

# 高通量生物序列比對平台: *myBLAST*



## *A Customized BLAST Platform For Genomics, Transcriptomics And Proteomics With Paralleled Computing On Your Desktop or Somewhere*

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Sep 17, 2014



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# What's BLAST

## BLAST (生物資訊學)

維基百科，自由的百科全書

生物資訊學中，**BLAST**(**B**asic **L**ocal **A**lignment **S**earch **T**ool") 它是一個用來比對**生物序列**的一級結構（如不同**蛋白質**的**胺基酸**序列或不同**基因**的**DNA**序列）的演算法。已知一個包含若干序列的資料庫，BLAST可以讓研究者在其中尋找與其感興趣的序列相同或類似的序列。例如如果某種非人動物的一個以前未知的基因被發現，研究者一般會在人類基因組中做一個BLAST搜索來確認人類是否包含類似的基因（通過序列的相似性）。BLAST演算法以及實現它的程序由**美國國家生物技術信息中心**（NCBI）的**Eugene Myers**、**Stephen Altschul**、**Warren Gish**、**David J. Lipman**及**Webb Miller**博士開發[1]的。

研究者利用BLAST來解決的其他問題有：

- 哪個**細菌物種**包含與**胺基酸**序列已知的某**蛋白質**有親緣關係的蛋白質？
- 被測序的一段**DNA**來自哪裡？
- 何種基因編碼的蛋白質表現出剛剛被確定的某種結構或**結構模體**？

.....等等。



# *Sequence in FASTA format*

- FASTA format

- an simplest incarnation of the FASTA format

```
>U54469.1  
CGGTTGCTTGGGTTTTATAACATCAGTCAGTGACAGGCATTTCCAGAGTTGCCCTGTTCAACAATCGATA  
GCTGCCTTTGGCCACCAAATCCCAAACCTTAATTAAAGAATTAAA.....
```

**>Definition Line  
sequence (60mer/lane)**

- a modified FASTA format

```
>gi|1322283|gb|U54469.1|DMU54469 Drosophila melanogaster eukaryotic  
initiation factor 4E (eIF4E) gene, alternative splice products, complete  
cds  
CGGTTGCTTGGGTTTTATAACATCAGTCAGTGACAGGCATTTCCAGAGTTGCCCTGTTCAACAATCGATA  
GCTGCCTTTGGCCACCAAATCCCAAACCTTAATTAAAGAATTAAATAATTTCG.....
```

# *FASTA Format (DNA)*

```
>gi|3954981|emb|AJ130968.1|MRO130968 M. rosenbergii partial  
mRNA for CHH gene
```

```
GCCATCCTCGACCAGTCCTGCAAAGGTATCTTCGACCGTGAGCTCTTCAAGAAGCTCGACCGT  
GTCTGCGACGATTGTTACAACCTCTACAGGAAGCCTTACGTCGCCATCGACTGCAGGGAGGGC  
TGCTACCAGAACTTGGTCTTCCGACAGTGCATCCAGGACCTCCAGTTGATGGACCAACTCGAC  
GAATACGCCAACGCTGTCCAGATCGTCGGGAAG
```

## Nuclecleic Acid Code:

A --> adenosine	M --> A C (amino)
C --> cytidine	S --> G C (strong)
G --> guanine	W --> A T (weak)
T --> thymidine	B --> G T C
U --> uridine	D --> G A T
R --> G A (purine)	H --> A C T
Y --> T C (pyrimidine)	V --> G C A
K --> G T (keto)	N --> A G C T (any)
- gap of indeterminate length	

# *FASTA Format (Protein)*

>sp|P05534|1A24\_HUMAN HLA class I histocompatibility antigen, A-24  
alpha chain OS=Homo sapiens GN=HLA-A

```
MAVMAPRTLVLGALALTQTWAGSHSMRYFSTSVSRPGRGEPFIAVGYVDDTQFVRFSDAASQRMEPRAPWIE  
QEGPEYWDEETGKVKAHSQTDRENLRALRYYNQSEAGSHTLQMMFGCDVGS DGRFLRGYHQYAYDGKDYIALKEDL  
RSWTAADMAAQITKRKWEAAHVAEQQRAYLEGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALG  
FYPAEITLTWQRDGEDQTQDTELVETRPAGDGTQKWA AVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS SQPTVPI  
VGIIAGLVLLGAVITGAVVA VMWRRNSSDRKGGSYSQAASSDSAQGS DVS LTACKV
```

Amino Acid Code:

A	alanine	P	proline
B	aspartate or asparagine	Q	glutamine
C	cystine	R	arginine
D	aspartate	S	serine
E	glutamate	T	threonine
F	phenylalanine	U	selenocysteine
G	glycine	V	valine
H	histidine	W	tryptophan
I	isoleucine	Y	tyrosine
K	lysine	Z	glutamate or glutamine
L	leucine	X	any
M	methionine	*	translation stop
N	asparagine	-	gap of indeterminate length

# *The Programs Of BLAST*

<b>Applications</b>	<b>Query Type</b>	<b>Database Type</b>
<b>blastn</b>	nucleotide	nucleotide
<b>blastp</b>	protein	protein
<b>blastx</b>	translated nucleotide	protein
<b>tblastn</b>	protein	translated nucleotide
<b>tblastx</b>	translated nucleotide	translated nucleotide

# NCBI BLAST

Perform BLAST on pre-defined Databases

## BLAST Assembled Genomes

Choose a species genome to search, or [list all genomic BLAST databases](#).

- [Human](#)
- [Mouse](#)
- [Rat](#)
- [Arabidopsis thaliana](#)
- [Oryza sativa](#)
- [Bos taurus](#)
- [Danio rerio](#)
- [Drosophila melanogaster](#)

## Basic BLAST

Choose a BLAST program to run.

- nucleotide blast** Search **nucleotide** database using a **nucleotide** query  
Algorithms: [blastn](#), [megablast](#), [discontiguous megablast](#)
- [protein blast](#) Search **protein** database using a **protein** query  
Algorithms: [blastp](#), [psi-blast](#), [phi-blast](#)
- [blastx](#) Search **protein** database using a **translated nucleotide** query
- [tblastn](#) Search **translated nucleotide** database using a **protein** query
- [tblastx](#) Search **translated nucleotide** database using a **translated nucleotide** query

## Specialized BLAST

Choose a type of specialized search (or database name in parentheses.)

- Make specific primers with [Primer-BLAST](#)
- Search [trace archives](#)
- Find [conserved domains](#) in your sequence (cds)
- Find sequences with similar [conserved domain architecture](#) (cdart)
- Search sequences that have [gene expression profiles](#) (GEO)
- Search [immunoglobulins](#) (IgBLAST)
- Search for [SNPs](#) (snp)
- Screen sequence for [vector contamination](#) (vecscreen)
- [Align](#) two (or more) sequences using BLAST (bl2seq)
- Search [protein](#) or [nucleotide](#) targets in PubChem BioAssay
- Search SRA [transcript libraries](#)
- Constraint Based Protein [Multiple Alignment Tool](#)

NCBI/ BLAST/ blastn suite

blastn | [blastp](#) | [blastx](#) | [tblastn](#) | [tblastx](#) BLASTN program

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#) [Query subrange](#)

From

To

Or, upload file [選擇檔案](#) 未選擇任何檔案

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Database  Human genomic + transcript  Mouse genomic + transcript  Others (nr etc.):

Organism   Exclude

Exclude  Models (XM/XP)  Uncultured/environmental sample sequences

Limit to  Sequences from type material

Entrez Query  [YouTube](#) [Create custom database](#)

Program Selection

Optimize for  Highly similar sequences (megablast)  More dissimilar sequences (discontiguous megablast)  Somewhat similar sequences (blastn)

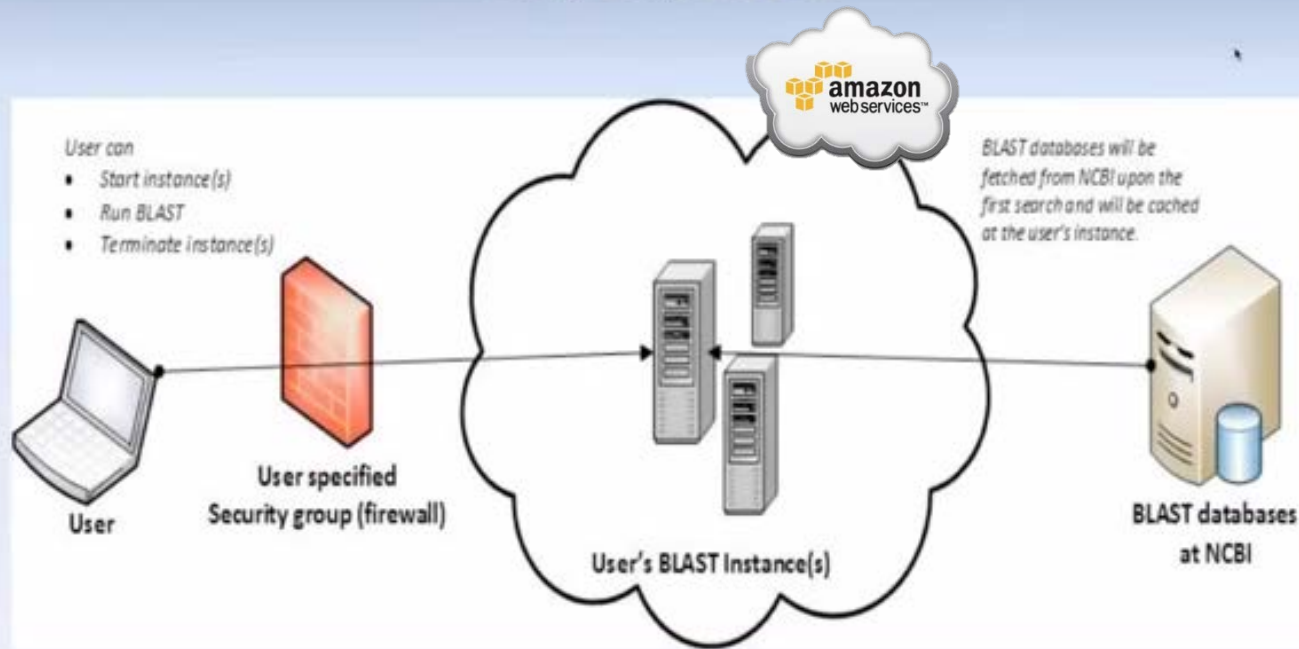
Choose a BLAST algorithm

**BLAST** Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)  Show results in a new window

Specify and shrink Database

# NCBI BLAST in the Cloud

July 30, 2014



7/30/14

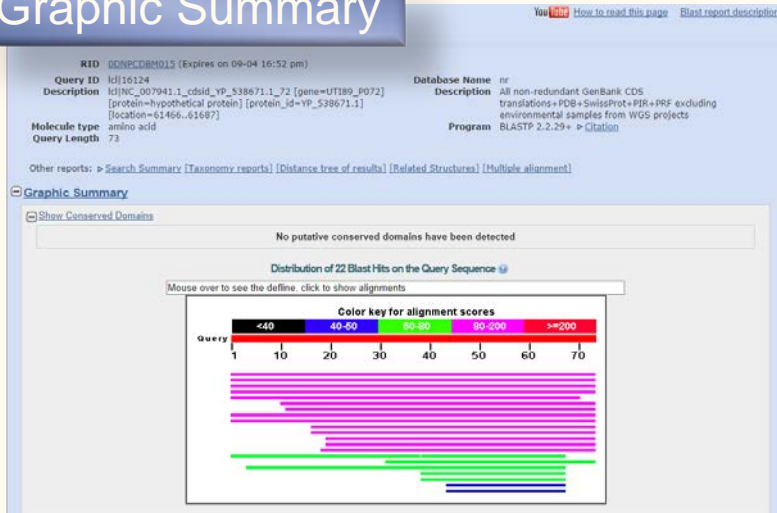


1



# Typical BLAST Output

## Graphic Summary



## Hits in detail

Sequences producing significant alignments:

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

Alignments [Download](#) [GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> <a href="#">MULTISPECIES: hypothetical protein [Escherichia]</a>	149	149	100%	1e-44	100%	<a href="#">WP_001336408.1</a>
<input type="checkbox"/> <a href="#">hypothetical protein [Escherichia coli]</a>	148	148	100%	2e-44	100%	<a href="#">WP_001431134.1</a>
<input type="checkbox"/> <a href="#">hypothetical protein [Escherichia coli]</a>	146	146	100%	1e-43	99%	<a href="#">WP_001746024.1</a>
<input type="checkbox"/> <a href="#">hypothetical protein AC16_4947 [Escherichia coli 2-177-06 S3_C2]</a>	143	143	100%	2e-42	97%	<a href="#">KDX40558.1</a>
<input type="checkbox"/> <a href="#">hypothetical protein [Yersinia pestis]</a>	128	128	95%	1e-36	91%	<a href="#">WP_011171999.1</a>

## Pairwise Alignment

[Download](#) [GenPept](#) [Graphics](#) [Next](#) [Previous](#) [Descriptions](#)

MULTISPECIES: hypothetical protein [Escherichia]  
 Sequence ID: [ref|WP\\_001336408.1](#) Length: 73 Number of Matches: 1  
[See 18 more title\(s\)](#)

Range 1: 1 to 73 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
149 bits(375)	1e-44	Compositional matrix adjust.	73/73(100%)	73/73(100%)	0/73(0%)

```

Query 1  MAGLSGWRFRVFEVASDRPFRRATNLSRNDINVRALLAHLHYHVKVLSAQHVDVLSGVRTL 60
          MAGLSGWRFRVFEVASDRPFRRATNLSRNDINVRALLAHLHYHVKVLSAQHVDVLSGVRTL
Sbjct 1  MAGLSGWRFRVFEVASDRPFRRATNLSRNDINVRALLAHLHYHVKVLSAQHVDVLSGVRTL 60

Query 61  RKQHVGWISGQSKW 73
          RKQHVGWISGQSKW
Sbjct 61  RKQHVGWISGQSKW 73
  
```

**Related Information**

- [Gene](#) - associated gene details
- [Identical Proteins](#) - Proteins identical to the subject

# The Output: Pair wise , Local Alignment

Source of database      Accession #      Name of sequence      Species

```
>prfl|1802398A crustacean hyperglycemic hormone [Orconectes limosus]
Length = 72
Score = 115 bits (286), Expect = 6e-26
Identities = 49/71 (69%), Positives = 58/71 (81%)
Query: 2  ILDQSCKGIFDRELFKKLDRVCDDCYNLYRKPYVAIDCREGICYQNLVFRQCIODLQLMDQ 61
+ DQ+CKGI+DR +FKKLD RVC+DCYNLYRKPYVA CR+ CY N VFRQC+ DL L+D
Sbjct: 2  VFDQACKGIYDRAIFKKLDRVCEDCYNLYRKPYVATTCRQNCYANSVFRQCLDDLLIDV 61
Query: 62  LDEYANAVQIV 72
LDEY + VQ V
Sbjct: 62  LDEYISGVQTV 72
```

Full length

Start point of sequence

End point of sequence

Identical sequence

Similarity Sequence

# Submit Multiple Seqs to NCBI BLAST

- 145 Protein sequences vs. nr Database
- After 15 minutes, we got

NCBI/ BLAST/ blastp suite/ Formatting Results - 0DSX0DCJ014

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

**There was a problem with the search. Please, contact [Help Desk](#) and include RID 0DSX0DCJ014**

**Informational Message: [blastsrv4.REAL]: Error: CPU usage limit was exceeded, resulting in SIGXCPU (24).**

145 sequences (lcl|NC\_007941.1\_cdsid\_YP\_538600.1\_1...

**Results for:** \*1:lcl|72572 lcl|NC\_007941.1\_cdsid\_YP\_538600.1\_1 [gene=UTI89\_P001] [protein=hypothetical protein] [protein\_id=YP...(196aa)]

**RID** 0DSX0DCJ014 (Expires on 09-04 17:47 pm)

<b>Query ID</b>	lcl 72572	<b>Database Name</b>		<b>Description</b>	<a href="#">See details</a>
<b>Description</b>	lcl NC_007941.1_cdsid_YP_538600.1_1 [gene=UTI89_P001] [protein=hypothetical protein] [protein_id=YP_538600.1] [location=1..591]	<b>Program</b>	BLASTP 2.2.29+		<a href="#">Citation</a>
<b>Molecule type</b>	amino acid				
<b>Query Length</b>	196				

**No significant similarity found. For reasons why, [click here](#)**

Other reports: [Search Summary](#)



# *Issues Remained After BLAST*

- Input
  - Single sequence
  - Multiple sequences up to hundreds of thousands of seq.
- Where to perform computing
- Security/ Confidential of Data
- Databases
  - From NCBI existed DBs
  - Customized Databases
  - DBs Management/ re-use and backup
- Results
  - How to extract the information from BLAST result
  - Results management
  - Best hit for each query



# *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, even download the hits in fasta**
- A blast service can be **shared for small group / personal use**
- **Databases and results can be backup**
- **Run BLAST with handy platform**




# *myBlast vs. NCBI BLAST*



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


# myBLAST online Web -

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



Email

PWD

 [Has not registered?](#)  
[Forget password](#)

- [DB Management](#)
- [Upload DB](#)
- [Run BLAST](#)
- [View Results](#)
- [User Guide](#)

**:: Home ::**

"My BLAST" web tools .

You can build a customized database and run BLAST analysis.

Try this now!

**Here's BLAST result lists:**

Database Description	Submit Description	Date	Result	Download	delete
(6)HP 26695	(17)J99 blast 26695	2007-10-31 11:23			
(36)all sequences of FOSmid from shrimp	(37)Blast for Pen5-2	2007-12-28 02:19			
(36)all sequences of FOSmid from shrimp	(38)fosmid e				

**:: MyBLAST Results ::**


DB description: (6) HP 26695      Matche Sequences

Submit description: (17) J99 blast 26695      Top 3

Download Output Files ([text file](#)) or ([cvs file](#))

Seq.	Rank	Hits	E-value	Score	Bits	Match Length	Identities
gi 15611072 ref NP_222723.1  transcription antiterminationprotein NusB [Helicobacter pylori J99]	1	gi 15644635 ref NP_206803.1  transcription antitermination protein NusB [Helicobacter pylori 26695]	0.0	267.0	683	138	136/137 (99%), Positives = 136/137 (99%)
gi 15611073 ref NP_222724.1  riboflavin synthase subunit beta[Helicobacter pylori J99]	1	gi 15644636 ref NP_206804.1  riboflavin synthase subunit beta [Helicobacter pylori 26695]	0.0	294.0	753	156	147/155 (94%), Positives = 152/155 (98%)

# myBLAST Windows / Mac / Bio-Linux




**Hello!**  
Welcome to MyBLAST!!  
IP: 140.109.23.6

[DB Management](#)  
[Upload DB](#)  
[Run BLAST](#)  
[Jobs pending](#)  
[View Results](#)  
[User Guide](#)  
[Contact Us](#)

:: 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)

Available for

- Windows xp,vista,7,8
- Mac OSX 10.5
- Bio-Linux 7, 8 (ISO/OVA)
- Linux



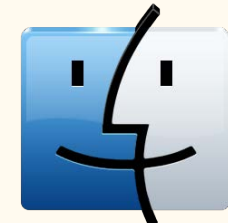
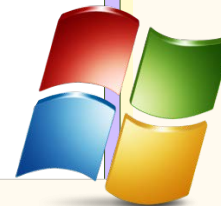
MyBlast Control Panel

MyBlast  
MySQL Community Server V.5.1.37  
Apache Tomcat Web Server V.5.5.27

Download ImportBackup Tools Help

SHUTDOWN  
MyBlast Home

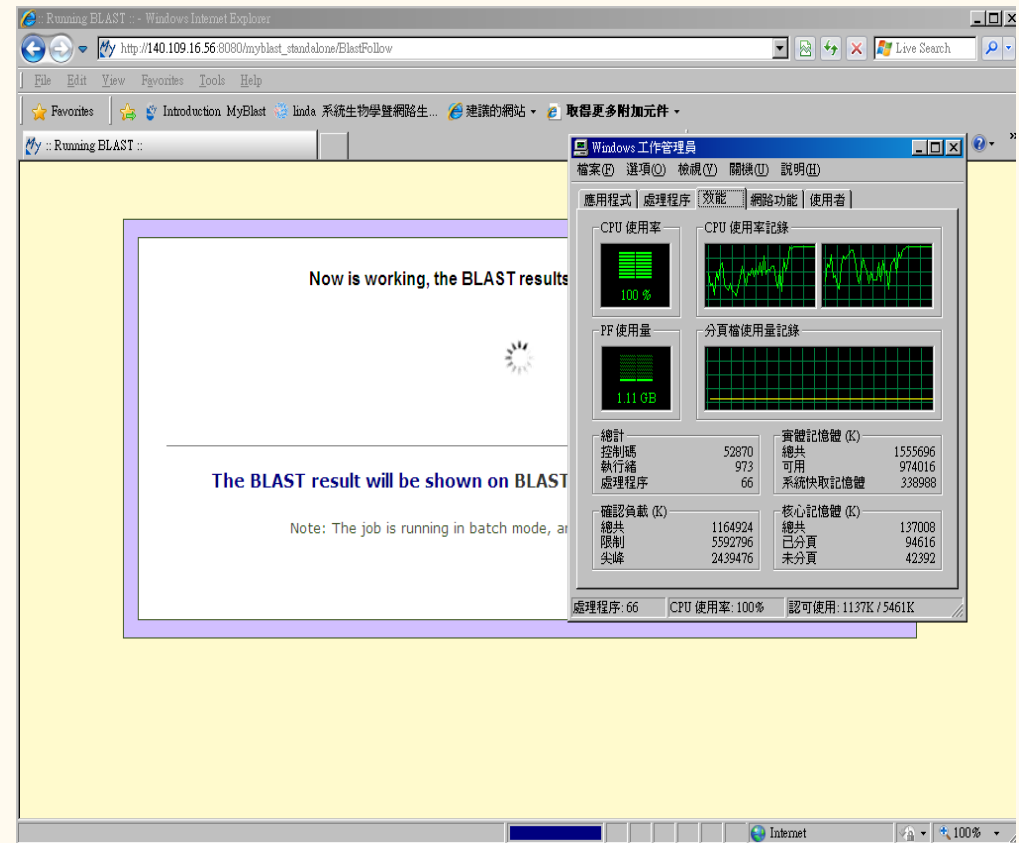
Powered by  
LAB OF  
System Biology & Network Biology  
Academia Sinica, TAMS-33  
系統生物學與網路生物學實驗室



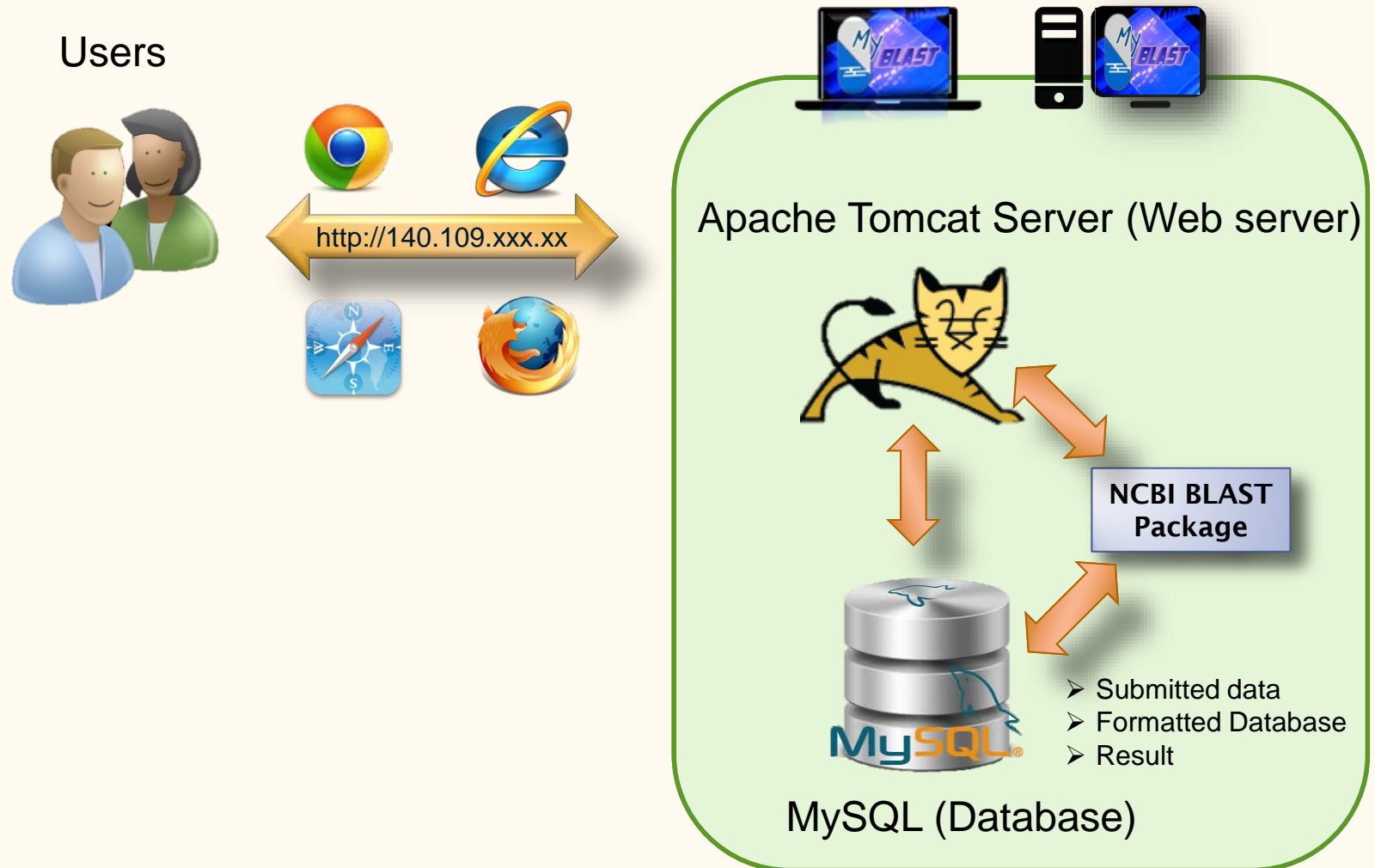


# *myBlast is Multi-Thread Processing*

- More efficiency
- Faster then before



# *myBlast as Web Application*



# myBlast Standalone Installation

## First, please visit us

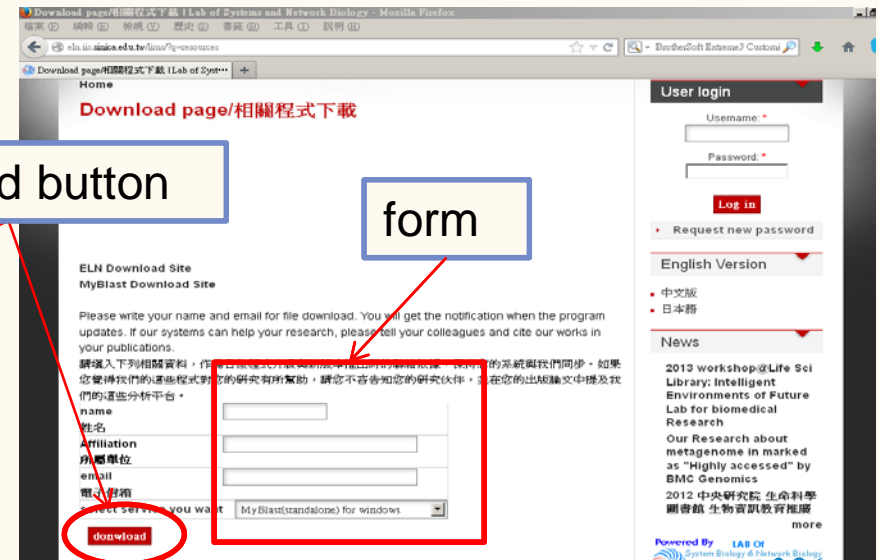
- ① Visit Lab of Systems Biology & Network Biology website

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



## Second, Download the file

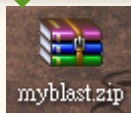
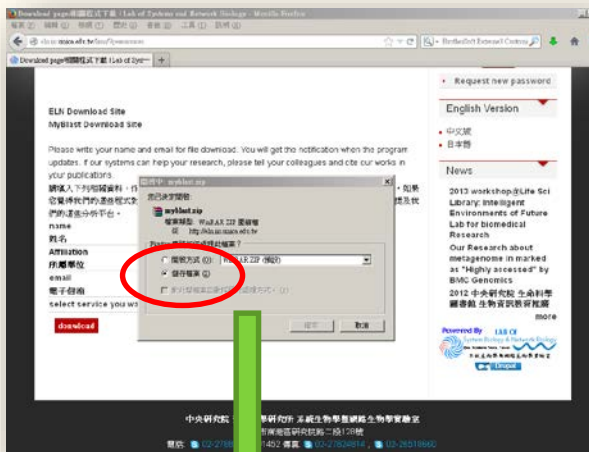
- ① Click the Download link on the top of the main page.
- ② Fill in the form, then submit it. The download process starts immediately.



# Unpack

## Download process

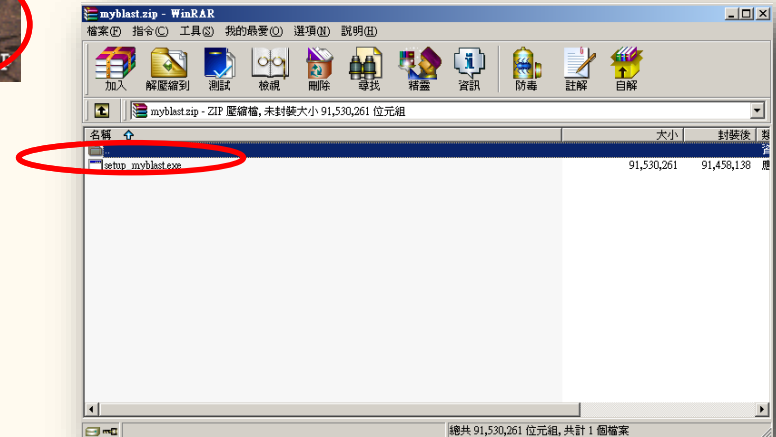
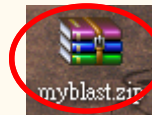
- ① The browser pop up the question. Click Save.
- ② Wait until the process done.



Myblast.zip save to the download folder.

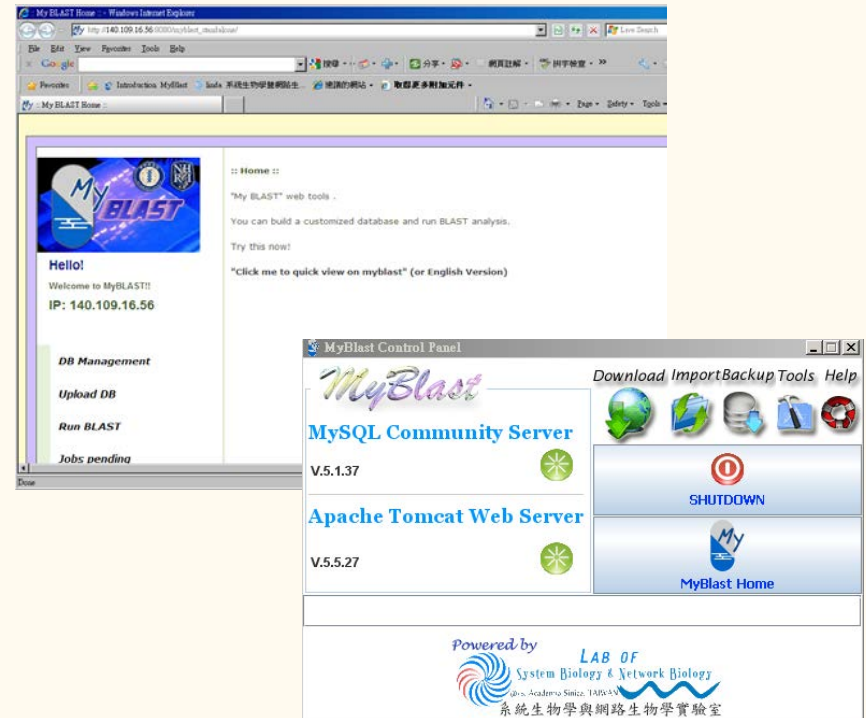
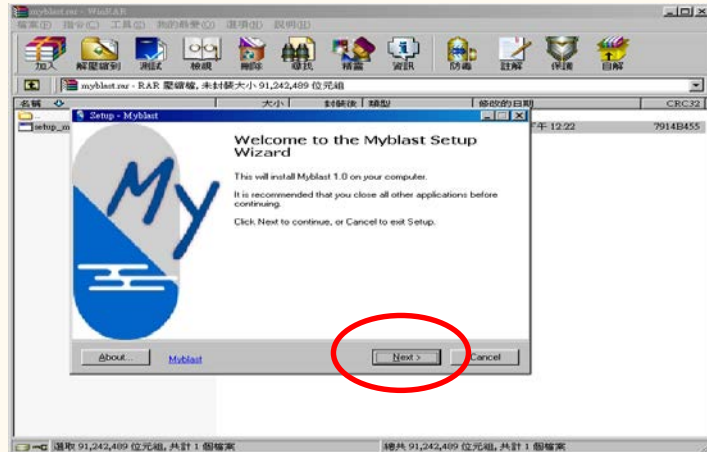
## Execute setup\_myblast.exe

- ① The setup\_myblast.exe is inside the myblast.zip
- ② Double click the myblast.zip
- ③ Execute this setup\_myblast.exe



# Follow The Setup Wizard

- Start from the welcome page
- At the end, the main page and the control panel start automatically



# Web Portal of myBLAST



**Hello!**

Welcome to MyBLAST!!

IP: 140.109.20.15 xxx

***DB Management***

***Upload DB***

***Run BLAST***

***Jobs pending***

***View Results***

***User Guide***

***Contact Us***

**:: Home ::**

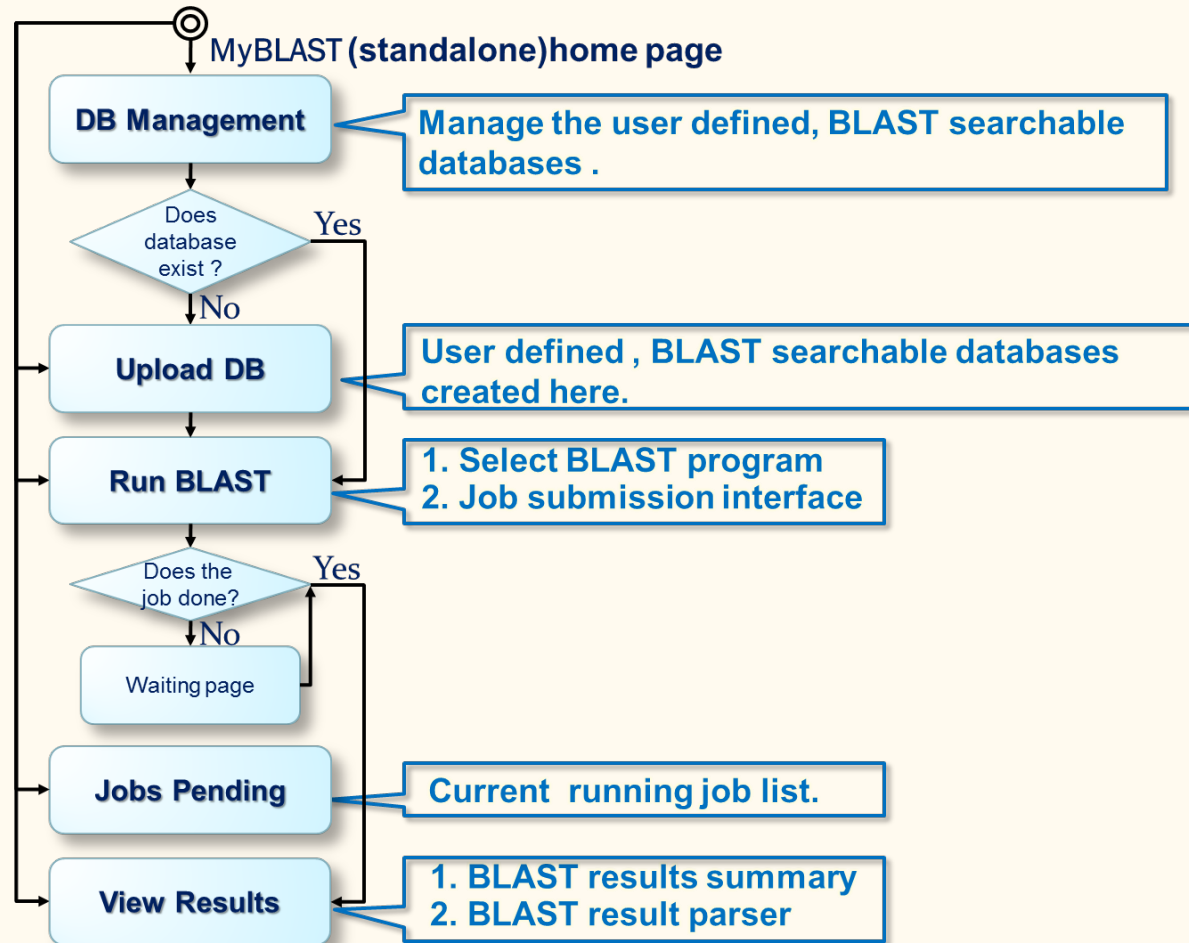
"My BLAST" web tools .

You can build a customized database and run BLAST analysis.

Try this now!

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

# Mechanisms inside myBLAST

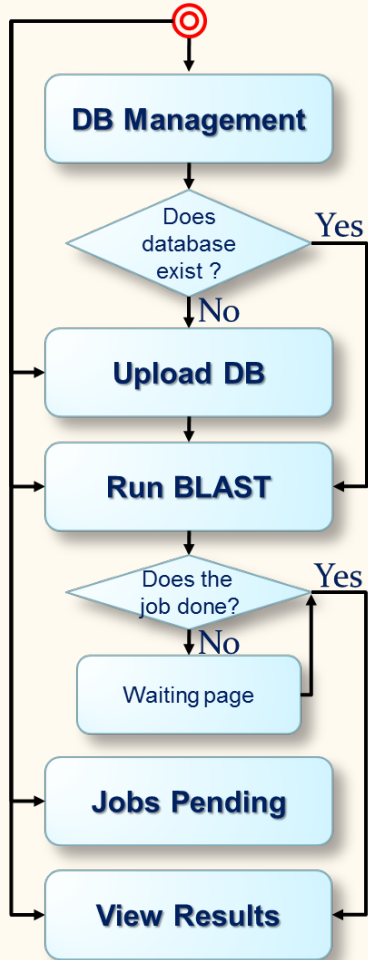
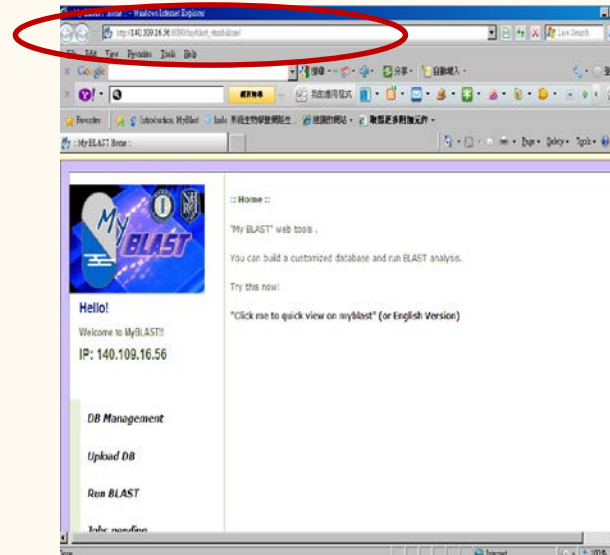


# How to Start

1. By clicking the **MyBlast Home** button in the myBlast ControlPanel.



2. Or typing URL [http://localhost:8080/myblast\\_standalone/](http://localhost:8080/myblast_standalone/)







# Share myBLAST by IP adress

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: 140.109.23.6**

**DB Management**

**Upload DB**

**Run BLAST**

**:: Home ::**

"My BLAST" web tools .

You can build a customized database and run BLAST analysis.

Try this now!

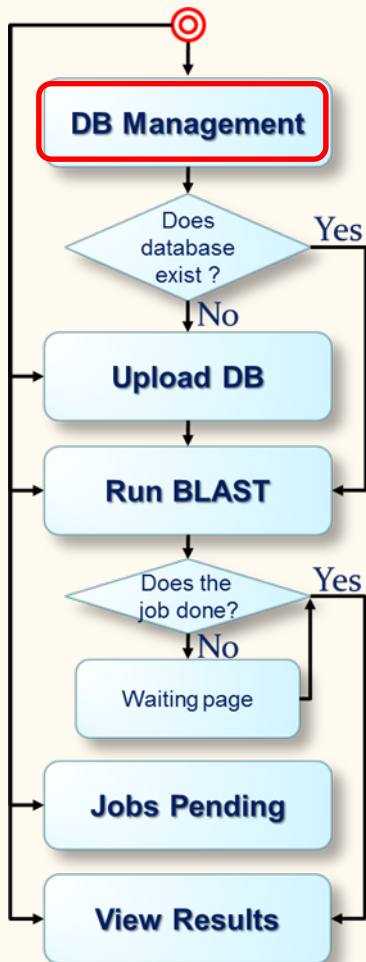
"Click me to quick view on myblast" (or English Version)

Share this website for others to perform BLAST on your machine

Local intranet 100%

# Database Management

- Manage the user defined, BLAST searchable databases



The screenshot shows the MyBLAST Database Management interface. On the left is a navigation menu with the following items: **DB Management** (circled in red), Upload DB, Run BLAST, Jobs pending, View Results, and User Guide. A green arrow points from the 'DB Management' menu item to the main content area. The main content area is titled ':: Database Management ::' and contains a table of database lists. Below the table are four icons: a green plus sign labeled 'Add', a red minus sign labeled 'Delete', a green magnifying glass labeled 'BLAST', and a green refresh icon labeled 'Job Restart'.

MyBLAST  
Hello!  
Welcome to MyBLAST!!  
IP: 140.109.23.6

:: Database Management ::

Here's your database lists:

DB_id	type	description	date	Edit	Download	Status	Detail	Delete
1	P	NCBI_alu.a	2013-09-03 17:18			Done!		<input type="checkbox"/>
2	N	NCBI_alu.n	2013-09-03 17:18			Done!		<input type="checkbox"/>

**DB Management** ← Add Delete BLAST Job Restart

# Manage User Defined 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

Your sequences was converted to database.

:: Database Management ::

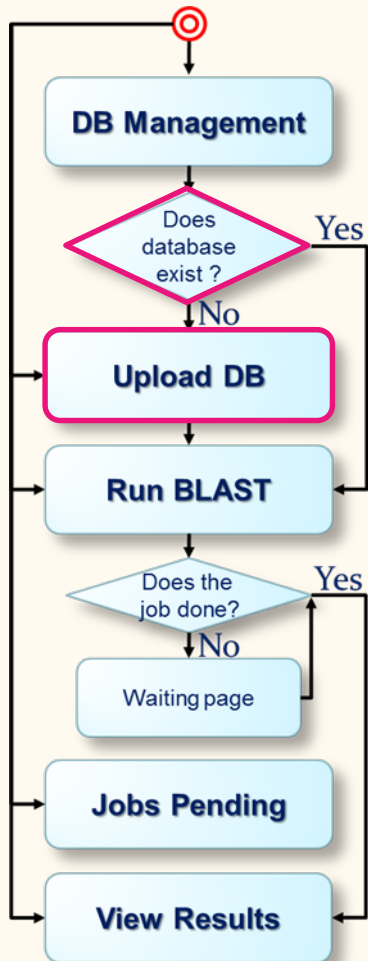
Here's your database lists:

DB_id	type	description	date	Edit	Download	Status	Detail	Delete
1	P	NCBI_alu.a	2013-09-03 17:18	①	②	Done!	③	④
2	N	NCBI_alu.n	2013-09-03 17:18			Done!		

⑤ Add      ④ Delete      ⑥ BLAST

DB Management  
Upload DB  
Run BLAST  
Jobs pending

# Customize Your Own Databases

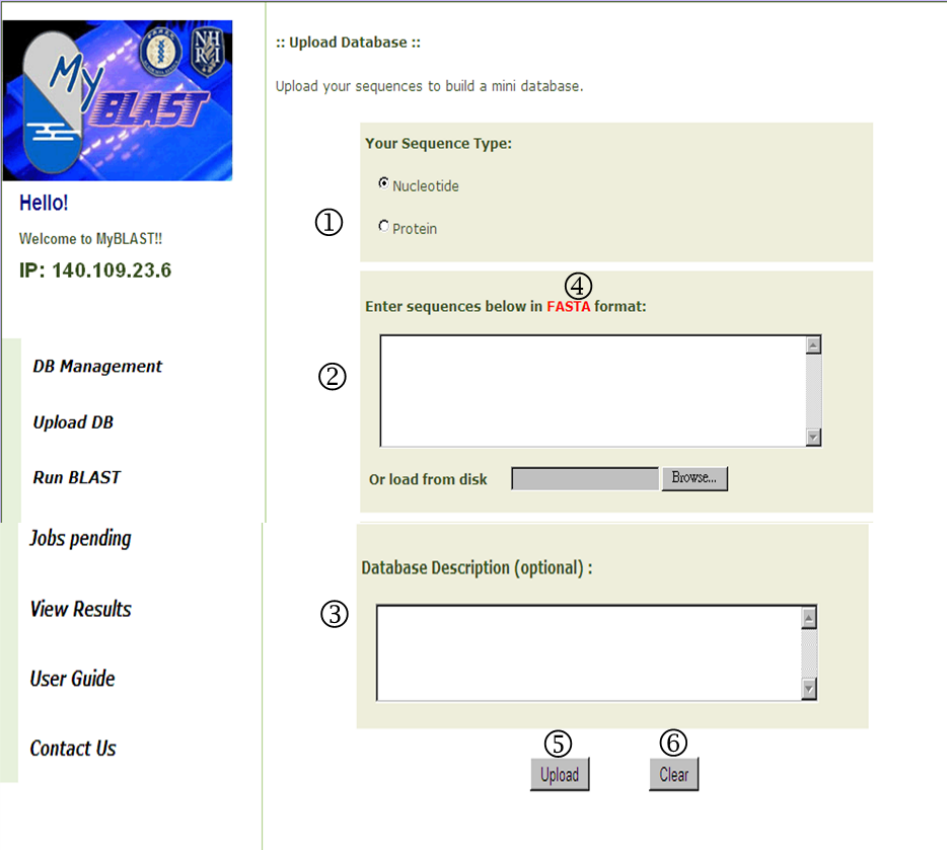


The screenshot shows the MyBLAST web interface. On the left is a navigation menu with the following items: **DB Management**, **Upload DB** (highlighted with a red border), **Run BLAST**, **Jobs pending**, **View Results**, **User Guide**, and **Contact Us**. The main content area is titled **:: Upload Database ::** and contains the following elements:

- A header image with the MyBLAST logo and the text: "Hello! Welcome to MyBLAST!! IP: 140.109.23.6".
- A section titled "Your Sequence Type:" with two radio buttons: "Nucleotide" (selected) and "Protein". A text box next to it says "Select the sequences type."
- A section titled "Enter sequences below in FASTA format:" with a large text input area.
- A section titled "Or load from disk" with a "Browse..." button and a text box that says "Input your sequences in this area."
- A section titled "Database Description (optional) :" with another large text input area.
- At the bottom, there are "Upload" and "Clear" buttons.

# Upload Data as Databases

- ① **Sequence Type**: Nucleotide or protein Enter sequences:
- ② **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 **Name of DB**: description of Database
- 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 contains the following elements:

- A header section with a logo and text: 'Hello! Welcome to MyBLAST!! IP: 140.109.23.6'.
- A 'Your Sequence Type:' section with two radio buttons: 'Nucleotide' (selected) and 'Protein'.
- A text input area for sequences, labeled 'Enter sequences below in FASTA format:' with a circled 4 above it.
- An 'Or load from disk' section with a text input field and a 'Browse...' button.
- A 'Database Description (optional):' section with a text input field, labeled with a circled 3 above it.
- At the bottom, two buttons: 'Upload' (labeled with a circled 5) and 'Clear' (labeled with a circled 6).

# Format Database



## Waiting page

**Your Sequence Type:**

Nucleotide

Protein

**Enter sequences below in FASTA format:**

Or load from disk

**Database Description (optional) :**

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



# Database Ready for Use



**Hello!**

Welcome to MyBLAST!!

**IP: 140.109.23.6**

**DB Management**

Upload DB

Run BLAST

Jobs pending

:: Database Management ::

Here's your database lists:

DB_id	type	description	date	Edit	Download	Status	Detail	Delete
1	P	NCBI_alu.a	2013-09-03 17:18			Done!		<input type="checkbox"/>
2	N	NCBI_alu.n	2013-09-03 17:18			Done!		<input type="checkbox"/>
3	P	hp26695	2013-09-04 14:19			Done!		<input type="checkbox"/>



Add



Delete

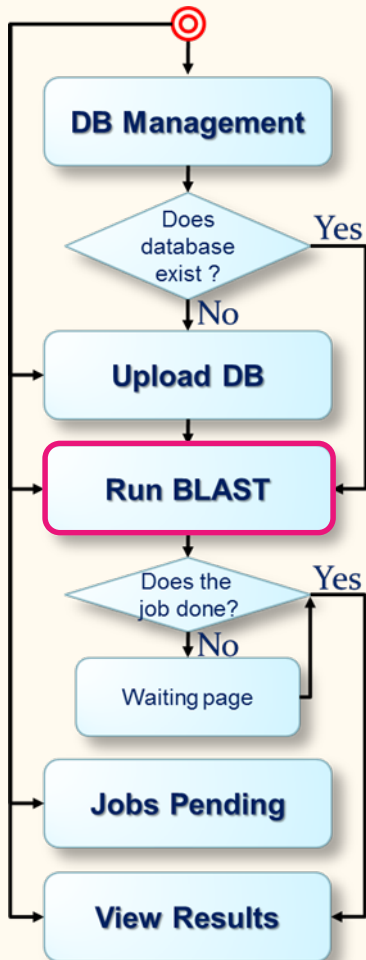


BLAST



Job Restart

# Run Your BLAST



Hello!

Welcome to MyBLAST!!

IP: 140.109.23.6

*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



# Job Submission

- ① Job note
- ② Copy and paste the FASTA format to the text area.
- ③ Or enter the full file path and file name.
- ④ Select Database
- ⑤ Max target
- ⑥ E-Value (ie: 1.0E-20)
- ⑦ Gap Creation
- ⑧ Word size
- ⑨ 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

Enter sequence below in **FASTA** format

```
>Acon2
GSAELGAACALLGRIPKKEEYMNLVSEKLESOKDKIYR
>025294
GVKEDDVHL
```

Or load it from disk  未選擇檔案。 ( )

Select Database:

Advanced Options:

④ Max target:

⑤ E-value:   ⑩

⑥ Matrix:

⑦ Gap creation:

⑧ Word size:

⑨  Turn off the low complexity filter



# Submit

## Select BLAST program

MyBLAST

Hello!  
Welcome to MyBLAST!!  
IP: 140.109.23.6

DB Management  
Upload DB  
Run BLAST  
Jobs pending  
View Results

:: Choose a BLAST program to run ::

Nucleotide BLAST	blastn megablast
Protein BLAST	<b>blastp</b>
Translated BLAST	blastx tblastn tblastx

:: Run blastp with your DB ::

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

Job Note:

Enter sequence below in **FASTA** format

```
>Acon2
GSAELGAACALLGRIPTKEEYNNLVSEKLESQDKIYR
>O25294
GVKEDDVHL
```

Or load it from disk  未選擇檔案。

Select Database:

Advanced Options:

Max target:   
E-value:   
Matrix:   
Gap creation:   
Word size:   
 Turn off the low complexity filter

Click the Submit button



# Searching and Results Presentation

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.



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

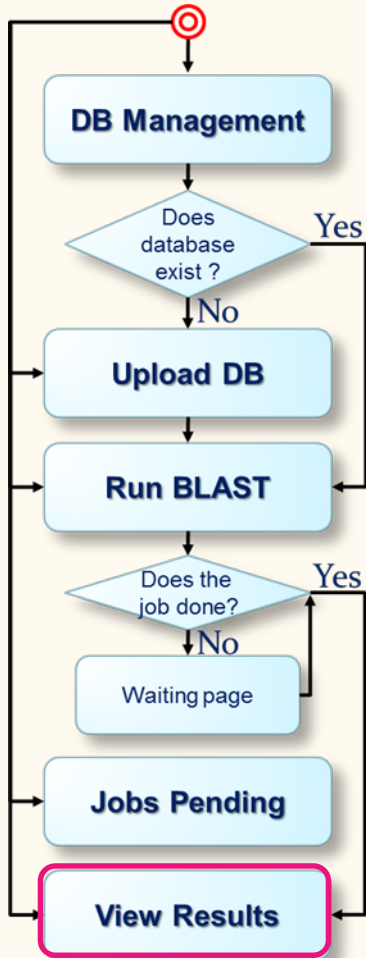
:: MyBLAST Results ::

DB description: (3) hp26695 Matche Sequences  
Submit description: (2) hp26695

Download Output Files ([text file](#)) or ([csv file](#))

Seq.	Rank	Hits	E-value	Score	Bits	Match Length	Identities
Acon2	1	3_d:\myblast\blastbase\blastdb\3 Aconitate hydratase 2 - Helicobacter pylori	5.0E-17	77.8	190	852	38/38 (100%), Positives = 38/38 (100%)
Acon2	2	484_d:\myblast\blastbase\blastdb\3 UvrABC system protein C - Helicobacter pylori	3.1	21.9	45	594	9/19 (47%), Positives = 13/19 (68%)
Acon2	3	37_d:\myblast\blastbase\blastdb\3 CAG pathogenicity island protein 23 - Helicobacter pylori	3.1	21.9	45	983	8/18 (44%), Positives = 13/18 (72%)
O25294	1	12_d:\myblast\blastbase\blastdb\3 Cytosol aminopeptidase - Helicobacter pylori	0.49	23.1	48	496	9/9 (100%), Positives = 9/9

# List of BLAST Result



**Hello!**  
 Welcome to MyBLAST!!  
 IP: 140.109.23.6

DB Management  
 Upload DB  
 Run BLAST  
 Jobs pending

**:: BLAST Results ::** All the BLAST results were saved in this page

Here's BLAST result lists:

Database Description	Submit Description	Date	Result ①	Detail ②	delete ③
(1)NCBI_alu.a	(1)test1	2013-09-03 17:47 ~ 2013-09-03 17:51 (0.07hr. Size:69.34MB)			<input type="checkbox"/>
(3)hp26695	(2)hp26695	2013-09-04 14:35 ~ 2013-09-04 14:35 (0.00hr. Size:0.01MB)			<input type="checkbox"/>

Delete ③
Click to see this result
View this BLAST command
Delete this result

# myBLAST Result

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

:: MyBLAST Results ::

DB description: (1) NCBI\_alu.a  
Submit description: (1) test1

Matche Sequences  
Top 3

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

**Top 1~10**

Seq.	Rank	Hits	E-value	Score	Bits	Match Length	Identities
gnl alu HSU14568_Alu_Sb_consensus_rf1	1	gnl alu HSU14568_Alu_Sb_consensus_rf1	3.0E-50	186.0	472	96	96/96 (100%), Positives = 96/96 (100%)
gnl alu HSU14568_Alu_Sb_consensus_rf1	2	gnl alu HSU14569_Alu_Sb1_consensus_rf1	3.0E-47	176.0	446	96	92/96 (95%), Positives = 92/96 (95%)
gnl alu HSU14568_Alu_Sb_consensus_rf1	3	gnl alu HSU14571_Alu_Sc_consensus_rf1	6.0E-41	155.0	392	95	82/95 (86%), Positives = 87/95 (91%)
gnl alu HSU14568_Alu_Sb_consensus_rf2	1	gnl alu HSU14568_Alu_Sb_consensus_rf2	1.0E-51	191.0	484	95	95/95 (100%), Positives = 95/95 (100%)

Download this "txt" result file

# Original output and CSV

BLASTP 2.2.9 [May-01-2004]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

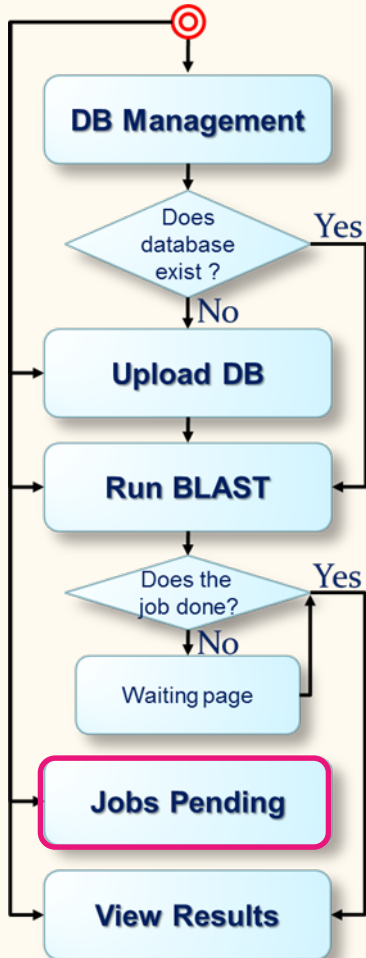
Query= spIP31946-1|1433B\_HUMAN Isoform Long of 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB (246 letters)

Database: C:\myblast\blastbase\blastdb\1 6432 sequences; 3,217,054 total letters

Sequences producing significant alignments:

	A	B	C	D	E	F	G	H
Score (bits)	Query ID	Rank	Hit	Score	Expect	bits	Identities	Length
2	spIP31946	1	gi 23222 gl	398	1.00E-112	1023	198/242 (81%), Positives =	245
3	spIP31946	2	gi 2210401	220	2.00E-58	561	108/122 (88%), Positives =	125
4	spIP31946	3	gi 2195195	33.1	0.045	74	50/257 (19%), Positives =	853
5	spIP31946	4	gi 5595757	30.8	0.22	68	33/187 (17%), Positives =	545
6	spIP31946	5	gi 5595757	30.8	0.22	68	33/187 (17%), Positives =	847
7	spIP31946	6	gi 5596032	28.5	1.1	62	18/90 (20%), Positives =	273
8	spIP31946	7	gi 1462582	27.7	1.9	60	23/128 (17%), Positives =	527
9	spIP31946	8	gi 1689852	27.3	2.5	59	33/138 (23%), Positives =	2569
10	spIP31946	9	gi 6110355	26.9	3.2	58	38/209 (18%), Positives =	1352
11	spIP31946	10	gi 6110347	26.9	3.2	58	38/209 (18%), Positives =	1360
12	spIP31946	1	gi 23222 gl	398	1.00E-112	1023	198/242 (81%), Positives =	245
13	spIP31946	2	gi 2210401	220	2.00E-58	561	108/122 (88%), Positives =	125

# Running/Pending Jobs



Hello!

Welcome to MyBLAST!!

IP: 140.109.23.6

*DB Management*

*Upload DB*

*Run BLAST*

*Jobs pending*

*View Results*

:: Search Management ::

CurrentTime: Wed Sep 04 16:04:19 CST 2013 , current running: 1

Here's your search lists:

#	DB_id	Program	Description	ProcessID	Start	Status	Detail	Delete
3	1	blastp		4104	2013-09-04 15:59	<input type="checkbox"/> Restart?		<input type="checkbox"/>
4	1	blastp		3232	2013-09-04 16:04	Running!		<input type="checkbox"/>



Add



Delete



BLAST



Job Restart

# myBLAST Control Panel

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

MyBlast Control Panel

MyBlast

MySQL Community Server V.5.1.37

Apache Tomcat Web Server V.5.5.27

Download Import Backup Tools Help

① ② ③ ④ ⑤

⑥ SHUTDOWN

⑦ MyBlast Home

⑩

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**Import Data**

1. Myblast mysql data backup file:

2. Click Import button ,data will clean and restore back.  
Please make sure you backup the latest data before import data.

MyBlast: d:\myblast

**Import** **Cancel** **Exit**

Message

2. Install Myblast

MyBlast - MyBlast

YouTube

Powered by **MyBlast Control Panel**

Download ImportBackupTools Help

**MyBlast**

Community Server

Tomcat Web Server

SHUTDOWN

MyBlast Home

**FTP Data**

Name	Type	~Size	process
alu.a.gz	Protien	~89KB	
alu.n.gz	DNA	~23KB	
drosoph.aa.gz	Protien	~4MB	
drosoph.rt.gz	DNA	~35MB	
env_nr.gz	Protien	~806MB	
env_nt.gz	DNA	~3GB	
est_human.gz	DNA	~1GB	
est_mouse.gz	DNA	~757MB	
est_others.gz	DNA	~10GB	

FTP site: ftp://ftp.ncbi.nih.gov/blast/db/FASTA/

1. Select files.

2. Save to: c:\tmp\

3. Set FormatDB dbname: (n1,n2...)

Download --> Unzip --> UploadDB --> Done

**Start** **Cancel** **Exit**

Message  
Wait to connect to ftp://ftp.ncbi.nih.gov/blast/db/FASTA/ ... Done!

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**Data Backup**

1. Myblast data backup file directory:

2. Click Backup button ,two data files will show on selected directory.

MyBlast: d:\myblast

**Backup** **Cancel** **Exit**

Message

**Setting**

Apache Tomcat Port 8080 (1~65536)

Mysql Port 3306 (1~65536)

**view ports** **Revert to defaults**

Changing ports will require restarting MyBlast.

**OK** **Cancel**

Message

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# Try To Restart Or Shutdown Servers

MyBlast Control Panel

MyBlast

Download ImportBackup Tools Help

MySQL Community Server V.5.1.37

Apache Tomcat Web Server V.5.5.27

RESTART

MyBlast Home

Shutdown tomcat and mysql.....2013/09/03 15:19:15

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MyBLAST Home

MyBLAST

Hello!

Welcome to MyBLAST!!

IP: 140.109.23.6

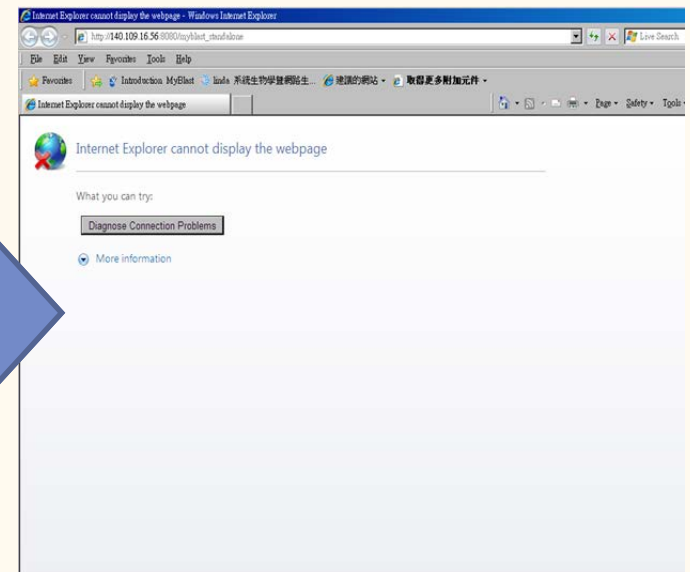
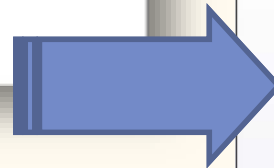
DB Management

Upload DB

Run BLAST

Jobs pending

# Try To Restart Or Shutdown Servers



# Close myBLAST Control Panel

A screenshot of the MyBlast Control Panel. The window title is "MyBlast Control Panel". The interface includes a "MyBlast" logo, a "MySQL Community Server" section with version "V.5.1.37" and a green star icon, and an "Apache Tomcat Web Server" section with version "V.5.5.27" and a green star icon. On the right, there are icons for "Download", "Import", "Backup", "Tools", and "Help". Below these are buttons for "SHUTDOWN" (with a red power icon) and "MyBlast Home" (with a blue "My" logo). A message box at the bottom is highlighted with a red border and contains the text: "Shutdown tomcat and mysql.....2013/09/03 15:19:15" and "Restart tomcat and mysql.....2013/09/03 15:20:31". The footer includes the text "Powered by LAB OF System Biology & Network Biology" and "Academia Sinica, TAIWAN" with a logo, and the Chinese text "系統生物學與網路生物學實驗室".

MyBlast Control Panel

MyBlast

MySQL Community Server  
V.5.1.37

Apache Tomcat Web Server  
V.5.5.27

Download Import Backup Tools Help

SHUTDOWN

MyBlast Home

Shutdown tomcat and mysql.....2013/09/03 15:19:15  
Restart tomcat and mysql.....2013/09/03 15:20:31

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Message

# *Play and Go*

- A. Get the FASTA data from NCBI or submit your own sequences
- B. Construct your own DB
- C. Run BLAST and View Results



# Download Big Data from NCBI as Database

The image shows a screenshot of the MyBlast Control Panel interface. The panel includes a navigation menu with 'Download' highlighted in a red box. Below the menu are buttons for 'SHUTDOWN' and 'MyBlast Home'. The main area displays 'MyBlast MySQL Community Server V.5.1.37' and 'Apache Tomcat Web Server V.5.27'. An orange arrow points from the 'Download' button to the 'FTP Data' dialog box.

**FTP Data**

Name	Type	~Size	process
alu.a.gz	Protien	~89KB	
alu.n.gz	DNA	~23KB	
drosoph.aa.gz	Protien	~4MB	
drosoph.nt.gz	DNA	~35MB	
env_nr.gz	Protien	~806MB	
env_nt.gz	DNA	~3GB	
est_human.gz	DNA	~1GB	
est_mouse.gz	DNA	~757MB	
est_others.gz	DNA	~10GB	

FTP site: ftp://ftp.ncbi.nih.gov/blast/db/FASTA/  
1. Select files.  
2. Save to: c:\tmp\  
3. Set FormatDB dbname: (n1,n2...)  
Download --> Unzip --> UploadDB --> Done

Start Cancel Exit

Message  
Wait to connect to ftp://ftp.ncbi.nih.gov/blast/db/FASTA/ ...Done!

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# Available Databases from NCBI

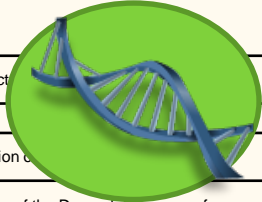
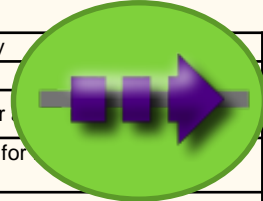


Table 4a. Contents of protein database files under the /db/FASTA directory

File	Content
alu.a.gz	Protein translation of alu elements
drosoph.aa.gz <sup>1</sup>	CDS translations of the Drosophila genome from drosophila.nt
env_nr.gz <sup>2</sup>	CDS translations of the environmental sequences from env_nt
igSeqProt.gz	Protein sequences for human and mouse immunoglobulin variable regions
mito.aa.gz <sup>1</sup>	CDS translations of the complete mitochondrial genomes
month.aa.gz	Protein sequences newly released or updated in the past 30 days
nr.gz <sup>2</sup>	Non-redundant protein sequences with entries from GenPept, Swissprot, PIR, PRF, PDB and RefSeq
pataa.gz <sup>2</sup>	Patent protein sequences submitted by USPTO or from EU/Japan patent agencies through EMBL and DDBJ
pdbaa.gz <sup>2</sup>	Protein sequences from PDB structure records
swissprot.gz <sup>2</sup>	The last major release of the Swiss-Prot database
yeast.aa.gz <sup>1</sup>	Protein translations of old baker yeast genomic contigs

Table 4b. Contents of nucleotide database files under the /db/FASTA directory

File	Content
alu.n.gz	Nucleotide sequences for alu elements
drosoph.nt.gz <sup>1</sup>	The old genomic contigs for drosophila melanogaster
env_nt.gz <sup>2</sup>	Nucleotide sequences from environmental samples
est_human.gz <sup>2</sup>	Human subset of the EST database
est_mouse.gz <sup>2</sup>	Mouse subset of the EST database
est_others.gz <sup>2</sup>	Non-human and non-mouse subset of the EST database
gss.gz <sup>2</sup>	Sequences from the GSS division of GenBank, EMBL and DDBJ
htgs.gz <sup>2</sup>	htgs database with high throughput genomic entries from the htg division of GenBank, EMBL and DDBJ
human_genomic.gz <sup>2</sup>	Human chromosome records from Reference as well as alternative assemblies
igSeqNt.gz	Nucleotide sequences for human and mouse immunoglobulin variable regions
mito.nt.gz <sup>1</sup>	Complete mitochondrial genomes
month.est_human.gz	Human est sequences released/updated in the past 30 days
month.est_mouse.gz	Mouse est sequences released/updated in the past 30 days
month.est_others.gz	Non-human and non-mouse est sequences released/updated in the past 30 days
month.gss.gz	gss sequences released/updated in the past 30 days
month.htgs.gz	htgs sequences released/updated in the past 30 days
month.nt.gz	Sequences from the nt database released/updated in the past 30 days
nt.gz <sup>2</sup>	Nucleotide sequence database contains entries from all traditional divisions of GenBank, EMBL and DDBJ. Sequences from bulk gss, sts, pat, est, htg divisions plus wgs and env_nt entries are excluded.



Footnote:

1. These sequence files are provided for test purpose, their contents are not up-to-date.
2. It is recommended that their pre-formatted counterparts described in Table 2 be used whenever possible.

More ...



# Load Data from NCBI

FTP Data

Name	Type	~Size	process
alu.a.gz	Protien	~89KB	
alu.n.gz	DNA	~23KB	
drosoph.aa.gz	Protien	~4MB	
drosoph.nt.gz	DNA	~35MB	
env_nr.gz	Protien	~806MB	
env_nt.gz	DNA	~3GB	
est_human.gz	DNA	~1GB	
est_mouse.gz	DNA	~757MB	
est_others.gz	DNA	~10GB	

FTP site: ftp://ftp.ncbi.nih.gov/blast/db/FASTA/  
1. Select 2 files.  
2. Save to: c:\tmp\  
3. Set FormatDB dbname: (n1,n2...)  
NCBI\_alu.a,NCBI\_alu.n  
Download --> Unzip --> UploadDB --> Done  
Start Cancel Exit

Message  
Wait to connect to ftp://ftp.ncbi.nih.gov/blast/db/FASTA/ ...Done!

FTP Data

Name	Type	~Size	process
alu.a.gz	Protien	~89KB	Done!(Do...
alu.n.gz	DNA	~23KB	start!(Do...
drosoph.aa.gz	Protien	~4MB	
drosoph.nt.gz	DNA	~35MB	
env_nr.gz	Protien	~806MB	
env_nt.gz	DNA	~3GB	
est_human.gz	DNA	~1GB	
est_mouse.gz	DNA	~757MB	
est_others.gz	DNA	~10GB	

FTP site: ftp://ftp.ncbi.nih.gov/blast/db/FASTA/  
✓ 1. Select 2 files.  
✓ 2. Save to: c:\tmp\  
✓ 3. Set FormatDB dbname: (n1,n2...)  
NCBI\_alu.a,NCBI\_alu.n  
Download --> Unzip --> UploadDB --> Done  
Start Cancel Exit

Remote system is UNIX type: LS  
Start to ftp alu.a.gz  
Save to c:\tmp\alu.a.gz...Done!  
Start to ftp alu.n.gz  
Save to c:\tmp\alu.n.gz...

99% 24465 byte.

FTP Data

Name	Type	~Size	process
alu.a.gz	Protien	~89KB	DB_id: 1
alu.n.gz	DNA	~23KB	DB_id: 2
drosoph.aa.gz	Protien	~4MB	
drosoph.nt.gz	DNA	~35MB	
env_nr.gz	Protien	~806MB	
env_nt.gz	DNA	~3GB	
est_human.gz	DNA	~1GB	
est_mouse.gz	DNA	~757MB	
est_others.gz	DNA	~10GB	

FTP site: ftp://ftp.ncbi.nih.gov/blast/db/FASTA/  
✓ 1. Select 2 files.  
✓ 2. Save to: c:\tmp\  
✓ 3. Set FormatDB dbname: (n1,n2...)  
NCBI\_alu.a,NCBI\_alu.n  
Download --> Unzip --> UploadDB --> Done  
Start Cancel Exit

FormatDB DB\_id: 1 done!  
Send out c:\tmp\alu.n data to MyBLAST server.Wait until FormatDB done!  
Please go to MyBLAST server DBmanagement to check db status!  
FormatDB DB\_id: 2 done!  
Go to myBLAST home page to RUN BLAST.





# Check the Database List


My BLAST Home :: - Mozilla Firefox

檔案 (F) 編輯 (E) 檢視 (V) 歷史 (S) 書籤 (B) 工具 (T) 說明 (H)

140.109.23.6:8080/myblast\_standalone/MainMenu?act=mng\_db\_list

BrotherSoft Extreme3 Customi

My :: My BLAST Home ::



**Hello!**

Welcome to MyBLAST!!

**IP: 140.109.23.6**

DB Management

Upload DB

Run BLAST

:: Database Management ::

Here's your database lists:

DB_id	type	description	date	Edit	Download	Status	Detail	Delete
1	P	NCBI_alu.a	2013-09-03 17:18			Done!		<input type="checkbox"/>
2	N	NCBI_alu.n	2013-09-03 17:18			Done!		<input type="checkbox"/>

Add    Delete    BLAST    Job Restart




# Perform BLASTP

My BLAST Home :: Mozilla Firefox

140.109.23.6:8080/myblast\_standalone/MainMenu?act=search\_program\_sel

My BLAST Home ::



**Hello!**  
Welcome to MyBLAST!!  
IP: 140.109.23.6

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

:: Choose a BLAST program to run ::

Nucleotide BLAST	blastn megablast
Protein BLAST	<b>blastp</b>
Translated BLAST	blastx tblastn tblastx

# Submit Query Sequences



My BLAST Home :: Mozilla Firefox

140.109.23.6:8080/myblast\_standalone/MainMenu/act-search\_page&program=blastp

My BLAST Home ::

**Hello!**  
Welcome to MyBLAST!!  
IP: 140.109.23.6

*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:  ↕

Word size:  ↕

Turn off the low complexity filter ↕



# Similarity Search

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.

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

:: MyBLAST Results ::

DB description: (1) NCBI\_alu.a  
Submit description: (1) test1  
Download Output Files ([text file](#)) or ([csv file](#))


Matche Sequences  
Top 3 [Go] [Download]

Seq.	Rank	Hits	E-value	Score	Bits	Match Length	Identities
gnl alu HSU14568_Alu_Sb_consensus_rf1	1	gnl alu HSU14568_Alu_Sb_consensus_rf1	3.0E-50	186.0	472	96	96/96 (100%), Positives = 96/96 (100%)
gnl alu HSU14568_Alu_Sb_consensus_rf1	2	gnl alu HSU14569_Alu_Sb1_consensus_rf1	3.0E-47	176.0	446	96	92/96 (95%), Positives = 92/96 (95%)
gnl alu HSU14568_Alu_Sb_consensus_rf1	3	gnl alu HSU14571_Alu_Sc_consensus_rf1	6.0E-41	155.0	392	95	82/95 (86%), Positives = 87/95 (91%)





# View the Results





**Hello!**  
Welcome to MyBLAST!!  
IP: 140.109.23.6

[DB Management](#)  
[Upload DB](#)

**:: BLAST Results ::**

Here's BLAST result lists:

Database Description	Submit Description	Date	Result	Detail	delete
(1)NCBI_alu.a	(1)test1	2013-09-03 17:47 ~ 2013-09-03 17:51 (0.07hr. Size:69.34MB)			<input type="checkbox"/>



[Back

**:: MyBLAST Results ::**

DB description: (1) NCBI\_alu.a      Matche Sequences

Submit description: (1) test1     

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

Seq.	Rank	Hits	E-value	Score	Bits	Match Length	Identities
gnl alu HSU14568_Alu_Sb_consensus_rf1	1	gnl alu HSU14568_Alu_Sb_consensus_rf1	3.0E-50	186.0	472	96	96/96 (100%), Positives = 96/96 (100%)
gnl alu HSU14568_Alu_Sb_consensus_rf1	2	gnl alu HSU14569_Alu_Sb1_consensus_rf1	3.0E-47	176.0	446	96	92/96 (95%), Positives = 92/96 (95%)
gnl alu HSU14568_Alu_Sb_consensus_rf1	3	gnl alu HSU14571_Alu_Sc_consensus_rf1	6.0E-41	155.0	392	95	82/95 (86%), Positives = 87/95 (91%)

# Flash Demo



## Hello!

Welcome to MyBLAST!!

IP: 140.109.23.6

*DB Management*

*Upload DB*

*Run BLAST*

*Jobs pending*

*View Results*

*User Guide*

:: Home ::

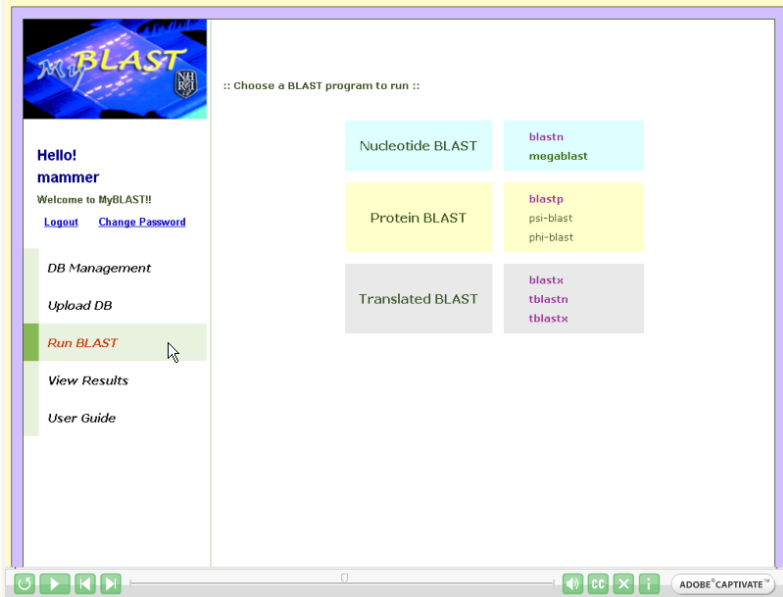
"My BLAST" web tools .

You can build a customized database and run BLAST analysis.

Try this now!

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

# Screen Casts for myBLAST



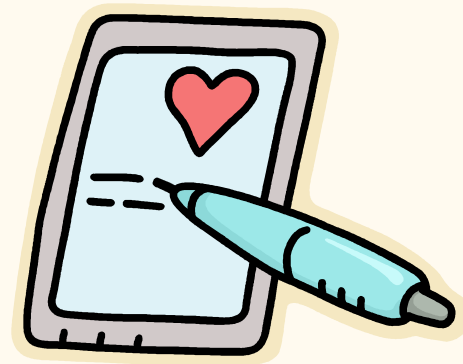
Web version



Standalone version for windows/MAC

# *Take Home Messages About myBlast*

- User defined /customized databases
- Managing these databases as well as the blast results conveniently
- Multi-Thread Processing (faster)
- Graphic User Interface (easier)
- Local computer or share at network (security)
- Backup for Databases and Blast Results





# Research Team



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National Health Research Institutes



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*Thanks for your Attention*



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