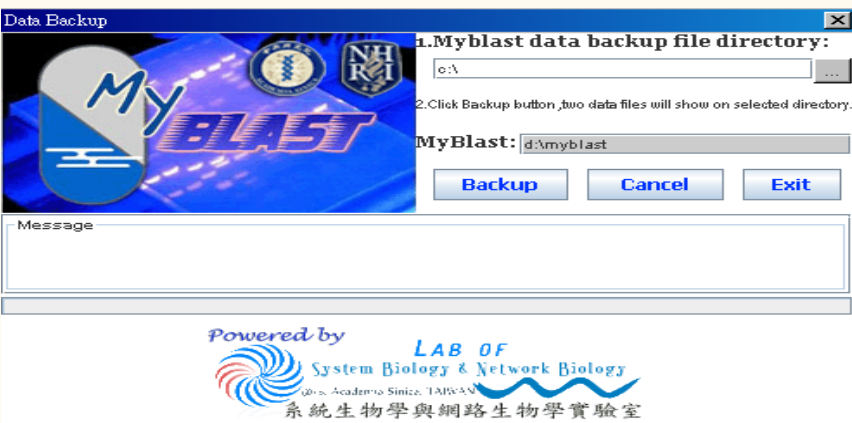
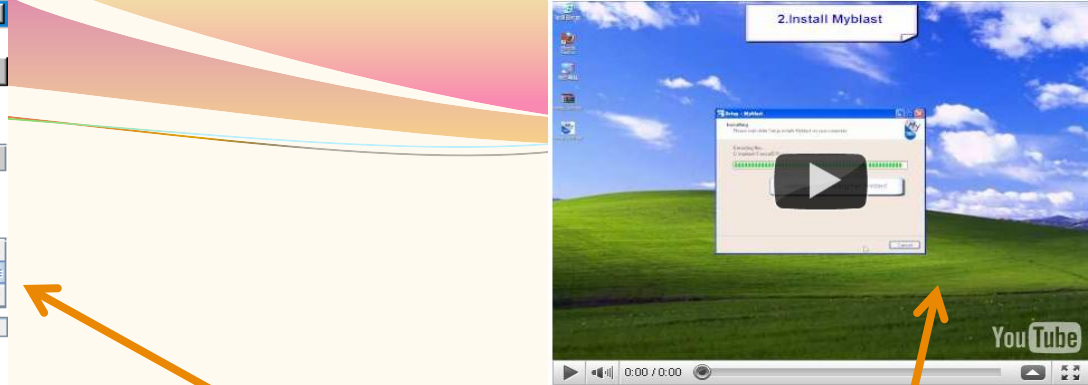
Shutdown tomcat and mysql.....2010/09/30 11:53:13
Restart tomcat and mysql.....2010/09/30 11:59:34

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系統生物學與網路生物學實驗室

Message



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系統生物學與網路生物學實驗室





Example :

Get the FASTA data from After GenBank .
Upload DB, Run BLAST and View Results.

Motivation :: AfterGenBank

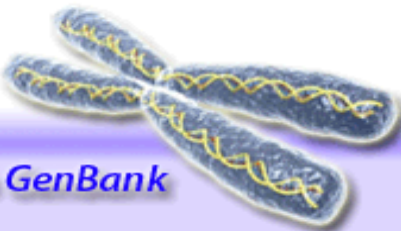
- A quick way to fetch the sequence features (5'UTR, 3' UTR, CDS, Translation) from GenBank only with mouse clicking not programming
- Provide most update collections for specific sequence features like 16s rRNA, ncRNA, etc which can be used to construct databases for search and blast (using myBLAST)
- Provide a friendly GUI to extract specific sequence features by submission of gene list.



Specificity of AfterGenbank

- Collect all the features existed in Genbank for 12 divisions
- Built-in BLAST with specific databases composed by selected features.
- Output in fasta and CSV can be used for further analysis
- Access :

<http://aftergenbank.nhri.org.tw/>



Step 1. choosing the specific division

Step 2. input search term

Search for Organism

Division: (eg. Vibrio cholerae)

- [Keyword : \(eg. toxic\)](#)
- [-AND Search](#)
- [-OR Search](#)
- [-Advanced Search](#)

- Select Division
- Bacterial
- Invertebrate
- Other Mammalian
- Patent
- Phage
- Plant
- Primate
- Rodent
- Synthetic
- Unannotated
- Viral
- Other Vertebrate

twelve divisions

- Type 1. Organism.
- Type 2. Organism a
- Type 3. Organism a
- Type 4. Keyword.
- Type 5. Accession n

Accession Number : (eg. AB016894)

-Accession Number Search

Use Accession Number: ?

Search for Accession number

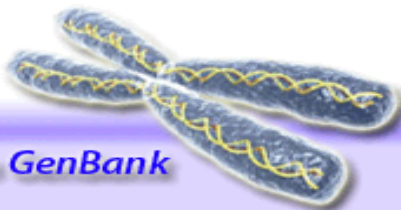
- 3'UTR
- 5'UTR
- 10 signal
- 35 signal
- attenuator
- C region
- CAAT
- CDS
- CDS_translation
- conflict
- D-loop
- D segment
- enhancer
- exon
- gap
- GC signal
- 5 segment
- LTR
- mat peptide
- misc feature
- misc recomb
- misc RNA
- misc signal
- misc structure
- modified base
- mRNA
- N region

Step 3. choosing the interested feature

Or load it from file

- primer bind
- promoter
- protein bind
- RBS
- rep origin
- repeat region
- rRNA
- S region
- tRNA
- unsure
- V region
- V segment
- variation

Step 4. submit



Search Result Page

Division : Bacterial Organism : *Vibrio cholerae*

Accession Number : EU523703 EU523704 EU523705 EU523706

Feature : 5'UTR.

7 feature(s) are found in this search. Total result number

Page 1 of 1 page(s)

Show 20 features in page Show not found Accession id

Select Page 1 All/Null Refresh the count

ALL (.fasta) ALL (.fasta) ALL (.CSV)

1.	EU523703	<i>Vibrio cholerae</i> strain NAG-V17 hemagglutinin protease regulatory protein (hapR) gene, complete cds.	<i>Vibrio cholerae</i>
<input type="checkbox"/>	Feature	5'UTR	
	Range	1..542	
	gene	hapR	
2.	EU523704	<i>Vibrio cholerae</i> strain TSI-4S hemagglutinating/protease regulatory protein-like (hapR) gene, partial sequence.	<i>Vibrio cholerae</i>
<input type="checkbox"/>	Feature	5'UTR	
	Range	1..542	
	gene	hapR	
3.	EU523705	<i>Vibrio cholerae</i> strain TSI-4B hemagglutinating/protease regulatory protein-like (hapR) gene, partial sequence.	<i>Vibrio cholerae</i>
<input type="checkbox"/>	Feature	5'UTR	
	Range	1..542	
	gene	hapR	
4.	EU523706	<i>Vibrio cholerae</i> strain CB1 hemagglutinin/protease regulatory protein (hapR) gene, complete cds.	<i>Vibrio cholerae</i>
<input type="checkbox"/>	Feature	5'UTR	

Search terms

Total result number

Show not found Accession id

Change page

Refresh the count

Result

Locus id

download file

The definition of Locus id

Organism

Feature

More annotation

AfterGenBank

- website

<http://aftergenbank.nhri.org.tw/>



The screenshot shows the AfterGenBank website in a Windows Internet Explorer browser window. The address bar is highlighted with a red box and contains the URL <http://aftergenbank.nhri.org.tw/AfterGenbank/>. The website header features the "AfterGenBank" logo, a stylized DNA double helix, and navigation links for "Repository", "BLAST", "Home", "Contact", "Tools", and "Help". Below the header, the text "GenBank Release 178.0(Release Date:June 15, 2010)" is displayed. The main search area includes a "Text Search Term" field with a "HELP" link, and several search criteria: "Division" (a dropdown menu), "Organism" (a text input field with examples like "Vibrio cholerae"), "Keyword" (a text input field with examples like "toxin, 16s rRNA"), and "Accession Number" (a text input field with examples like "AB016894"). Below these search fields, there are links for "-AND Search", "-OR Search", and "-Advanced Search", as well as a link for "-Accession Number Search". The "Feature Extract" section is visible at the bottom, showing a grid of checkboxes for various genomic features such as 3'UTR, 5'UTR, gene, ncRNA, and sig peptide.

• Let's try to click example1

After GenBank
annotated-Feature Extractor from GenBank

Repository
Home Contact Tools

GenBank Release 178.0(Release Date:June 15, 2010)

Text Search Term [HELP](#)

Division:

Organism: (eg. Vibrio cholerae)

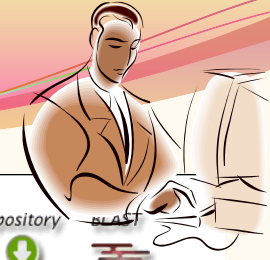
[Keyword](#) :(eg. toxin, 16s rRNA) [Accession Number](#) :(eg. AB016894)

-AND Search
-OR Search
-Advanced Search

-Accession Number Search

Feature Extract

<input type="checkbox"/> 3'UTR	<input type="checkbox"/> gene	<input type="checkbox"/> ncRNA	<input type="checkbox"/> sig peptide
<input checked="" type="checkbox"/> 5'UTR	<input type="checkbox"/> iDNA	<input type="checkbox"/> old sequence	<input type="checkbox"/> source
<input type="checkbox"/> -10 signal	<input type="checkbox"/> intron	<input type="checkbox"/> operon	<input type="checkbox"/> stem loop
<input type="checkbox"/> -35 signal	<input type="checkbox"/> J segment	<input type="checkbox"/> oriT	<input type="checkbox"/> STS
<input type="checkbox"/> attenuator	<input type="checkbox"/> LTR	<input type="checkbox"/> polyA signal	<input type="checkbox"/> TATA signal
<input type="checkbox"/> C region	<input type="checkbox"/> mat peptide	<input type="checkbox"/> polyA site	<input type="checkbox"/> terminator
<input type="checkbox"/> CAAT signal	<input type="checkbox"/> misc binding	<input type="checkbox"/> precursor RNA	<input type="checkbox"/> tmRNA
<input type="checkbox"/> CDS	<input type="checkbox"/> misc difference	<input type="checkbox"/> prim transcript	<input type="checkbox"/> transit peptide
<input type="checkbox"/> CDS_translation	<input type="checkbox"/> misc feature	<input type="checkbox"/> primer bind	<input type="checkbox"/> tRNA
<input type="checkbox"/> conflict	<input type="checkbox"/> misc recomb	<input type="checkbox"/> promoter	<input type="checkbox"/> unsure
<input type="checkbox"/> D-loop	<input type="checkbox"/> misc RNA	<input type="checkbox"/> protein bind	<input type="checkbox"/> V region
<input type="checkbox"/> D segment	<input type="checkbox"/> misc signal	<input type="checkbox"/> RBS	<input type="checkbox"/> V segment
<input type="checkbox"/> enhancer	<input type="checkbox"/> misc structure	<input type="checkbox"/> rep origin	<input type="checkbox"/> variation
<input type="checkbox"/> exon	<input type="checkbox"/> modified base	<input type="checkbox"/> repeat region	
<input type="checkbox"/> gap	<input type="checkbox"/> mRNA	<input type="checkbox"/> rRNA	
<input type="checkbox"/> GC signal	<input type="checkbox"/> N region	<input type="checkbox"/> S region	



Waiting page

After GenBank
nnotated-Feature Extractor from GenBank

Repository BLAST

Home Contact Tools Help



Division of Biostatistics and Bioinformatics
National Health Research Institutes
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Lasted Updated 2010/7/28

- Wait the result.

- Click Download.

Result page

After GenBank
nnotated-Feature Extractor from GenBank

Repository BLAST

Home Contact Tools Help

Search Result Page

Division : Bacterial Organism : Vibrio cholerae
Feature : 5'UTR.

18 feature(s) are found in this search.

Page 1 of 1 page(s).

Show 20 features in page

Select Page 1 All/Null

refresh 0 feature(s) are selected by user.

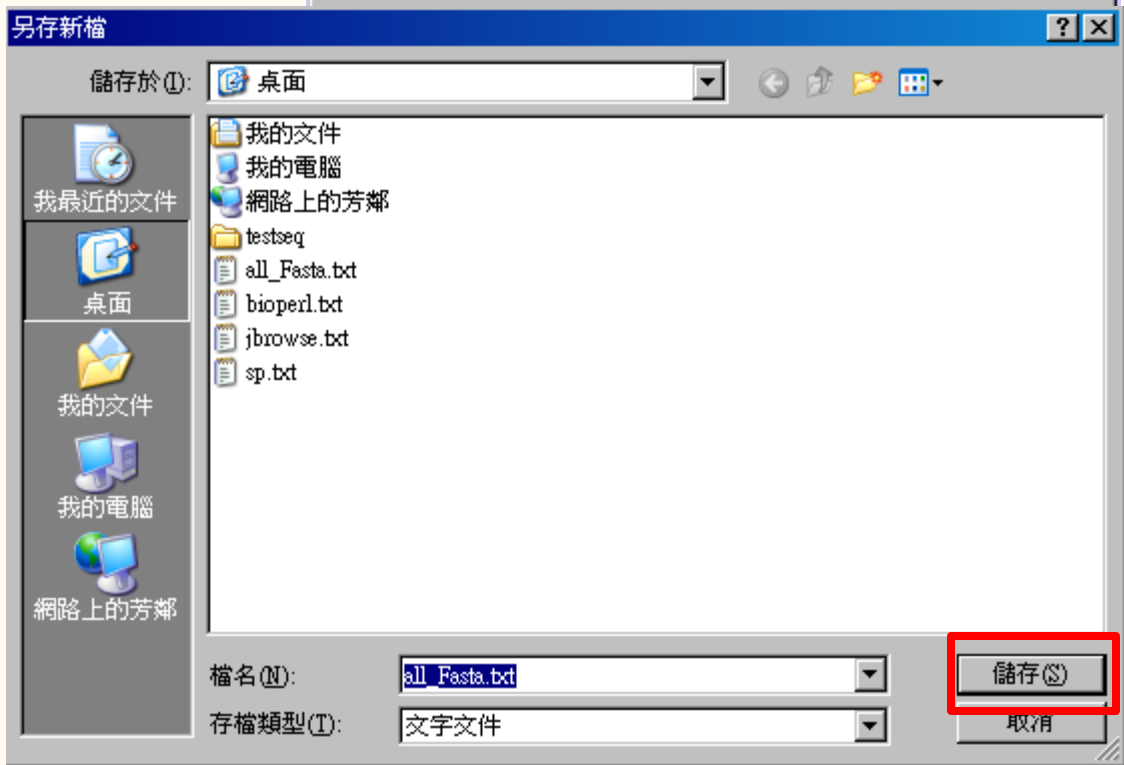
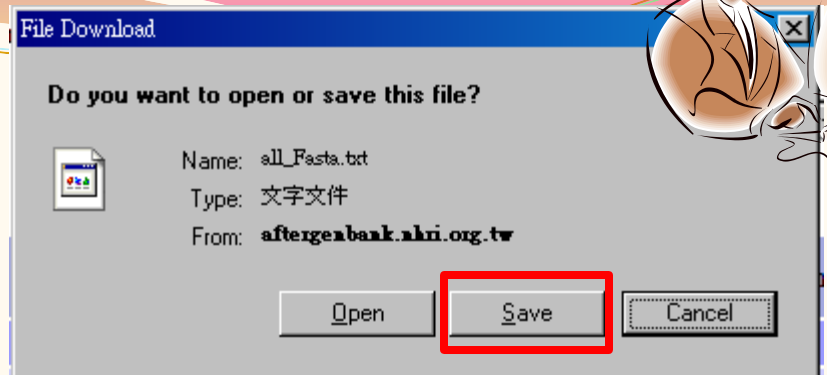
Download ALL (.fasta)

[Back to Search Page](#)

1.	EU523702	Vibrio cholerae strain 93Ag13 hemagglutinin/protease regulatory protein (hapR) gene, complete cds.	<i>Vibrio cholerae</i>
<input type="checkbox"/>	Feature	5'UTR	
	Range	1..542	
	gene	hapR	
2.	EU523703	Vibrio cholerae strain NAG-V17 hemagglutinin/protease regulatory protein (hapR) gene, complete cds.	<i>Vibrio cholerae</i>
<input type="checkbox"/>	Feature	5'UTR	
	Range	1..542	

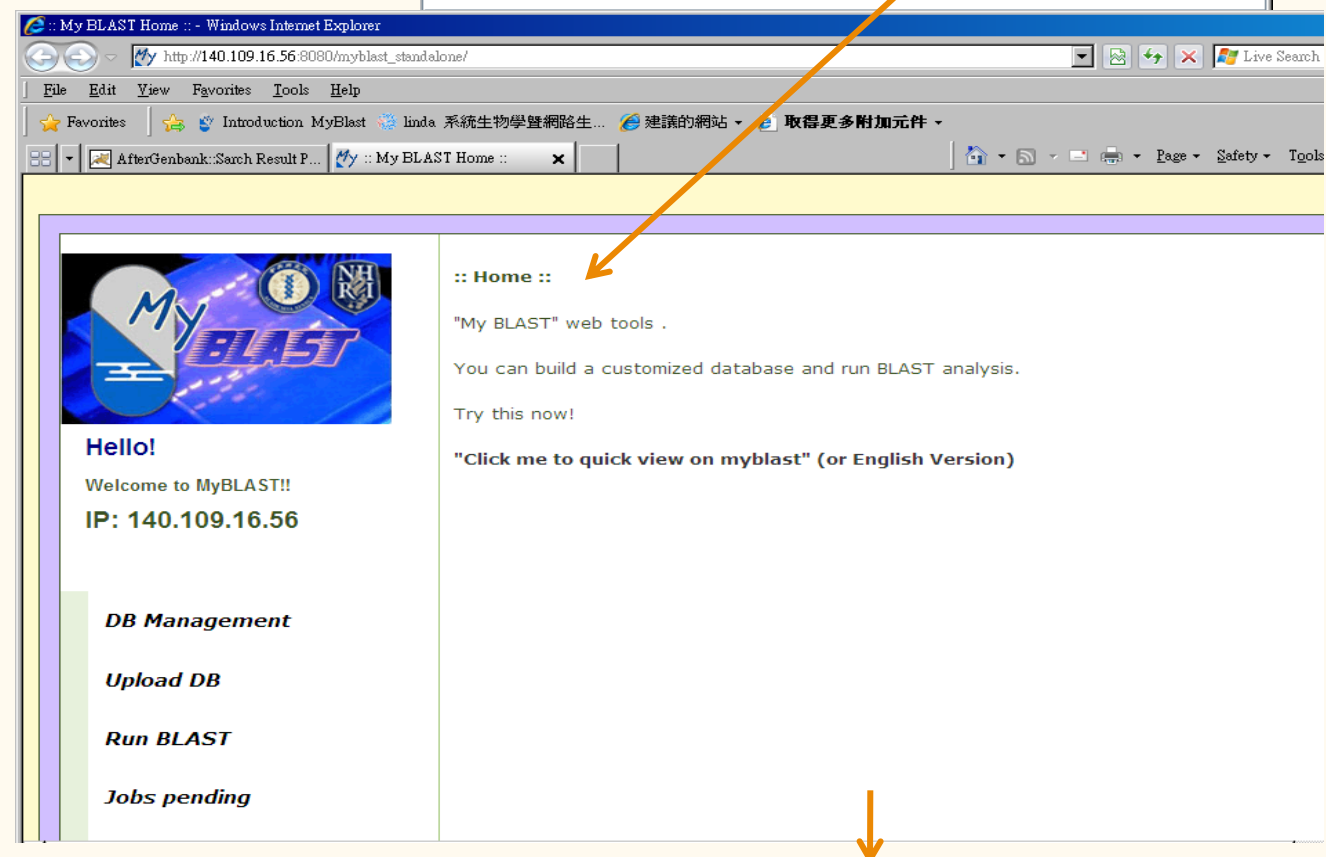
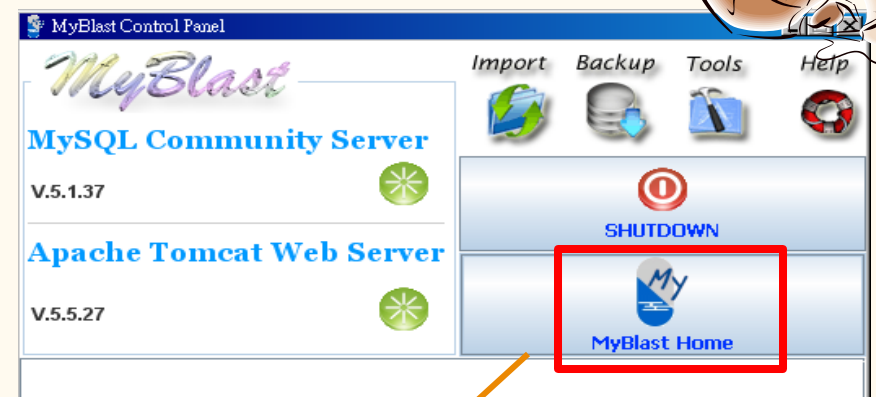


- **Save to the computer (Ex. desktop).**





- **MyBLAST website**
Open MyBlast ControlPanel.
Click Myblast Home button.





• Upload DB

My BLAST Home :: - Windows Internet Explorer
http://140.109.16.56:8080/myblast_standalone/MainMenu?act=upload_db_page

File Edit View Favorites Tools Help

AfterGenbank::Sarch Result P... My BLAST Home ::

Hello!
Welcome to MyBLAST!!
IP: 140.109.16.56

DB Management

- Upload DB**
- Run BLAST
- Jobs pending
- View Results

:: Upload Database ::

Upload your sequences to build a mini database.

Your Sequence Type:

Nucleotide
 Protein

Enter sequences below in FASTA format:

Or load from disk

Database Description (optional) :





• Upload DB

My BLAST Home :: - Windows Internet Explorer
http://140.109.16.56:8080/myblast_standalone/MainMenu?act=upload_db_page

File Edit View Favorites Tools Help

AfterGenbank::Sarch Result P... My BLAST Home ::

My BLAST

Hello!
Welcome to MyBLAST!!
IP: 140.109.16.56

DB Management

- Upload DB**
- Run BLAST
- Jobs pending
- View Results
- User Guide
- Contact Us

:: Upload Database ::

Upload your sequences to build a mini database.

Your Sequence Type:

Nucleotide
 Protein

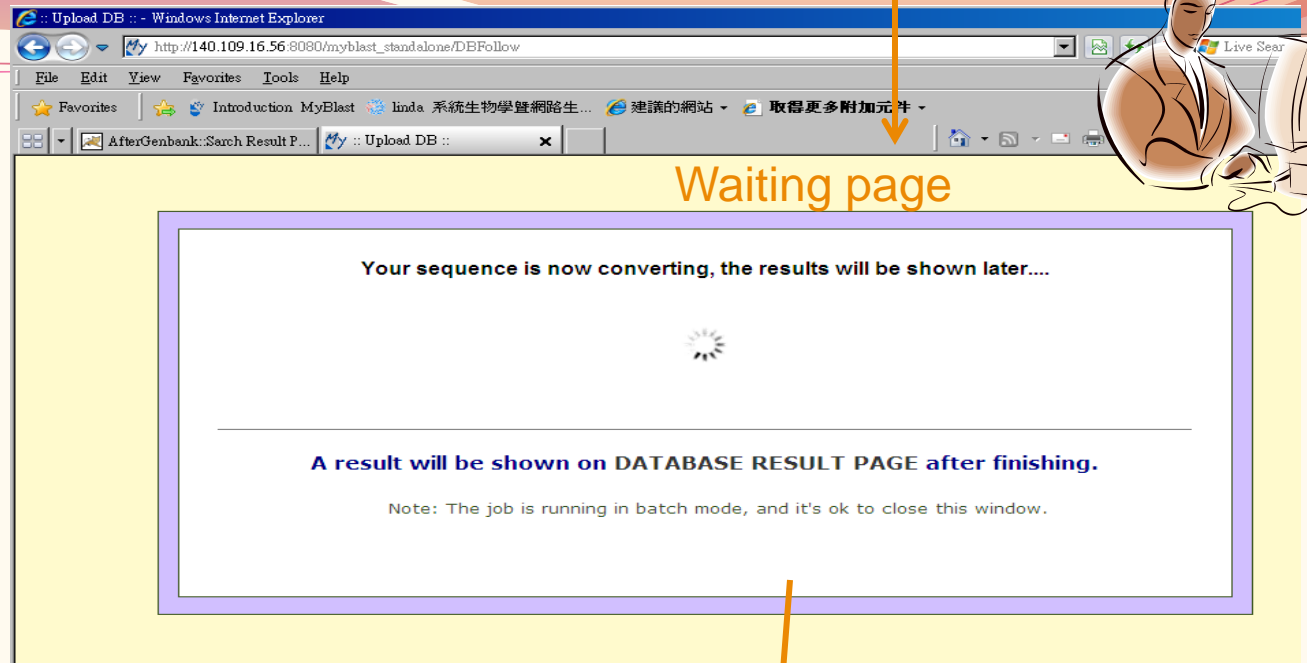
Enter sequences below in **FASTA** format:

Or load from disk

Database Description (optional) :



- **Upload DB**




Windows Internet Explorer
http://140.109.16.56:8080/myblast_standalone/DBFollow

File Edit View Favorites Tools Help

Waiting page

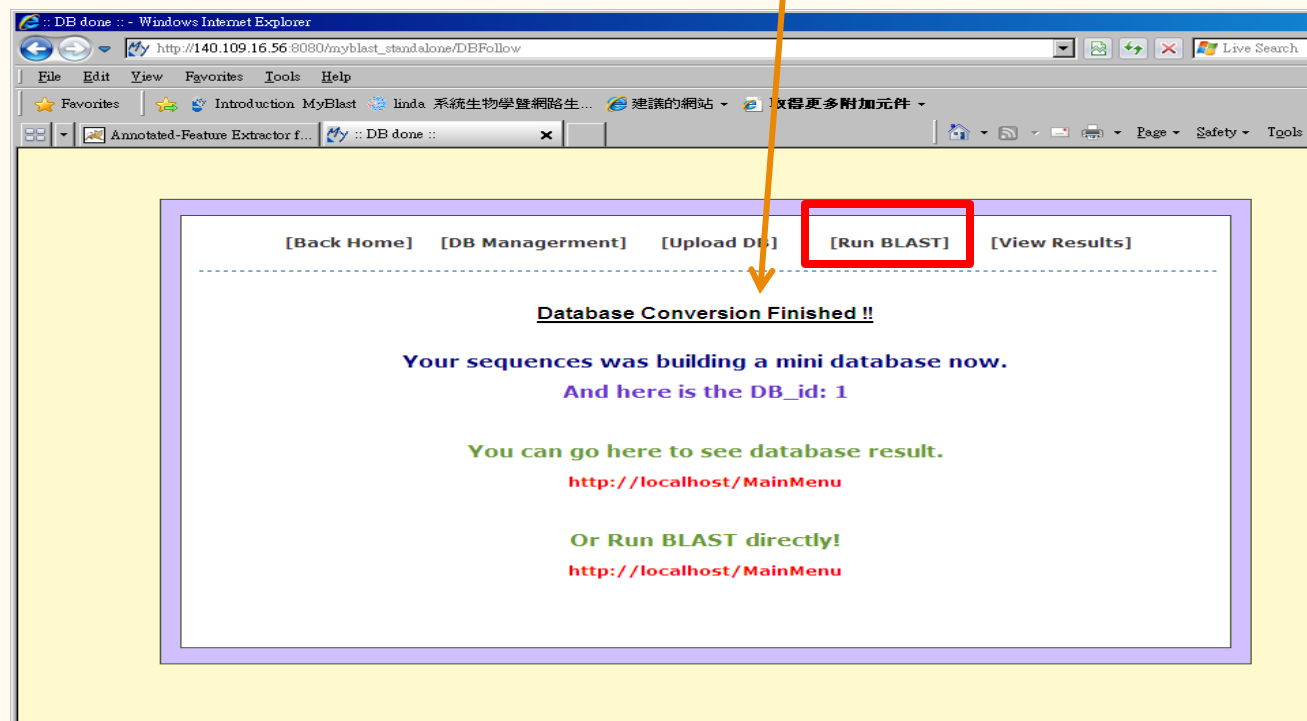
Your sequence is now converting, the results will be shown later....



A result will be shown on DATABASE RESULT PAGE after finishing.

Note: The job is running in batch mode, and it's ok to close this window.

An illustration of a person in a suit is visible in the top right corner of the browser window.



Windows Internet Explorer
http://140.109.16.56:8080/myblast_standalone/DBFollow

File Edit View Favorites Tools Help

[Back Home] [DB Management] [Upload DB] [Run BLAST] [View Results]

Database Conversion Finished !!

Your sequences was building a mini database now.
And here is the DB_id: 1

You can go here to see database result.
<http://localhost/MainMenu>

Or Run BLAST directly!
<http://localhost/MainMenu>

The [Run BLAST] link in the navigation bar is highlighted with a red box, and an arrow points from this box to the 'Database Conversion Finished !!' message.

- **Run BLAST**

My BLAST Home :: - Windows Internet Explorer

http://140.109.16.56:8080/myblast_standalone/MainMenu?act=search_program_sel

File Edit View Favorites Tools Help

★ Favorites Introduction MyBlast linda 系統生物學暨網路生... 建議的網站 取得更多附加元件

Annotated-Feature Extractor f... My BLAST Home ::

My BLAST

Hello!

Welcome to MyBLAST!!

IP: 140.109.16.56

DB Management

Upload DB

Run BLAST

Jobs pending

:: Choose a BLAST program to run ::

Nucleotide BLAST	blastn megablast
Protein BLAST	blastp
Translated BLAST	blastx tblastn tblastx

• Run BLAST

My BLAST Home :: - Windows Internet Explorer
http://140.109.16.56:8080/myblast_standalone/MainMenu?act=search_page&program=blastp

File Edit View Favorites Tools Help

Introduction MyBlast linda 系統生物學暨網路生... 建議的網站 取得更多附加元件

Annotated-Feature Extractor f... My BLAST Home ::

My BLAST

Hello!

Welcome to MyBLAST!!
IP: 140.109.16.56

- DB Management
- Upload DB
- Run BLAST
- Jobs pending
- View Results
- User Guide
- Contact Us

:: Run blastp with your DB ::

Program: blastp (search protein databases using a protein query)

Job Note:

Enter sequence below in FASTA format

Or load it from disk:

Select Database:

Advanced Options:

Max target:

E-value:

Matrix:

Gap creation: Existence: 11 Extension: 1

Word size:

Turn off the low complexity filter

- Run BLAST

Running BLAST :: - Windows Internet Explorer

http://140.109.16.56:8080/myblast_standalone/ElastFollow

File Edit View Favorites Tools Help

Now is working, the BLAST results will be shown later....

The BLAST result will be shown on BLAST RESULT PAGE after finishing.

Note: The job is running in batch mode, and it's ok to close this window.

Waiting page

BLAST Results :: - Windows Internet Explorer

http://140.109.16.56:8080/myblast_standalone/ElastFollow

File Edit View Favorites Tools Help

[Back Home] [Upload DB] [Run BLAST] [View Results]

MyBLAST Results ::

DB description: (1) Vibrio cholerae

Submit description: (1) First

Download Output Files (text file) or (csv file)

Matche Sequences: Top 3

Seq.	Rank	Hits	E-value	Score	Bits	Match Length	Identities
Ic 5"UTR_1 EU523702(1..542) Vibrio cholerae strain 93Ag13hemagglutinin/teprotease regulatory protein (hapR) gene, completecds. Vibrio cholerae	1	5"UTR_1 cholerae strain 93Ag13 hemagglutinin/teprotease regulatory protein (hapR) gene, complete cds. Vibrio cholerae	0.0	1219.0	3154	542	542/542 (100%), Positives = 542/542 (100%)
Ic 5"UTR_1 EU523702(1..542) Vibrio cholerae strain 93Ag13hemagglutinin/teprotease	2	5"UTR_18 cholerae strain 93Ag19 hemagglutinin/teprotease regulatory protein	0.0	1217.0	3150	542	541/542 (99%), Positives =

Result page



View Results

MyBLAST Home

http://140.109.16.56:8080/myblast_standalone/MainMenu?act=result_list_page

File Edit View Favorites Tools Help

DB Management

Upload DB

Run BLAST

:: BLAST Results ::

Here's BLAST result lists:

Database Description	Submit Description	Date	Result	Detail	delete
(1)Vibrio cholerae	(1)First	2010-09-30 15:59 ~ 2010-09-30 15:59 (0.00hr. Size:0.46MB)			<input type="checkbox"/>

Delete

BLAST Results

http://140.109.16.56:8080/myblast_standalone/BlastFollow?act=result&submit_id=1&job_id=1

File Edit View Favorites Tools Help

[Back Home] [Upload DB] [Run BLAST] [View Results]

:: MyBLAST Results ::

DB description: (1) Vibrio cholerae

Submit description: (1) First

Matche Sequences: Top 3 [Go] [Download]

Download Output Files (text file) or (csv file)

Seq.	Rank	Hits	E-value	Score	Bits	Match Length	Identities
lcl 5"UTR_1 EU523702(1..542) Vibrio cholerae strain 93Ag13hemagglutinin/protease regulatory protein (hapR) gene, completecds. Vibrio cholerae	1	5"UTR_1 cholerae strain 93Ag13 hemagglutinin/protease regulatory protein (hapR) gene, complete cds. Vibrio cholerae	0.0	1219.0	3154	542	542/542 (100%), Positives = 542/542 (100%)
lcl 5"UTR_1 EU523702(1..542) Vibrio cholerae strain 93Ag13hemagglutinin/protease	2	5"UTR_18 cholerae strain 93Ag19 hemagglutinin/protease regulatory protein	0.0	1217.0	3150	542	541/542 (99%), Positives =

Result page



Flash Demo



[Search](#) [Repository](#) [BLAST](#) [Demo](#)

Introduction

Search



Hello!

Welcome to MyBLAST!!

IP: 140.109.16.56

DB Management

Upload DB

Run BLAST

Jobs pending

:: Home ::

"My BLAST" web tools .

You can build a customized database and run BLAST analysis.

Try this now!

[Click me to quick view on myblast" \(or English Version\)](#)

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