

# Similarity Search and Phylogenetic Analysis

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LAB OF System Biology & Network Biology

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National Health Research Institutes

# Brief on Our Research Works



### 我們的最新消息

標題	發表時間▼	作者
2009中央研究院 生命科學圖書館 生物資訊教育推廣	11/13/2009 - 16:47	admin
myBLAST下載及線上說明/ Myblast download and Online Help	10/30/2009 - 15:18	admin
Online Videos for ELN/ ELN 線上教學	10/29/2009 - 16:30	admin
Open House 2009	10/29/2009 - 12:39	admin
國立台灣大學暑期課程:2009年轉錄體學(Transcriptome/Transcriptomics)分析技術	07/20/2009 - 13:20	admin
Our works for research community	10/27/2008 - 13:42	admin
實驗室簡介	10/27/2008 - 12:17	admin
Introduction of Our Laboratory	10/27/2008 - 12:15	admin
國立台灣大學暑期課程:2008年轉錄體學(Transcriptome/Transcriptomics)分析技術	08/11/2008 - 17:25	admin
恭賀林仲彥老師獲得中華民國專利:「電腦輔助引子設計之裝置與方法以及偵測嚴重急性性呼吸道症候群冠狀病毒之組合物」	06/03/2008 - 14:09	admin

1 2 下一頁 > 最後一頁 >

### 行事曆

◀ 12月 2009

一	二	三	四	五	六	日
	1	2	3	4	5	6
7	8	9	10	11	12	13
14	15	16	17	18	19	20
21	22	23	24	25	26	27
28	29	30	31			

### 搜尋

# Schedule Today

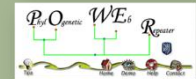
9:50~10:40

序列比對簡介與上機實習 (*myBLAST*)



11:00~11:20

生物巨分子序列親緣分析流程之整合與最佳化系統  
(POWER)



11:30~12:00

最佳化分子親緣關係分析平台(PALM)



# 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
GCTGCCTTTGGCCACCAAATCCCAAACCTAATTAAAGAATTAAA.....
```

**>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
GCTGCCTTTGGCCACCAAATCCCAAACCTAATTAAAGAATTAAATAATTTCG.....
```

# FASTA Format (DNA)

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

```
GCCATCCTCGACCAGTCCTGCAAAGGTATCTTCGACCGTGAGCTCTTCAAGAAGCTCGACCGT
GTCTGCGACGATTGTTACAACCTCTACAGGAAGCCTTACGTGCGCCATCGACTGCAGGGAGGGC
TGCTACCAGAACTTGGTCTTCCGACAGTGCATCCAGGACCTCCAGTTGATGGACCAACTCGAC
GAATACGCCAACGCTGTCCAGATCGTCGGGAAG
```

A --> adenosine

C --> cytidine

G --> guanine

T --> thymidine

U --> uridine

R --> G A (purine)

Y --> T C (pyrimidine)

K --> G T (keto)

- gap of indeterminate length

M --> A C (amino)

S --> G C (strong)

W --> A T (weak)

B --> G T C

D --> G A T

H --> A C T

V --> G C A

N --> A G C T (any)

# FASTA Format (Protein)

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

```
MAVMAPRTLVLLLSGALALTQTWAGSHSMRYFSTSVSRPGRGEPFIAVGYVDDTQFVRFSDAASQRMEPRAPWIEQE  
GPEYWDEETGKVKAAHSQTDRENLRALRYYNQSEAGSHTLQMMFGCDVGS DGRFLRGYHQYAYDGKDYIALKEDLRS  
WTAADMAAQITKRKWEAAHVAEQQRAYLEGT CVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFY  
PAEITLTWQRDGEDQTQDTELVETRPAGDGT FQKWA AVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS SQPTVPIVGIIA  
GLVLLGAVITGAVVAAMWRRNSSDRKGGSY SQAASSDSAQGS DVSLTACKV
```

A alanine

B aspartate or asparagine

C cystine

D aspartate

E glutamate

F phenylalanine

G glycine

H histidine

I isoleucine

K lysine

L leucine

M methionine

N asparagine

P proline

Q glutamine

R arginine

S serine

T threonine

U selenocysteine

V valine

W tryptophan

Y tyrosine

Z glutamate or glutamine

X any

\* translation stop

- gap of indeterminate length



# The Programs of BLAST

Application	Query Type	Database Type
<b>blastn</b>	NA	NA
<b>blastp</b>	Protein	Protein
<b>blastx</b>	NA	Protein
<b>tblastn</b>	Protein	NA
<b>tblastx</b>	NA	NA



# 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 a **nucleotide** database using a **nucleotide** query  
*Algorithms: blastn, megablast, discontinuous 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 (b2seq)
- Search [protein](#) or [nucleotide](#) targets in PubChem BioAssay
- Search SRA [transcript libraries](#)
- Constraint Based Protein [Multiple Alignment Tool](#)

## BLAST Human Sequences.

Enter an accession, gi, or a sequence in FASTA format:

Or, choose a file to upload

 瀏覽...

Set subsequence: (optional)

From:  To:

Database:

genome (all assemblies) 11426 sequences

Program:

megaBLAST: Compare highly related nucleotide sequences

### Optional parameters

Expect	Filter	Descriptions	Alignments
0.01	default	100	100

Advanced options:

Begin Search

Clear Input

auto-check for results

# BLAST Result

Pull-down menu for each result

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

5 sequences (B.D00331.1|HPBADW3 Hepatitis...

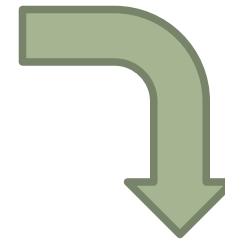
Results for: 1.lc18075 B.D00331.1HPBADW3 Hepatitis B virus genome, complete genome(3215bp) [What's this?](#)

**Query ID**  
**Description**  
**Molecule type**  
**Query Length**

1.lc18075 B.D00331.1HPBADW3 Hepatitis B virus genome, complete genome(3215bp)  
 2.lc18076 B.M54923.1HPBADWZ Hepatitis B virus (subtype adw), complete genome(3215bp)  
 3.lc18077 B.D00329.1HPBADW1 Hepatitis B virus (HBV) genome, complete genome(3215bp)  
 4.lc18078 B.D00330.1HPBADW2 Hepatitis B virus genome, complete genome(3215bp)  
 5.lc18079 C.X01587.1HBVADR4 Hepatitis B virus subtype adw4 (HBV)(3214bp)

Other reports: [▶ Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#)

- ▶ [Graphic Summary](#)
- ▶ [Descriptions](#)
- ▶ [Alignments](#)



▼ [Graphic Summary](#)

Distribution of 10 Blast Hits on the Query Sequence [?](#)

Mouse over to see the define, click to show alignments

Color key for alignment scores

Score Range	Color
<40	Black
40-50	Blue
50-80	Green
80-200	Red
>=200	Dark Red

Query 0 600 1200 1800 2400 3000

▼ [Descriptions](#)

Legend for links to other resources: [U](#) UniGene [G](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer

Sequences producing significant alignments:  
(Click headers to sort columns)

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
D00331.1	Hepatitis B virus subtype ADW genomic DNA, complete genome, clon	5938	5938	100%	0.0	100%	
AB033554.1	Hepatitis B virus DNA, complete genome, isolate:RTB299	5838	5838	100%	0.0	99%	
AP011085.1	Hepatitis B virus DNA, complete genome, strain: B0612746(JKT)F	5827	5827	100%	0.0	99%	
AB493832.1	Hepatitis B virus DNA, complete genome, isolate: P19	5753	5753	100%	0.0	98%	
AB033555.1	Hepatitis B virus DNA, complete genome, isolate:PAD744	5722	5722	100%	0.0	98%	
EF473971.1	Hepatitis B virus isolate 2059Java, complete genome	5710	5710	100%	0.0	98%	
EF473972.1	Hepatitis B virus isolate 1839Java, complete genome	5694	5694	100%	0.0	98%	<a href="#">G</a>
M54923.1	Hepatitis B virus (subtype adw), complete genome	5688	5688	100%	0.0	98%	
AB493835.1	Hepatitis B virus DNA, complete genome, isolate: P30	5666	5666	100%	0.0	98%	
AB493836.1	Hepatitis B virus DNA, complete genome, isolate: P57	5635	5635	100%	0.0	98%	

# Link to Map Viewer

Entrez Genome view - Netscape

http://www.ncbi.nlm.nih.gov/mapview/map\_search.cgi?chr=hum\_chr\_inf&RD=1075684236-31166-31991711190.BLASTQ34CLE

NCBI Genome

Published Nucleotide Protein Genome Structure PopSet Taxonomy OMM Help

Search for  on chromosome(s)  assembly All Find

Show linked entries Help FTP MapViewer home  Advanced search

**Homo sapiens genome view**  
build 34 version 2 statistics

BLAST search the human genome

Color key for scores: < 40 40-50 50-80 80-200 > 200

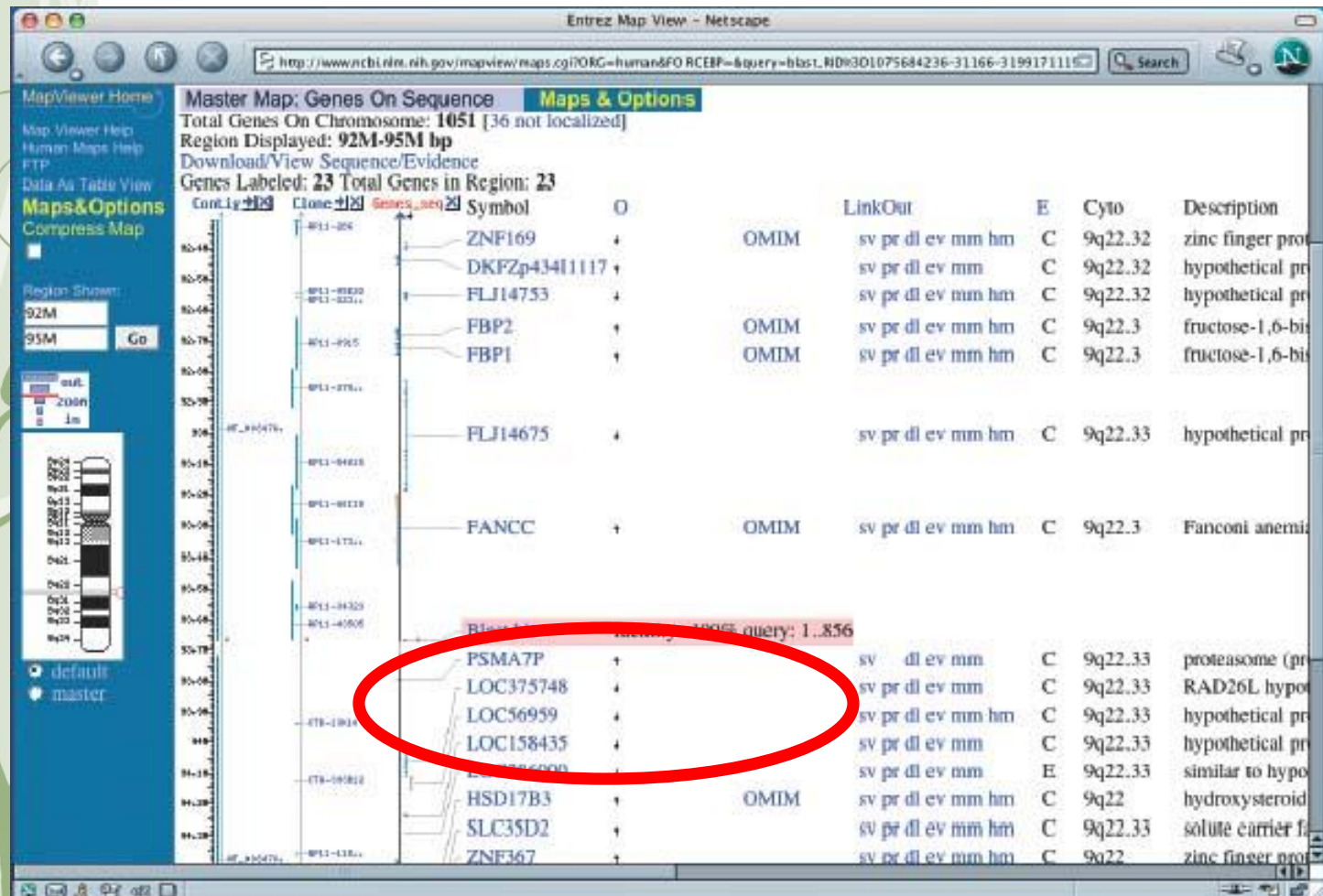
Back to BLAST alignments page

**BLAST search results: 2 BLAST hits found**  
Query BAC clone

Sort results by score

Chr	Hit GI	Hits	Score	E value	Map element
9	29734309	1	1646	0.0	NT_008476 Homo sapiens chromosome 9 genomic contig
not mapped	37540119	1	1646	0.0	NT_079537 Homo sapiens chromosome 9 genomic contig

# Location of Hit on Chr. 9



# The Output : Pairwise, Local Alignment

Source of database      Accession #      Name of sequence      Species

```
>prfl|1802398A crustacean hyperglycemic hormone [Orconectes limosus]  
Length = 72
```

Full length

```
Score = 115 bits (286), Expect = 6e-26  
Identities = 49/71 (69%), Positives = 58/71 (81%)
```

```
Query: 2  ILDQSCKGIFDRELFKFLDRVCDDCYNLYRKPYVAIDCREGICYQNLVFRQCIODLQLMDQ 61  
+ DQ+CKGI+DR +FKFLDRVC+DCYNLYRKPYVA CR+ CY N VFRQC+ DL L+D  
Sbjct: 2  VFDQACKGIYDRAIFKFLDRVCEDCYNLYRKPYVATTCRQNCYANSVFRQCLDDLLIDV 61
```

```
Query: 62  LDEYANAVQIV 72  
LDEY + VQ V  
Sbjct: 62  LDEYISGVQTV 72
```

Start point of sequence      Identical sequence      End point of sequence      Similarity Sequence

# Motivation of *my*BLAST

- 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** password-protected 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






# Characteristics of myBLAST

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

# myBLAST (Customized BLAST Framework)

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



Email

PWD

[Login](#) [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

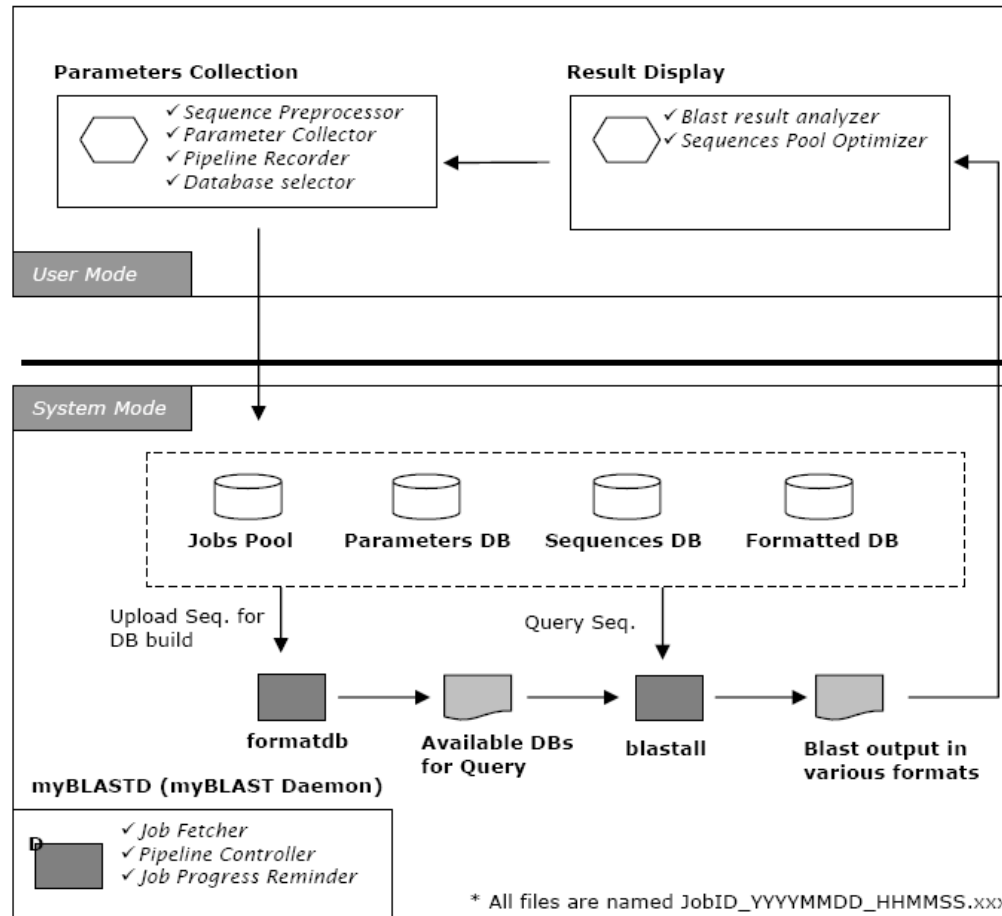
Submit description: (17) J99 blast 26695      Top 3

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%)



# Inside of myBlast



Hexagon : Web applications    Square : Program    Cylinder : Database    Shaded square : Output file

# Customized Databases



**Hello!**

Welcome to MyBLAST!!

IP: localhost

**DB Management**

**Upload DB**

**Run BLAST**

**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  浏览...

### Database Description (selected) :

Upload

Clear

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.

[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>

# Databases Manager



Hello!

Welcome to MyBLAST!!

IP: localhost

**DB Management**

**Upload DB**

**Run BLAST**

**View Results**

**User Guide**

**Contact Us**

:: Database Management ::

Protein

Here's your database lists:

DB_id	type	description	date	Edit	Download	Delete
1	P	Human Kinase	2009-12-01 06:16			
2	P	my first protein DB	2009-12-03 20:11			
3	N	my first DNA database	2009-12-03 20:14			



Add



Delete



BLAST

Nucleic Acids

# Select Database for Searching

## Select DB and Query to perform BLAST

### Select BLAST Program

Nucleotide BLAST

blastn  
megablast

Protein BLAST

blastp

Translated BLAST

blastx  
tblastn  
tblastx

Program: blastn (search nucleotide databases using a nucleotide query)

Job Note

Enter sequence below in **FASTA** format

Or load it from disk

Select Database:

Advanced Options:

Max target:

E-value:

Match/Mismatch  
penalty:

Gap creation:

Word size:

Turn off the low complexity filter

### BLAST running

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.

# Output Download

:: BLAST Results ::

Here's BLAST result lists:

Database Description	Submit Description	Date	Result	Download	delete
(1)Human Kinase	(1)test Human kinase DB	2009-12-01 06:17			
(1)Human Kinase	(2)my first protein search	2009-12-03 20:29			

Delete

# Result Viewer and Manager

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

**:: MyBLAST Results ::**

DB description: (1) Human Kinase  
Submit description: (2) my first protein search  
Download Output Files (**text file**) or (**cvs file**)

Matche Sequences  
Top 1

**Output Selector**

Seq.	Rank	Hits	E-value	Score	Bits	Match Length	Identities
sp P31946-1 1433B_HUMAN Isoform Long of 14-3-3 proteinbeta/alpha OS=Homo sapiens GN=YWHAB	1	gi 23222 gb CAA39840.1 14.3.3 protein cds_translation from X056468.126..863 Human mRNA for 14.3.3 protein, a protein kinase regulator. Homo sapiens (human)	1.0E-112	398.0	1023	245	198/242 (81%), Positives = 222/242 (91%)
sp P31946-2 1433B_HUMAN Isoform Short of 14-3-3 proteinbeta/alpha OS=Homo sapiens GN=YWHAB	1	gi 23222 gb CAA39840.1 14.3.3 protein cds_translation from X056468.126..863 Human mRNA for 14.3.3 protein, a protein kinase regulator. Homo sapiens (human)	1.0E-112	398.0	1023	245	198/242 (81%), Positives = 222/242 (91%)
sp P62258 1433E_HUMAN 14-3-3 protein epsilon OS=Homo sapiensGN=YWHAE	1	gi 23222 gb CAA39840.1 14.3.3 protein cds_translation from X056468.126..863 Human mRNA for 14.3.3 protein, a protein kinase regulator. Homo sapiens (human)	8.0E-85	308.0	788	245	154/236 (65%), Positives = 190/236 (80%), Gaps = 2/236 (0%)

# 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= sp|P31946-1|1433B\_HUMAN Isoform Long of 14-3-3 protein  
beta/alpha OS=Homo sapiens GN=YWHAB  
(246 letters)

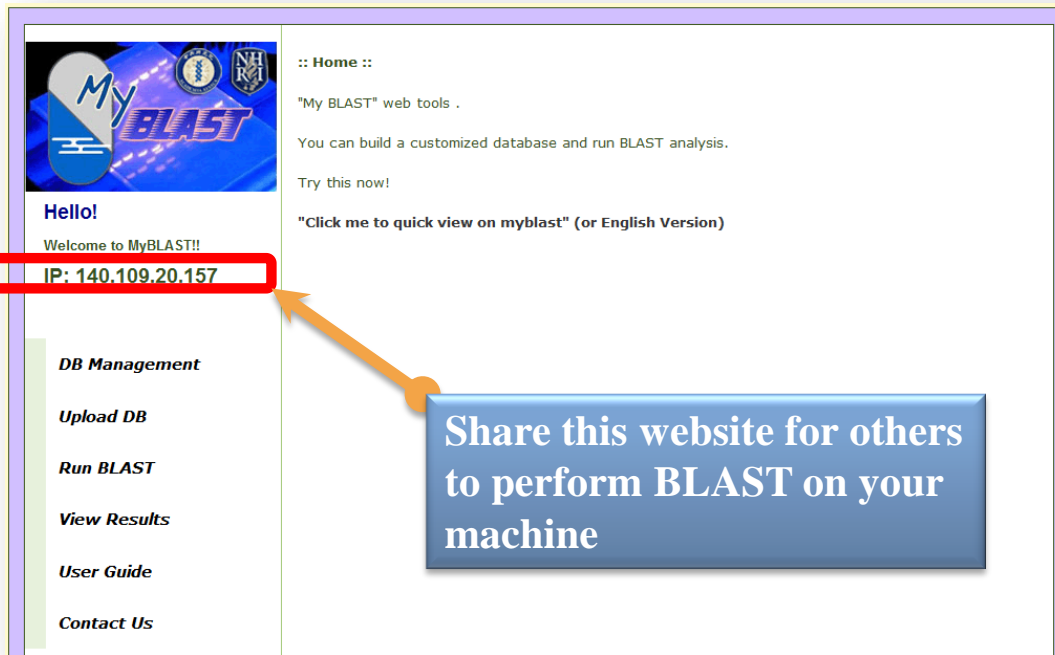
Database: C:\myblast\blastbase\blastdb\1  
6432 sequences; 3,217,054 total letters

Sequences producing significant alignments:

	Score	E
	(bits)	Value
gi 23222 gb CAA39840.1 14.3.3 protein cds_translation from X5646...	398	e-112
gi 221040138 gb BAH11832.1  from AK294647 158..535 Homo sapiens ...	220	2e-058
gi 219519599 gb AAI44068.1 TAOK1 protein cds_translation from BC...	33	0.045
gi 55957574 gb CAI16449.1 CANCER antigen  cds_translation from ...	31	0.22
gi 559575761 gb CAI16451.1 CANCER antigen  cds_translation from ...		
gi 55960327 gb CAI16114.1 NOVEL protein cds_translation from AL5...		
gi 14625824 gb AAK71522.1 MOESIN/ANAPLASTIC lymphoma kinase fusi...		
gi 168985265 gb CAQ09178.1 MYOSIN XVIII cds_translation from AL...		
gi 6110355 gb AAF03785.1 TRAF2 and NCK interacting kinase, splic...		
gi 6110347 gb AAF03782.1 TRAF2 and NCK interacting kinase, splic...		
gi 152012527 gb AAI50257.1 TRAF2 and NCK interacting kinase cds...		

	A	B	C	D	E	F	G	H
	Query ID	Rank	Hit	Score	Expect	bits	Identities	Length
1	sp P31946	1	gi 23222 gl	398	1.00E-112	1023	198/242 (81%), Positives =	245
2	sp P31946	2	gi 2210401	220	2.00E-58	561	108/122 (88%), Positives =	125
3	sp P31946	3	gi 2195195	33.1	0.045	74	50/257 (19%), Positives =	853
4	sp P31946	4	gi 5595757	30.8	0.22	68	33/187 (17%), Positives =	545
5	sp P31946	5	gi 5595757	30.8	0.22	68	33/187 (17%), Positives =	847
6	sp P31946	6	gi 5596032	28.5	1.1	62	18/90 (20%), Positives =	273
7	sp P31946	7	gi 1462582	27.7	1.9	60	23/128 (17%), Positives =	527
8	sp P31946	8	gi 1689852	27.3	2.5	59	33/138 (23%), Positives =	2569
9	sp P31946	9	gi 6110355	26.9	3.2	58	38/209 (18%), Positives =	1352
10	sp P31946	10	gi 6110347	26.9	3.2	58	38/209 (18%), Positives =	1360
11	sp P31946	1	gi 23222 gl	398	1.00E-112	1023	198/242 (81%), Positives =	245
12	sp P31946	2	gi 2210401	220	2.00E-58	561	108/122 (88%), Positives =	125

# myBLAST for Windows



**MyBLAST**

**Hello!**  
Welcome to MyBLAST!!  
**IP: 140.109.20.157**

**DB Management**

- Upload DB
- Run BLAST
- 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)



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

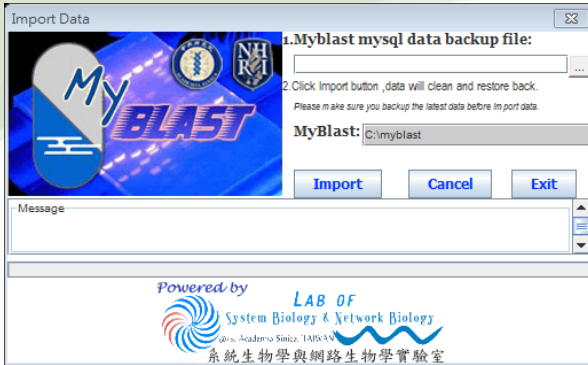
Restart tomcat and mysql..... 2009/11/20 12:58:14

Powered by LAB OF System Biology & Network Biology Academia Sinica, TAMS-330 系統生物學與網路生物學實驗室

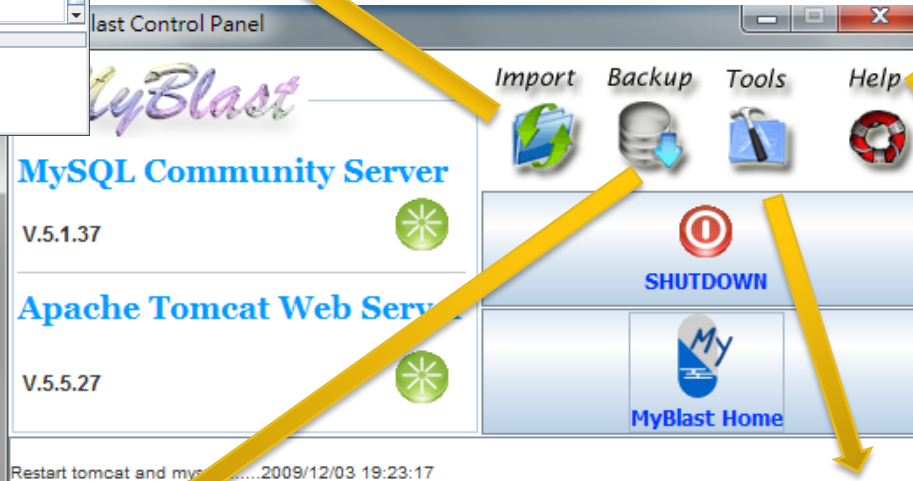
Screen casts and download URL: <http://eln.iis.sinica.edu.tw/>



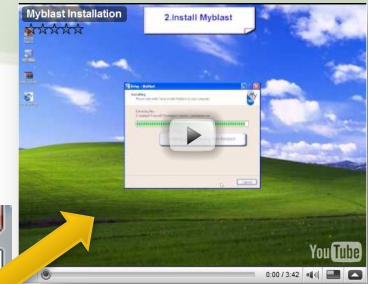
# Control Panel



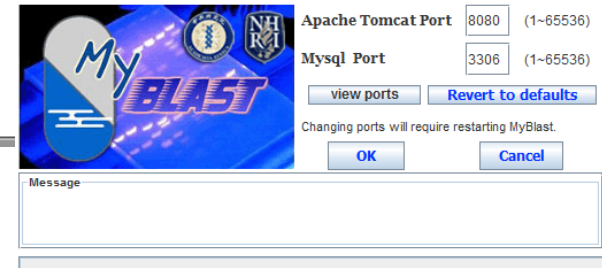
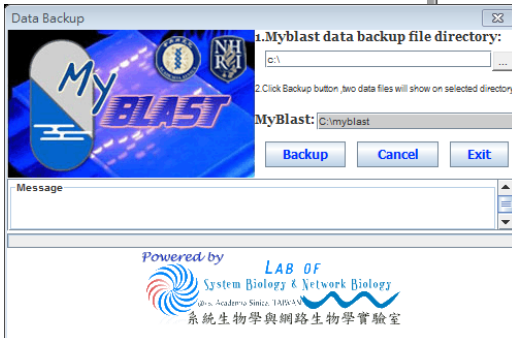
Import DBs and previous Result



Backup DBs and previous Result



HELP in Flash



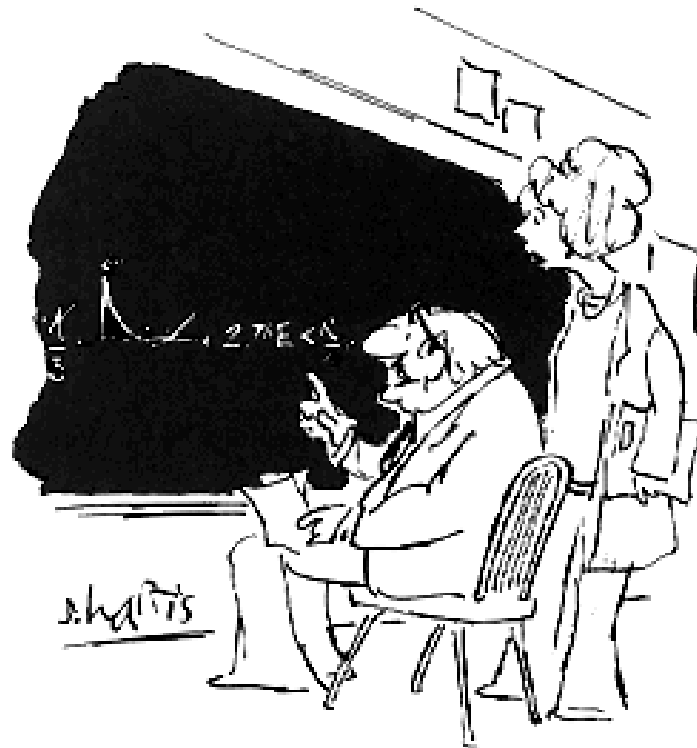
Port Setting

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# Flash Demo for MyBLAST



# *Give It a Try & Take a Break*



"The beauty of this is that it is only of theoretical importance, and there is no way it can be of any practical use whatsoever."