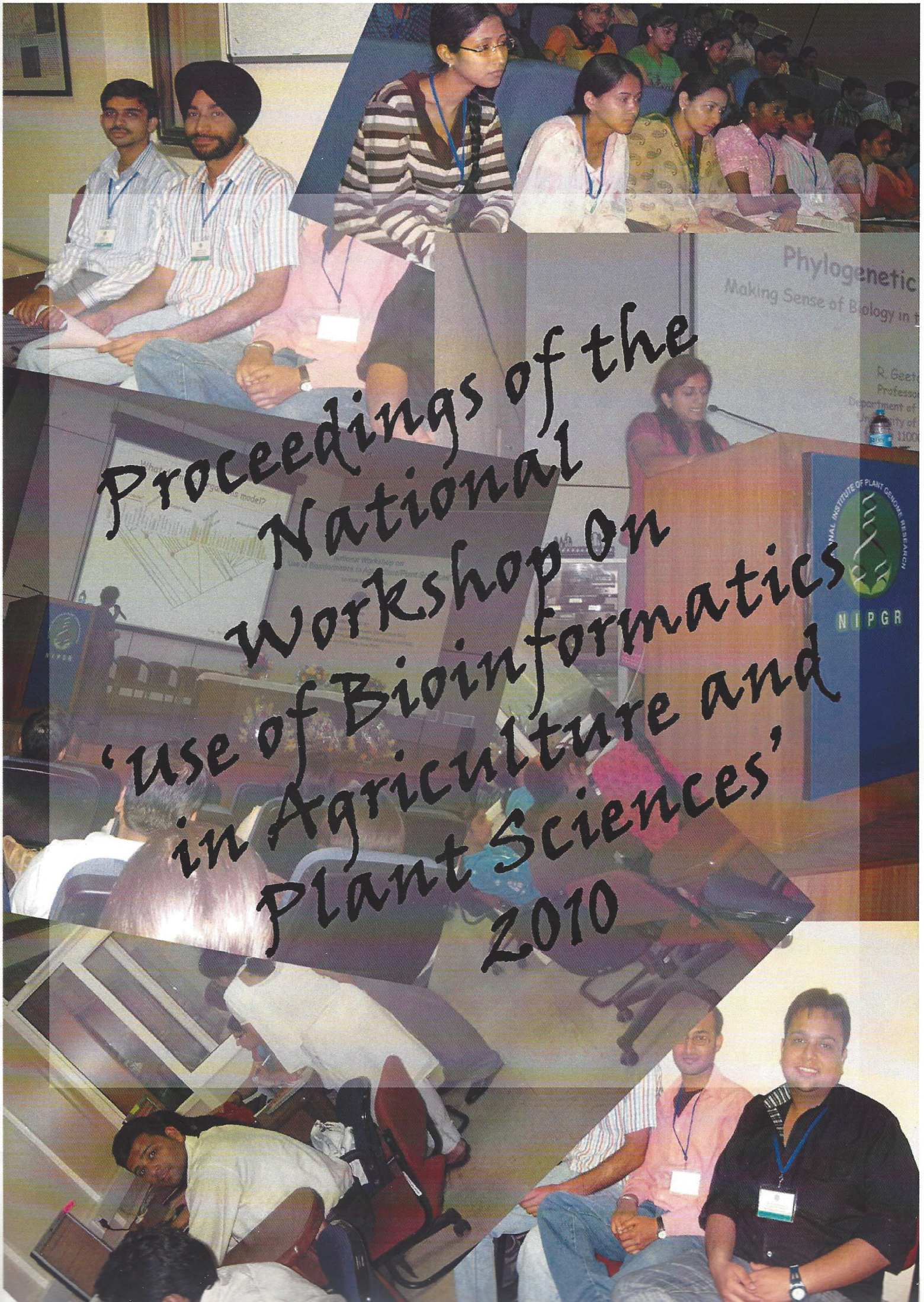


Proceedings of the National Workshop on 'Use of Bioinformatics in Agriculture and Plant Sciences' 2010

The BTIS-NET Sub-DIC at NIPGR organized the second Bioinformatics Workshop titled 'Use of Bioinformatics in Agricalture/ Plant Sciences' on 12-13th March 2010.

The endeavor of the organizing committee is to make this workshop an annual event, as per the BTIS-NET scheme, for Ph.D. scholars, postdoctoral researchers and teachers from various colleges and universities, in order to provide an opportunity to all participants to bene?t from the rich experience and expertise available in bioinformatics in India.

Twenty two participants were selected for the current workshop based upon abstracts received from all candidates (page X). The Inaugural session of the event was held at 10 am on the 12th of March, 2010. The welcome address was delivered by the Sub-DIC coordinator, while Prof. R. Geeta, renowned plant biologist and phylogeneticist from Univ of Delhi, Dept of Botany, delivered the Inaugural lecture titled "Phylogenetic Biology: Making Sense of Biology in the Light of Evolution". She stressed upon the need for young scienti?c minds to hypothesize and to remain aware of past research when designing experiments, giving examples from the her wide experience and her work in the evolution of the monocot leaf and the Angiosperm endosperm.

The remaining sessions of the workshop included, alternatively, three lecture sessions and five tutorial sessions (Page X). Young scientists working in the area of plant computational biology were invited for the lecture sessions, whereas previously designed hands-on practicals were imparted in the tutorial sessions. These included tutorials on Sequence Analysis, Data Interpretation, EST data analysis and structure prediction as well as modeling exercises.

During the First lecture session, Dr. G. Yadav, NIPGR, gave a lecture titled "Bioinformatics in Agriculture", describing the varied applications of computational biology in emerging areas like precision agriculture, crop improvement and evolutionary studies. Dr. S. M. Leighton, Univ of Delhi, in her lecture entitled "Bioinformatics and the pedagogy of Plant Sciences" described with examples, various steps in the design and implementation of a bioinformatics problem and its solution using freely available online programs and databases.

The first tutorial session gave the participants insights into sequence data retrieval and analysis, using web based tools. The next practical session included an exercise to enable the participants to carry out this analysis, using the example of wheat protein agglutinin.

On the second day of the workshop, participants were given a tutorial on EST data analysis and the methods involved therein. Later they were introduced to the concept of and protein structure. Exercises were designed using the example of wheat protein. The last hands-on session involved protein family analysis and phylogenetics. Summary slides from all lectures have been provided on Page X.

The second lecture session held on this day included a lecture by Dr. D. Chattopadhyay, NIPGR. His talk was titled 'Next generation sequencing and its applications in genomics and epigenomics'. Dr. Chattopadhyay elaborated upon the history of genome sequencing, the methods involved and described in details the applications of the new and futuristic methods with speci?c examples from plant genomes.

The valedictory session included an informal interaction with all participants who appreciated all the sessions and gave positive feedback on the workshop. On behalf of the Sub-DIC, I thank all participants as well as the NIPGR administration for making this event a success.

Gitanjali Yadav

(Staff Scientist & Workshop Coordinator)

Protein structure prediction and visualization

This exercise is concerned with various online tools available to study a protein structure. It is shown where you can find these tools, how to use them and most importantly how to interpret the results.

Part I: Predict the secondary structure of a protein sequence

Part 2: From the Primary Structure to the 3-D Structure

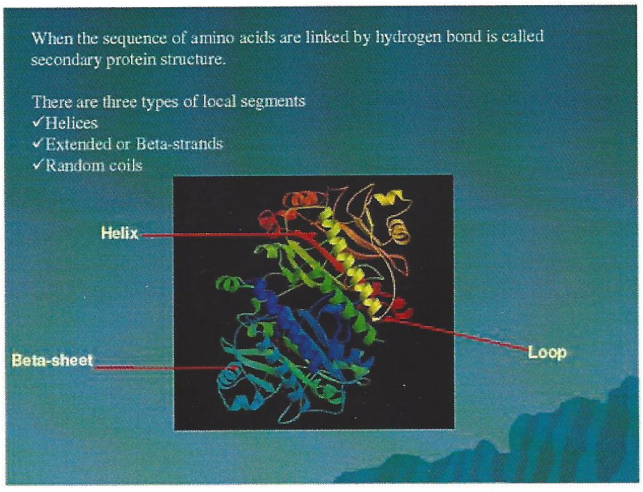
Part III: Visualization of protein 3D structure

Part IV(a): Gene and Protein sequences

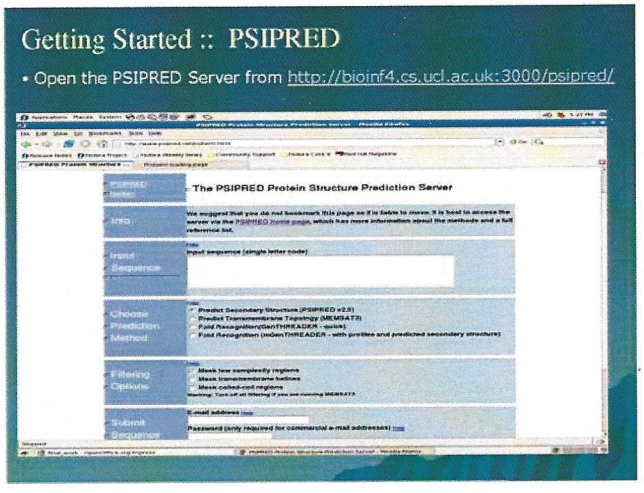
Part IV(b): Translation of the nucleotide sequence

Part V: View the overall information of PDB

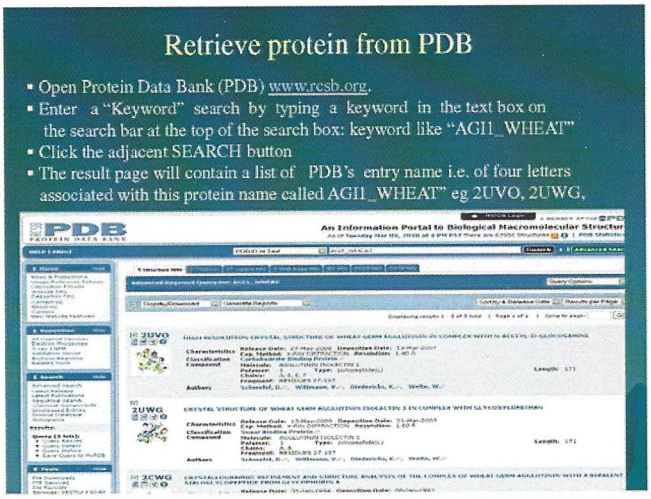
1.)



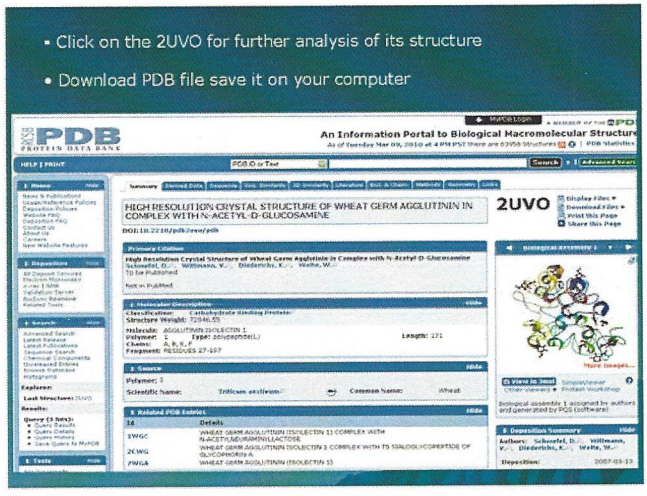
2.)



3.)

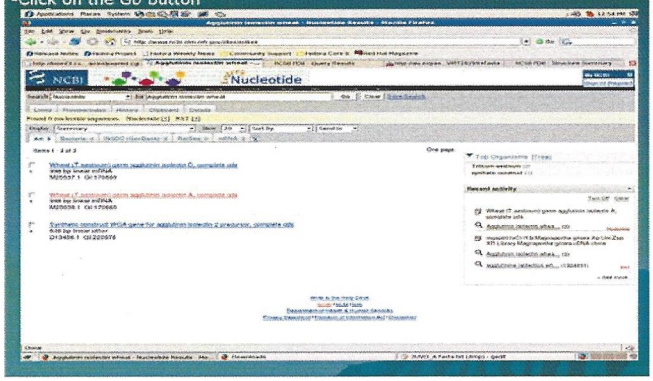


4.)



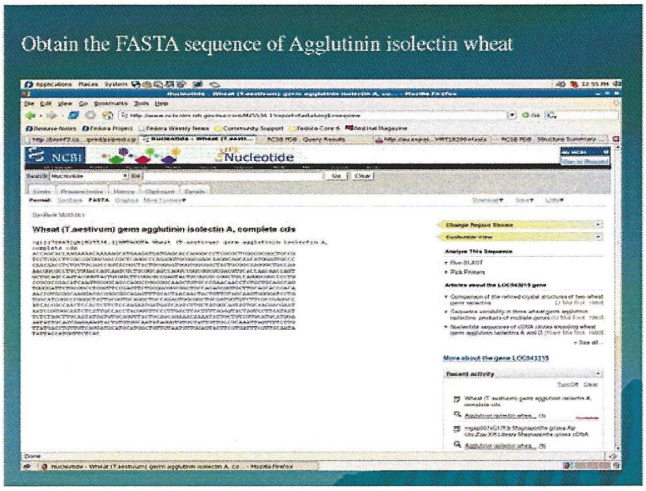
5.)

- Point your web browser to the following URL: http://www.ncbi.nlm.nih.gov/
- In the top search box select Nucleotide and enter the text "Agglutinin isolectin wheat"
- Click on the *Go* button



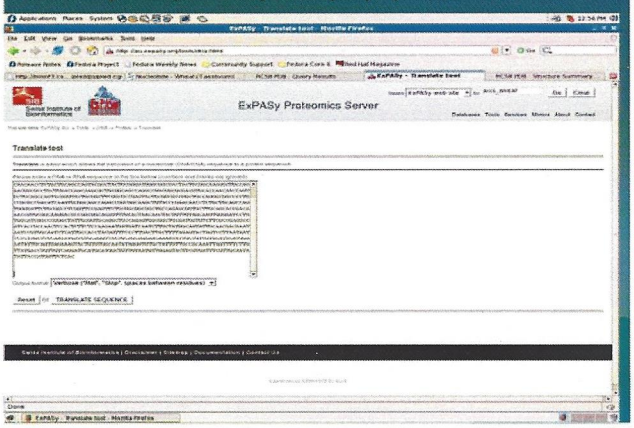
6.)

Obtain the FASTA sequence of Agglutinin isolectin wheat



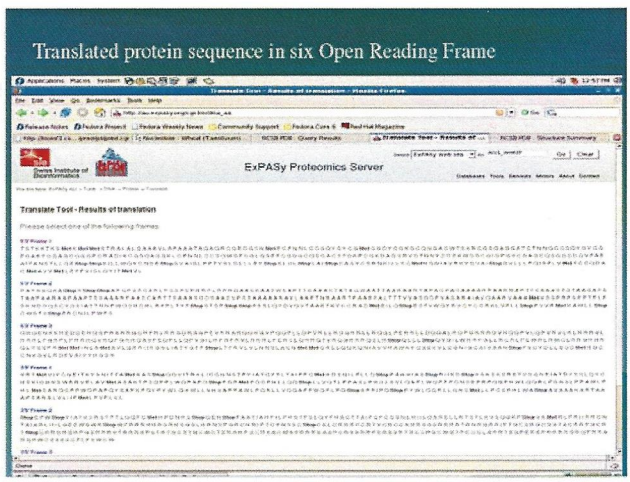
7.)

Translate gene to protein sequence by expasy tool.



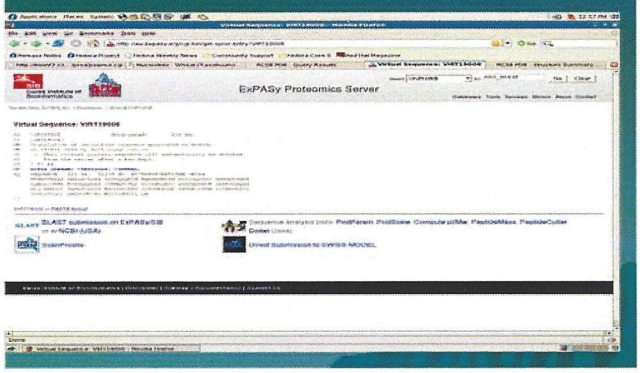
8.)

Translated protein sequence in six Open Reading Frame

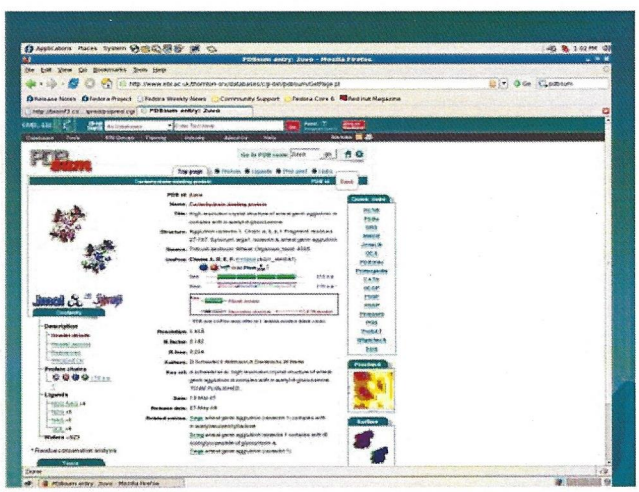


9.)

- ✓Click on any frame six of them.
- ✓The result page highlights the Methionine residues, or the starting point of the protein sequence.
- ✓Click the first 'M' in the sequence.

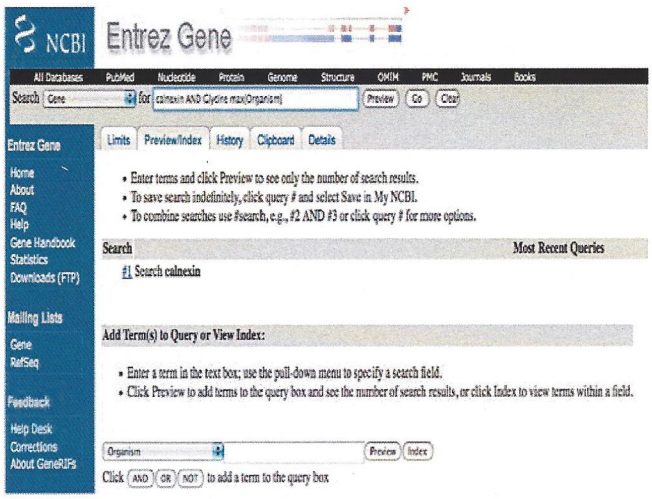


10.)

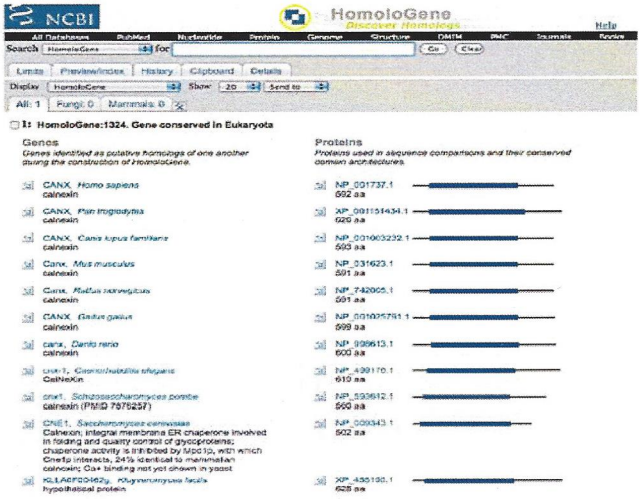


Biological Data Retrieval & Analysis

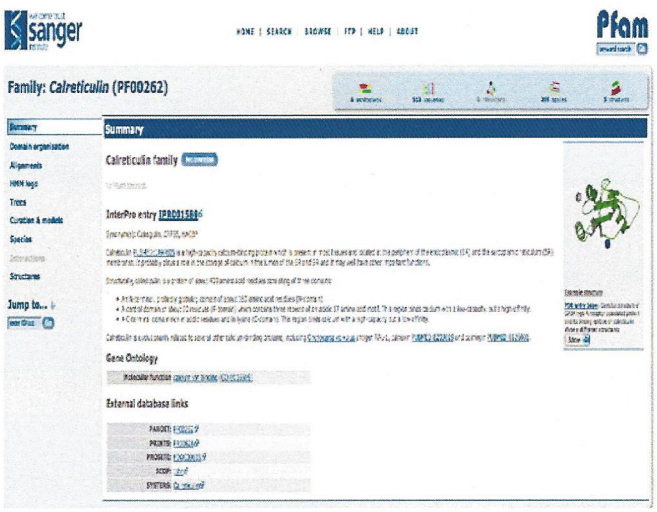
1.)



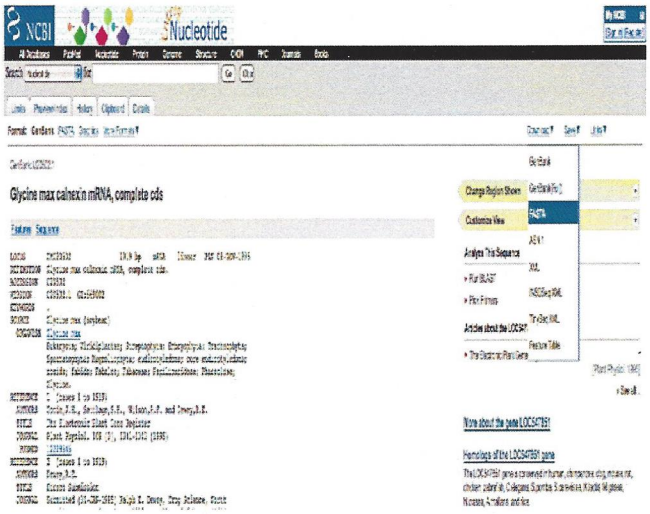
2.)



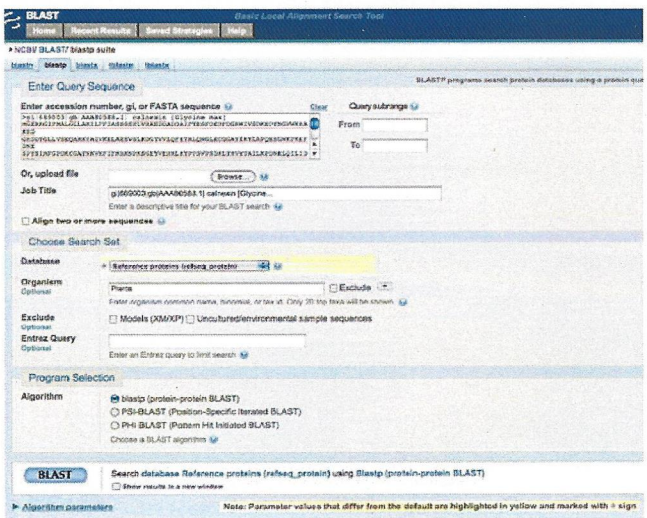
3.)



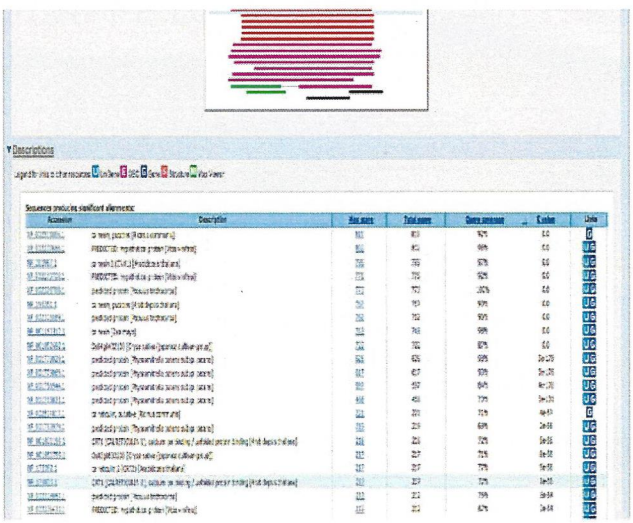
4.)



5.)



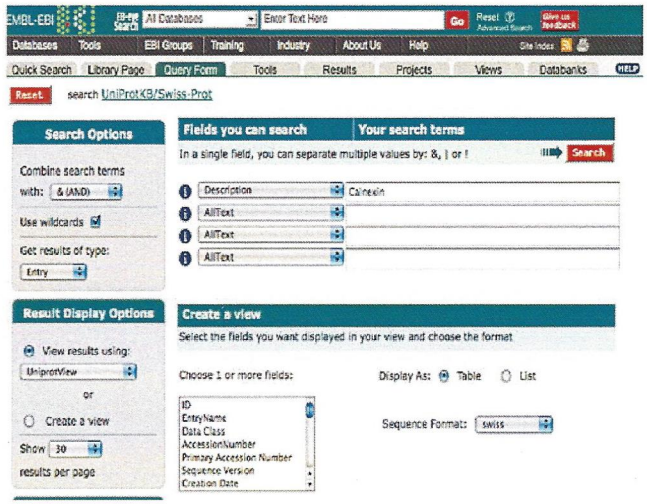
6.)



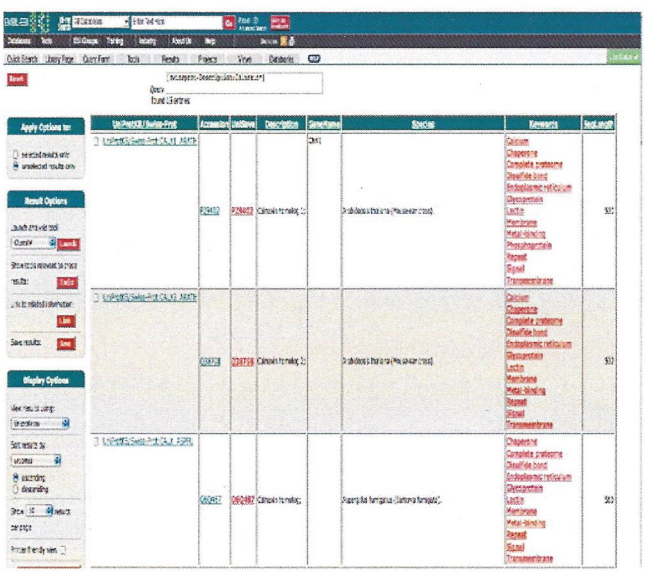
7.)

```
>ref|XP_002511066.1| calnexin, putative [Ricinus communis]
Length=542

 GENE ID: 8275467 RCOM_1503060 | calnexin, putative [Ricinus communis]

 Score =  810 bits (2091),  Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 403/507 (79%), Positives = 456/507 (89%), Gaps = 6/507 (1%)

Query  1    MGERKGIPMALGLLAMILFFIASSSSHLVRASDDADDAIFYESSPDESDFDGNWIVSDKEDY  60
            MGE K I + L L      +F +A  S   +RA  D D+ IFYESSP++ F+GNW +S K+DY
Sbjct  1    MGEAKRISLRLALL----VFLVAFVSFVQLRADSD-DNKIFYESSPEDSFEGNWTLSAKDDY  55

Query  61   NGVWKHAKSDGHDDYGLLVSSQARKYAIVKELAESVSLKDGTVVLQFETRLQNGLECGGA  120
             G WKHAKS+GHD+YGLLVSE+ARKYAIVKEL E   +LKDGT+VLQFETR QNGLECGGA
Sbjct  56   NGEWKHAKSEGHDEYGLLVSEKARKYAIVKELDEPATLKDGTIVLQFETRPQNGLECGGA  115

Query  121  YIKYLRPQESGWKPKEFDNESPYSIMFGPDKCGATNKVHPIFKHKNPKSGEYVEHHLKYP  180
            Y+KYLRPQE+GW PK+FDN+SPYSIMFGPDKCGATNKVHPI KHKNPKSGEY+EHHLKYP
Sbjct  116  YLKYLRPQEAGWIPKDFDNDSPYSIMFGPDKCGATNKVHPILKHKNPKSGEYIEHHLKYP  175

Query  181  PSVPSDKLTHVYTAILKPDNELQILIDGEEKKKANFLSSDDFEPPLIPSKTIPDPDDKKP  240
            PSVPSDKLTHVYTAILKPDNELQILIDGEEKKKANFLSSDDFEPPL+P+KTIPDPDDKKP
Sbjct  176  PSVPSDKLTHVYTAILKPDNELRILVDGEEKKKANFLSSDDFEPPLVPAKTIPDPDDKKP  235

Query  241  EDWDERAKIPDPSAVKPDDWDEDAPMEILDEEAEKPEGWLDDEPEEIDDPEAKPEDWDD  300
            EDWDERAKIPDP+AVKPDDWDEDAPMEI+DE+AEKPEGWLDDEPEEIDDP+A KPEDWDD
Sbjct  236  EDWDERAKIPDPMAVKPDDWDEDAPMEIVDEDAEKPEGWLDDEPEEIDDPDAAKPEDWDD  295

Query  301  EEDGEWEAPKIINPKCMAAPGGCEWKRPTKHNPAYKGKWSAPYIDNPSYKGIWKPHEIPN  360
            EEDGEWEAPKI+NPKCE APGCGEWKRP KHNPAYNGKW AP IDNP+YKGIWKP+EIPN
Sbjct  296  EEDGEWEAPKIDNPKCEIAPGCGEWKRPMKHNPAYNGKWHAPLIDNPNYKGIWKPQEIPN  355

Query  361  PEYFELAKPDFEPIAAIGIEIWTMQDGILFDNVLIANDDKVAKSYRETTWKPKFTVEKDK  420
            P YFEL KPDFEPIAA+GIEIWTMQDGILF +-LIA+D+KVAES R+T WKPKF  EK+K
Sbjct  356  PNYFELEKPDFEPIAAVGIEIWTMQDGILFGHILIADEKVAESLRQTAWKPKFIAEKEK  415

Query  421  LKAEEEAATGSDGISGPQKKVEDLLYKIADIFFLSEHKSKIFDLIEKAEKQPNLTIGILV  480
             KA E+AA GSDG++GPQKKVEDLLY++ADIFFLSEHK KI D+IEK EKQPNLTIGILV
Sbjct  416  QKA-EDAAAGSDGLAGPQKKVEDLLYQVADIFFLSEHKDKIIDIIEKGEKQPNLTIGILV  474

Query  481  AVVVVFVSIFFRLIFGGKKPAKVEKKP  507
            ++VVV  ++ F+++FGGKKPAKVE+KP
Sbjct  475  SIVVVIFTVLPKILFGGKKPAKVEEKP  501
```

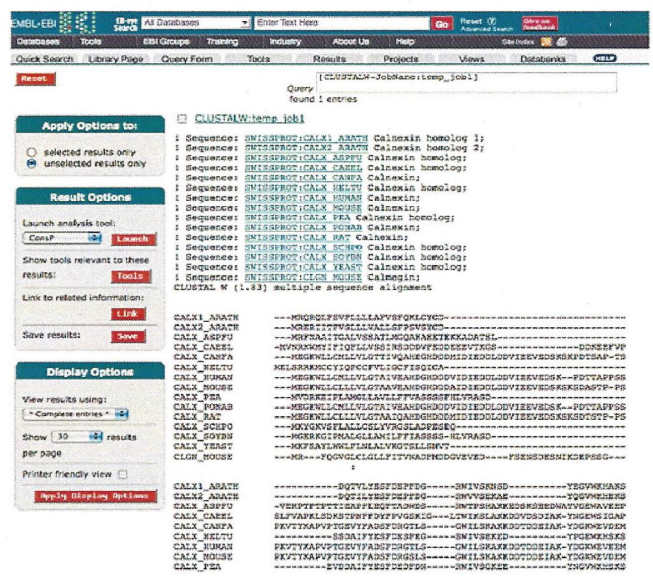
8.)



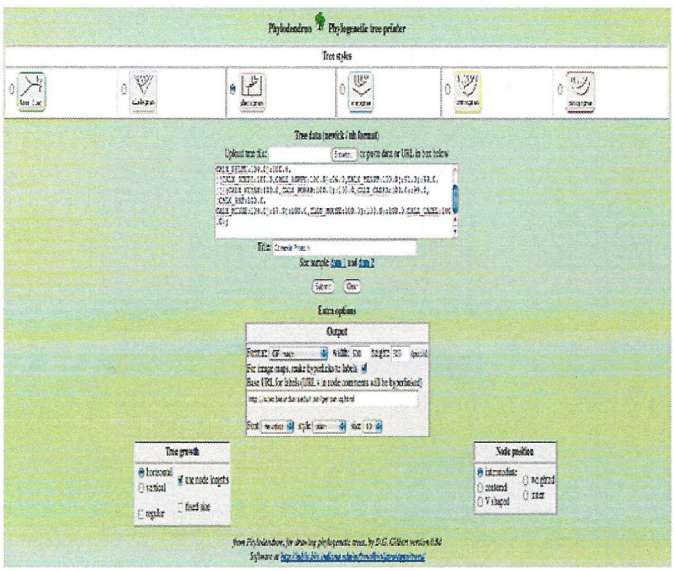
9.)



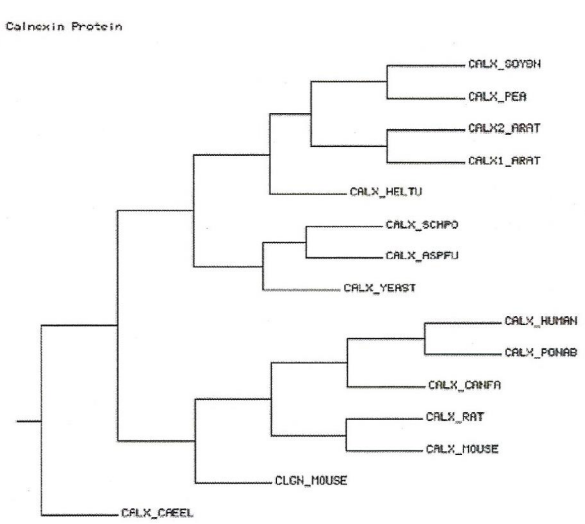
10.)



11.)



12.)

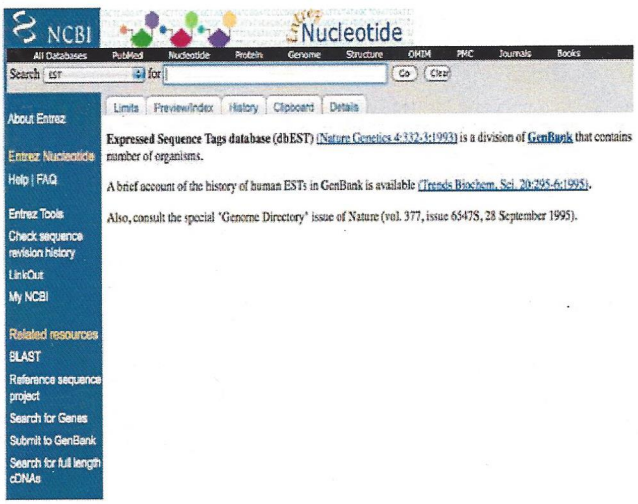


Methods for Analysis of EST Data

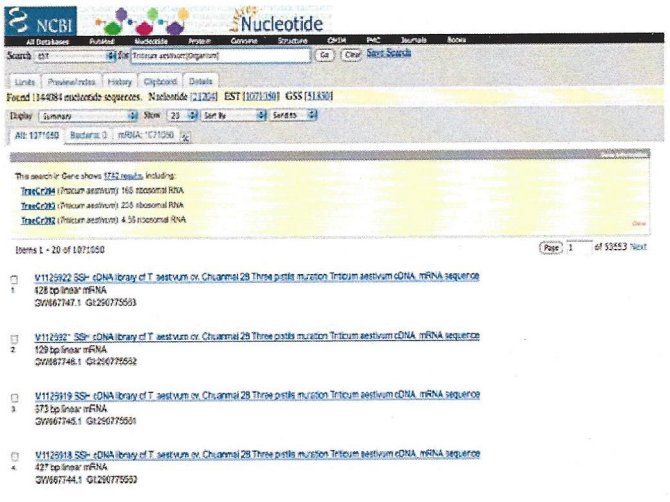
The Practical exercises discussed below will help us analyze EST data available publicly. We will analyze the High-throughput data for an agricultural crop, *Triticum aestivum* for being specific to one organism related to agriculture. Various tools available online will be used to retrieve analyze and annotate the EST data.

ESTs are short (200-800 nucleotide bases in length), unedited, randomly selected single-pass sequence reads derived from cDNA libraries. High-throughput ESTs can be generated at a reasonably low cost from either the 50 or 30 end of a cDNA clone to get an insight into transcriptionally active regions in any organism.

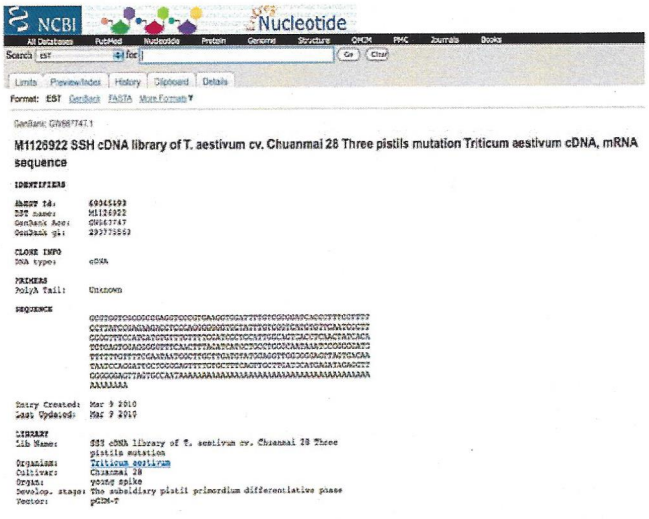
1.)



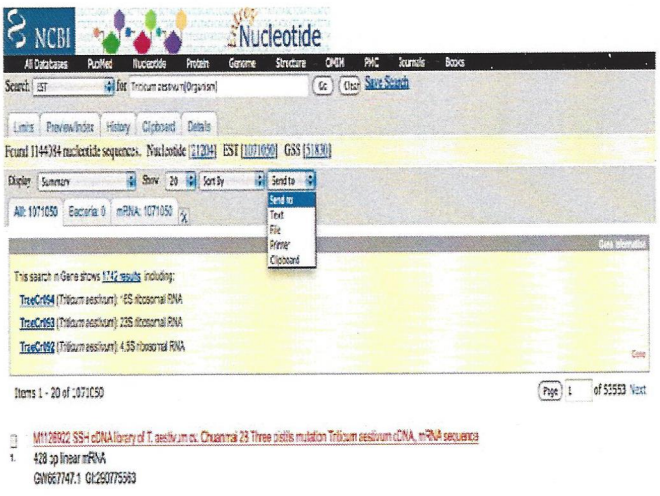
2.)



3.)



4.)



Working with a Single Protein Sequence

This exercise is concerned with various online tools available to study a protein before designing a new experiment in the lab. It is shown where you can find these tools, how to use them and most importantly how to interpret the results.

Part I : Predicting the main physico-chemical properties of a protein

Part II: Digesting a protein in a computer

Protease digestions — where you use an enzyme to cut your protein in specific ways — can be useful if you're only interested in carrying out experiments on a portion of your protein.

Part III: Primary Structure Analysis

A primary structure analysis is conducted to find segments in a protein that display a special composition. These segments can reveal some interesting properties of your protein.

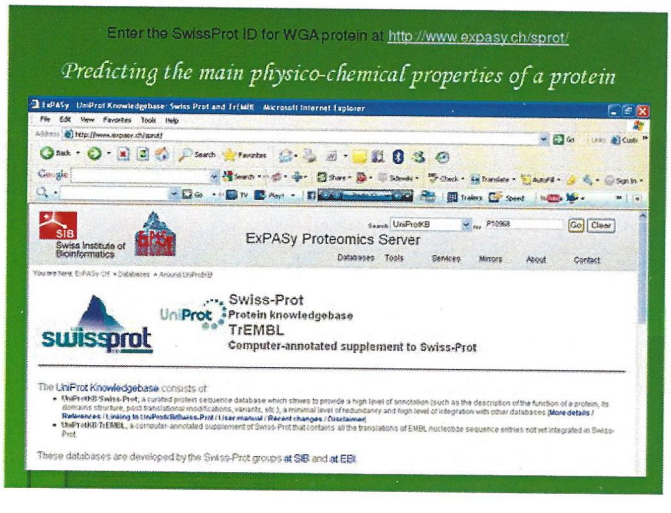
Note : For the following analysis , obtain the protein sequence Q39817 (CALX_SOYBN) from SwissProt.

Part IV: Predicting post-translational modifications in your protein.

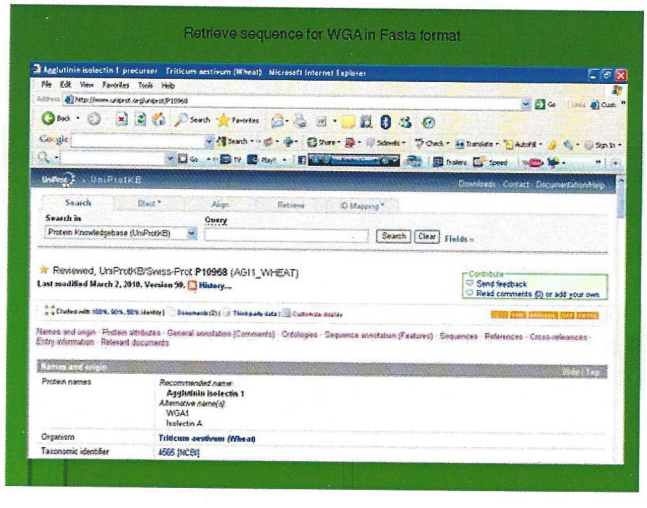
Part V: Finding Known Domains in your Protein

Note: In many interesting domains, a particular type of amino acid is overrepresented. For instance, there are more leucines than expected by chance in the leucine zippers, or more glycines than expected by chance in the glycine-rich domains — and so on — for many domains. Because repeated residues make a sequence simpler, sequences that contain them are described as low-complexity. If you keep the Apply Low Complexity Filter box checked, you may lose these domains.

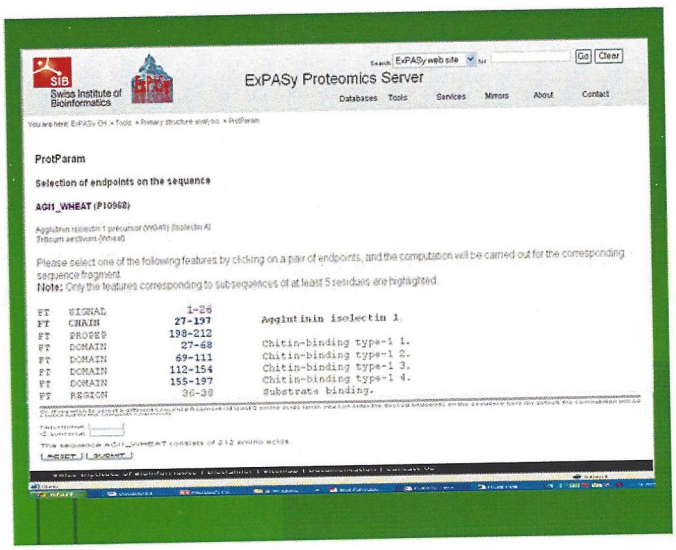
1.)



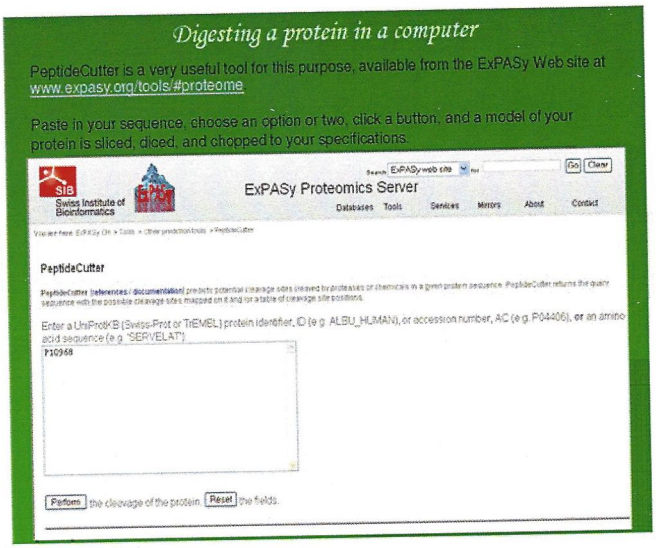
2.)



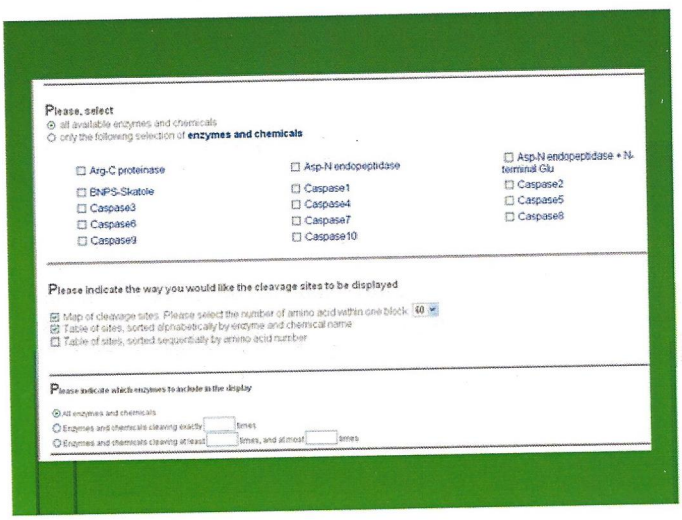
3.)


ExPASy Proteomics Server
ProtParam
Selection of endpoints on the sequence
AG1I_WHEAT (P10968)
Please select one of the following features by clicking on a pair of endpoints, and the computation will be carried out for the corresponding sequence fragment.
Note: Only the features corresponding to subsequences of at least 5 residues are highlighted.
FT SIGNAL 1-26
FT CHAIN 27-197 Agglutinin isolectin 1.
FT PROPEP 198-212
FT DOMAIN 27-68 Chitin-binding type-1 1.
FT DOMAIN 69-111 Chitin-binding type-1 2.
FT DOMAIN 112-154 Chitin-binding type-1 3.
FT DOMAIN 155-197 Chitin-binding type-1 4.
FT REGION 36-38 Substrate binding.

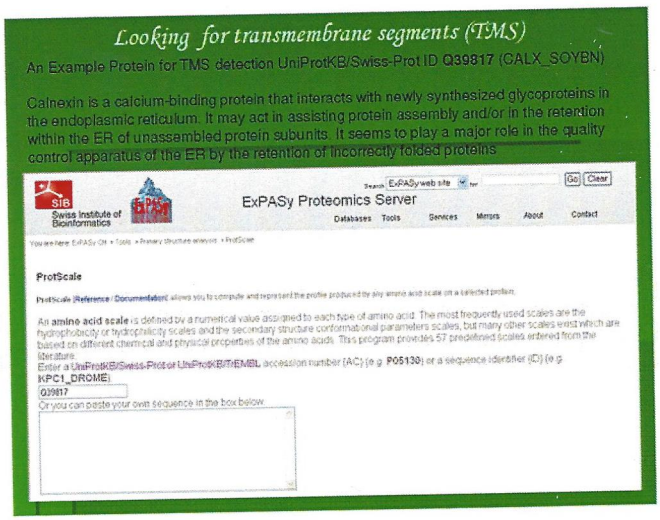
4.)


Digesting a protein in a computer
PeptideCutter is a very useful tool for this purpose, available from the ExPASy Web site at www.expasy.org/tools/#proteome
Paste in your sequence, choose an option or two, click a button, and a model of your protein is sliced, diced, and chopped to your specifications.
ExPASy Proteomics Server
PeptideCutter
Enter a UniProtKB (Swiss-Prot or TrEMBL) protein identifier, ID (e.g. ALBU_HUMAN), or accession number, AC (e.g. P04406), or an amino acid sequence (e.g. SERVELAT):
P10968
Perform the cleavage of the protein. Reset the fields.

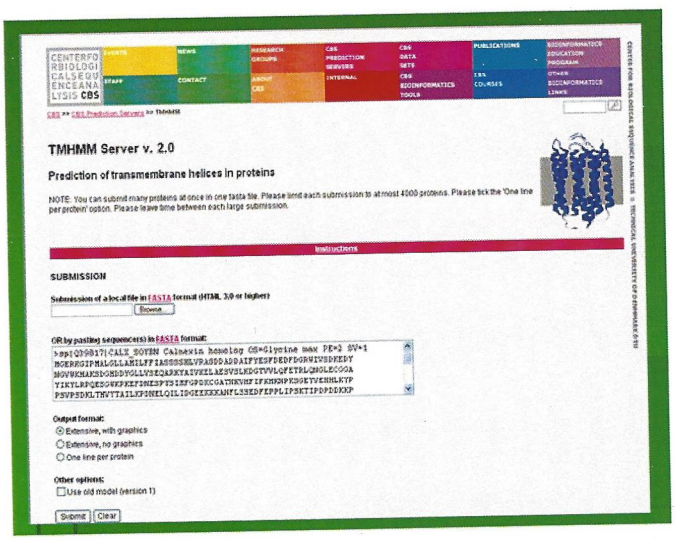
5.)


Please, select
all available enzymes and chemicals
only the following selection of enzymes and chemicals
Arg-C proteinase
Asp-N endopeptidase
Asp-N endopeptidase + N-terminal Glu
BNPS-Skatole
Caspase1
Caspase2
Caspase3
Caspase4
Caspase5
Caspase6
Caspase7
Caspase8
Caspase9
Caspase10
Please indicate the way you would like the cleavage sites to be displayed
Map of cleavage sites. Please select the number of amino acid within one block: 60
Table of sites, sorted alphabetically by enzyme and chemical name
Table of sites, sorted sequentially by amino acid number
Please indicate which enzymes to include in the display
All enzymes and chemicals
Enzymes and chemicals cleaving exactly times
Enzymes and chemicals cleaving at least times, and at most times

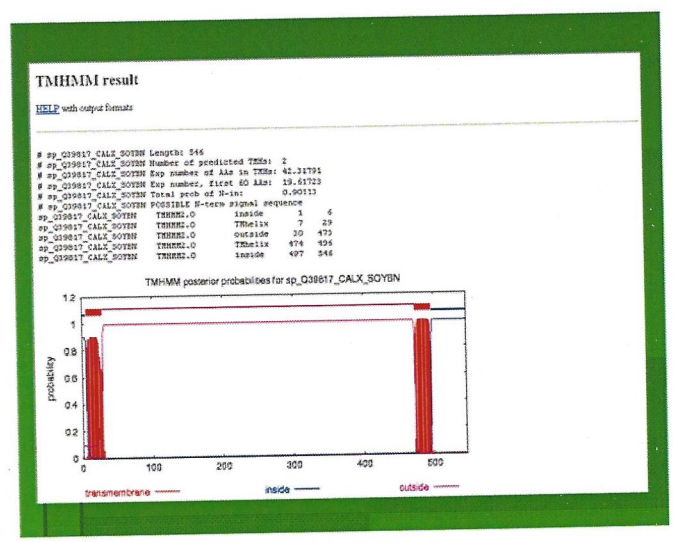
6.)


Looking for transmembrane segments (TMS)
An Example Protein for TMS detection UniProtKB/Swiss-Prot ID Q39817 (CALX_SOYBN)
Calnexin is a calcium-binding protein that interacts with newly synthesized glycoproteins in the endoplasmic reticulum. It may act in assisting protein assembly and/or in the retention within the ER of unassembled protein subunits. It seems to play a major role in the quality control apparatus of the ER by the retention of incorrectly folded proteins
ExPASy Proteomics Server
ProtScale
An amino acid scale is defined by a numerical value assigned to each type of amino acid. The most frequently used scales are the hydrophobicity or hydrophilicity scales and the secondary structure conformational parameters scales, but many other scales exist which are based on different chemical and physical properties of the amino acids. This program provides 57 predefined scales ordered from the literature.
Enter a UniProtKB/Swiss-Prot or UniProtKB/TrEMBL accession number (AC) (e.g. P05130) or a sequence identifier (ID) (e.g. KPC1_DROME):
Q39817
Or you can paste your own sequence in the box below:

7.)


TMHMM Server v. 2.0
Prediction of transmembrane helices in proteins
NOTE: You can submit many proteins at once in one fasta file. Please limit each submission to at most 4000 proteins. Please tick the 'One line per protein' option. Please leave time between each large submission.
Instructions
SUBMISSION
Submission of a local file in FASTA format (HTML 3.0 or higher):
Browse...
OR by pasting sequence(s) in FASTA format:
>sp|Q39817|CALX_SOYBN Calnexin Homolog OS=Glycine max PE=2 SV=1
Output format:
Extensive, with graphics
Extensive, no graphics
One line per protein
Other options:
Use old model (version 1)
Submit
Clear

8.)


TMHMM result
HELP with output formats
sp_Q39817_CALX_SOYBN Length: 546
sp_Q39817_CALX_SOYBN Number of predicted TMHs: 2
sp_Q39817_CALX_SOYBN Exp number of AAs in TMHs: 42.31791
sp_Q39817_CALX_SOYBN Exp number, first 60 AAs: 19.61723
sp_Q39817_CALX_SOYBN Total prob of N-in: 0.90113
sp_Q39817_CALX_SOYBN POSSIBLE N-term signal sequence
sp_Q39817_CALX_SOYBN TMHMM2.0 inside 1 6
sp_Q39817_CALX_SOYBN TMHMM2.0 TMhelix 7 29
sp_Q39817_CALX_SOYBN TMHMM2.0 outside 30 473
sp_Q39817_CALX_SOYBN TMHMM2.0 TMhelix 474 496
sp_Q39817_CALX_SOYBN TMHMM2.0 inside 497 546
TMHMM posterior probabilities for sp_Q39817_CALX_SOYBN
probability
transmembrane
inside
outside

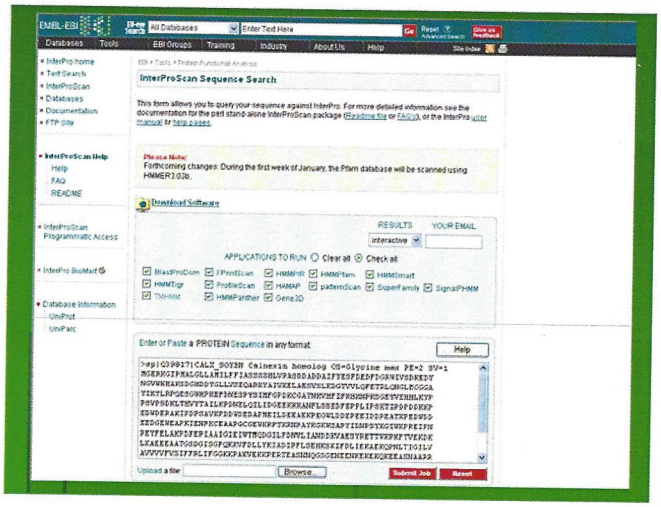
9.)

Finding Known Domains in your Protein

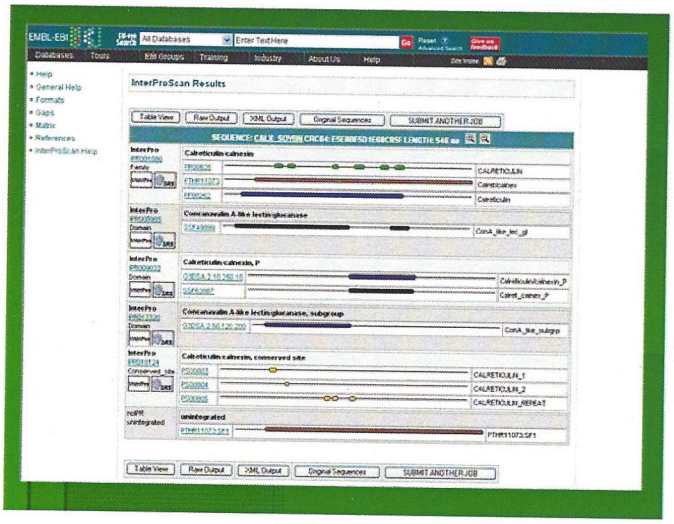
The Main Domain Collection

Name	Web Address	Number of Domains	Generation
PROSITE-Profile (IP)	www.expasy.org/prosite	616	Manual
PlamA (IP)	www.sanger.ac.uk/Software/Pfam	7973	Manual
PRINTs (IP)	www.bioinf.man.ac.uk/dbbrowser/PRINTS	1900	Manual
PRODOM (IP)	protein.toulouse.inra.fr/prodom/current/html/home.php	736000	Automatic
SMART (IP)	smart.embl-heidelberg.de	685	Manual
COGs	www.ncbi.nlm.nih.gov/COG/new/	4852	Manual
TIGRFAM (IP)	www.tigr.org/TIGRFAMs	2453	Manual
BLOCKs	blocks.fhcrc.org/	12548	Automatic

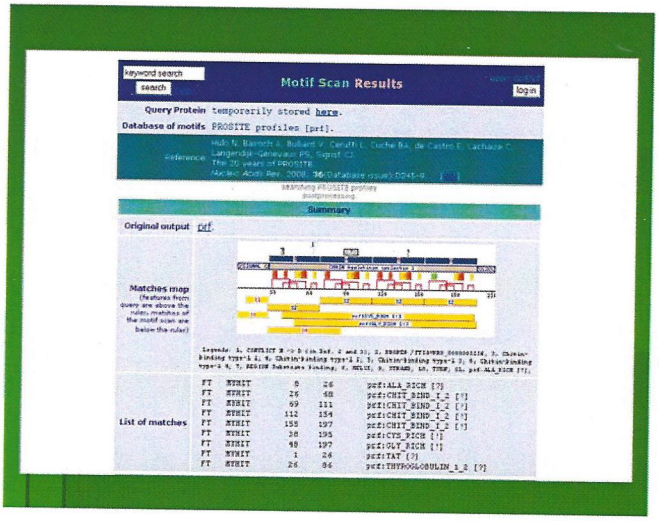
10.)



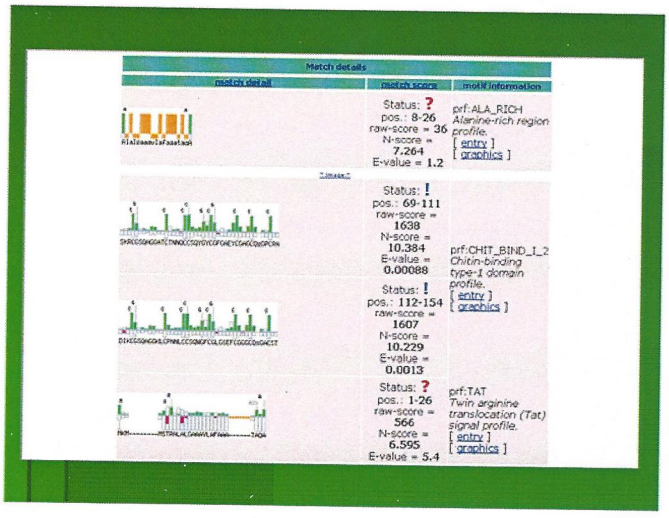
11.)



12.)



13.)



14.)

More Protein Analysis for Free over the Internet

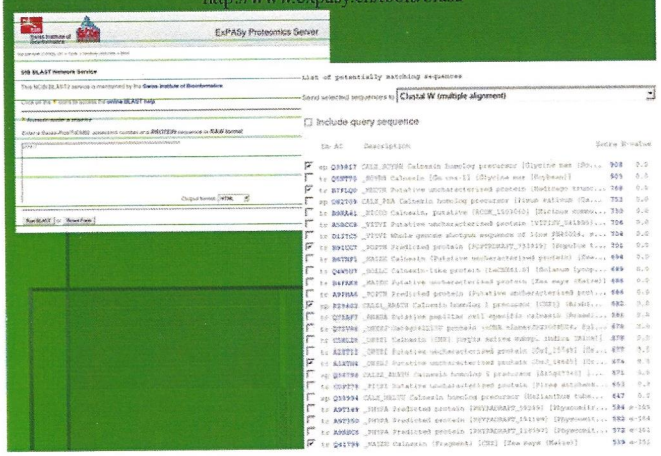
Name	Site	Description
ExPASy	www.expasy.org/tools	Proteins
Pbil	npsa-pbil.ibcp.fr	Proteins
PIR	pir.georgetown.edu	Proteins
CBS	www.cbs.dtu.dk/services	Proteins
Hits	hits.ish-sib.ch/	Proteins
InterPro	www.ebi.ac.uk/interpro/scan.html	Domains
CD search	http://www.ebi.ac.uk/InterProScan/	Domains

Protein Family Analysis & Phylogenetics

1.)

Gathering sequences with online BLAST servers

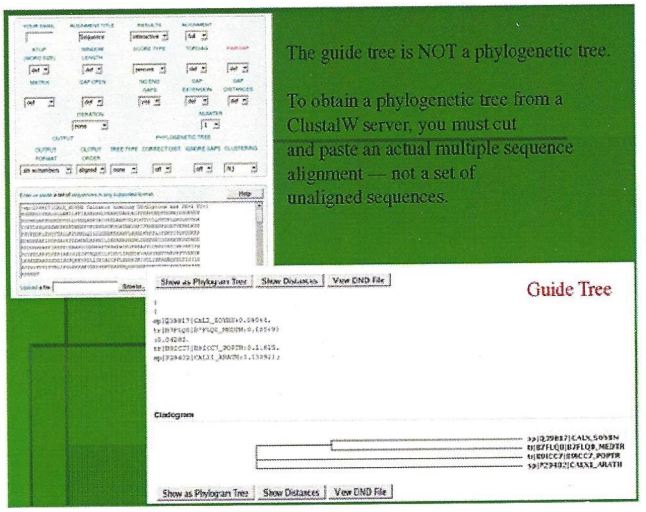
http://www.expasy.ch/tools/blast/



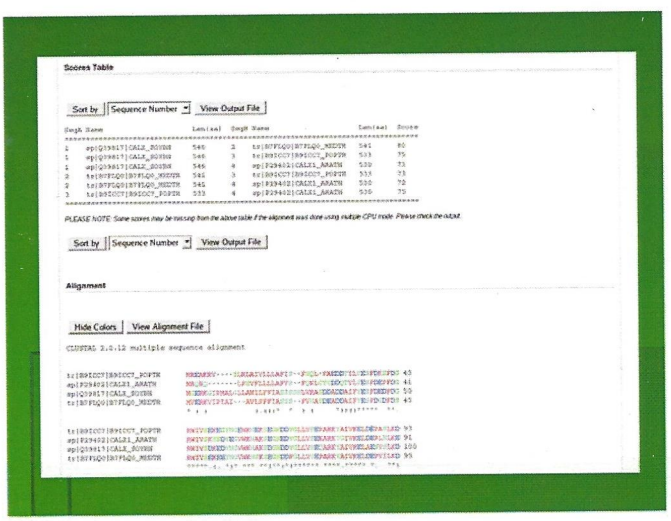
2.)

The guide tree is NOT a phylogenetic tree.

To obtain a phylogenetic tree from a ClustalW server, you must cut and paste an actual multiple sequence alignment — not a set of unaligned sequences.



3.)



4.)

Aligning sequences & structures with Tcoffee

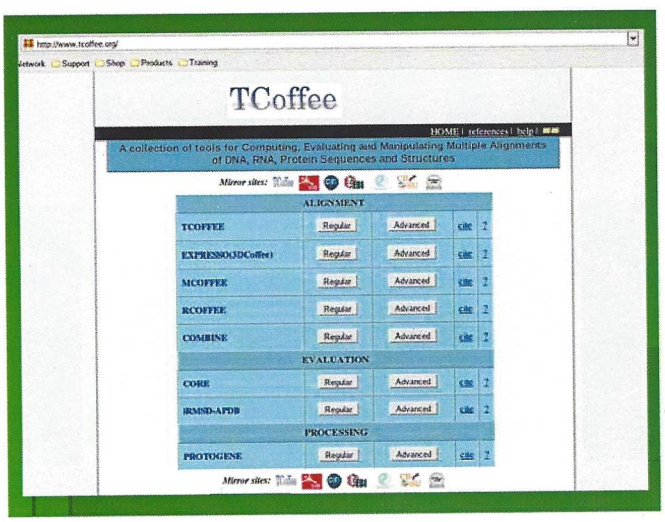
It uses a principle that's a bit similar to ClustalW, but it yields more accurate alignments at the cost of a slightly longer running time.

Tcoffee builds a progressive alignment like ClustalW, but it compares segments across the entire sequence set.

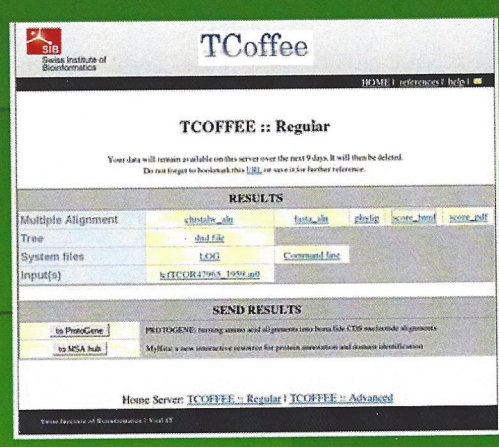
Available Tools on www.tcoffee.org

Usage	*Description*
TCOFFEE	Produce a multiple sequence alignment with Tcoffee.
CORE	Evaluate the reliability of an existing multiple alignment.
MCOFFEE	Run any requested Multiple Sequence Alignment package and combine all the output into one final alignment.
EXPRESSO	Incorporate all the available structural information in your alignment. Will produce the best sequence alignments if the structures are available.

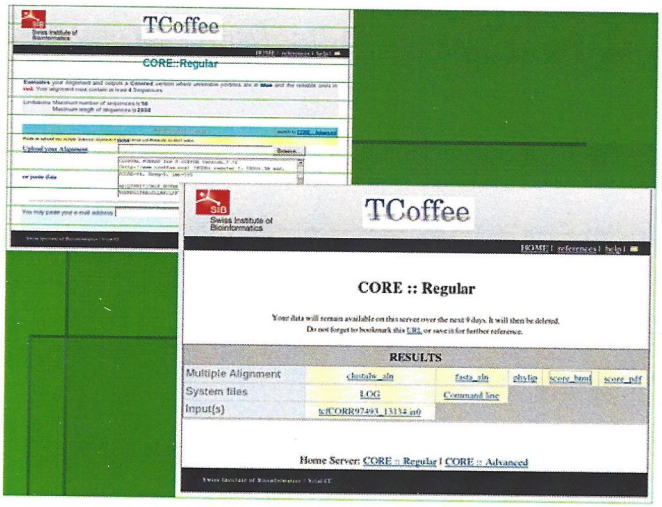
5.)



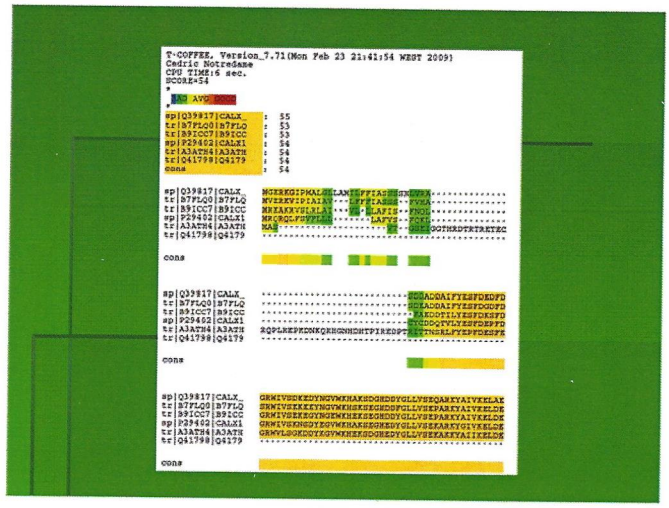
6.)



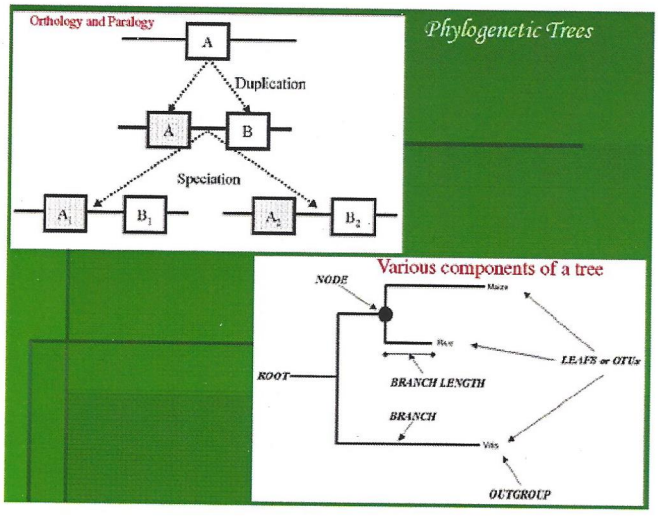
7.)


TCoffee
CORE::Regular
TCoffee
CORE :: Regular
Your data will remain available on this server over the next 9 days. It will then be deleted.
Do not forget to bookmark this URL or save it for further reference.
RESULTS
Multiple Alignment
clustalw_aln
fasta_aln
phylip
score_html
score_pdf
System files
LOG
Command line
Input(s)
tcfCORR97493_13334.arp
Home Server: CORE :: Regular | CORE :: Advanced

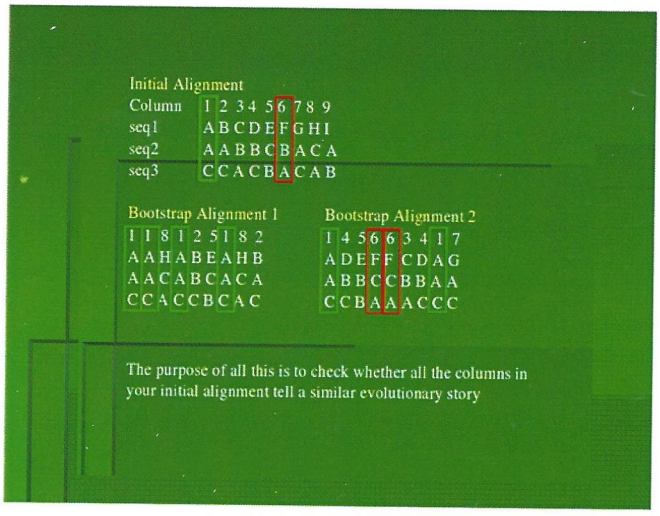
8.)


T-COFFEE, Version_7.71(Mon Feb 23 21:41:54 WEST 2009)
Cedric NotreGame
CPU TIME:6 sec.
SCORE=54
cons

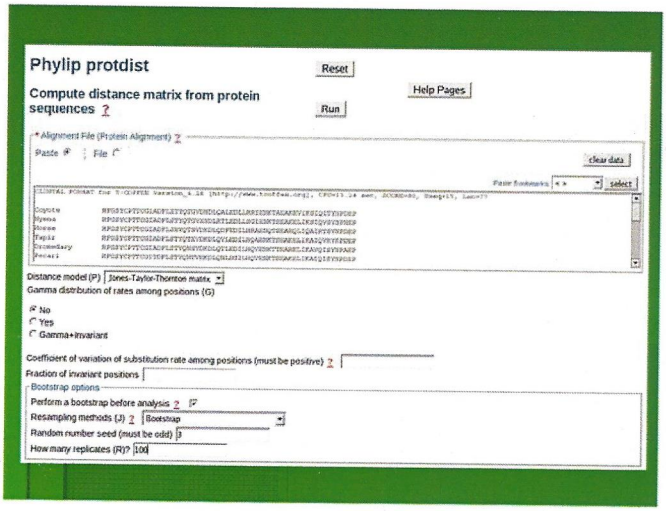
9.)


Orthology and Paralogy
Duplication
Speciation
Phylogenetic Trees
Various components of a tree
NODE
ROOT
BRANCH LENGTH
BRANCH
LEAFS or OTUs
OUTGROUP

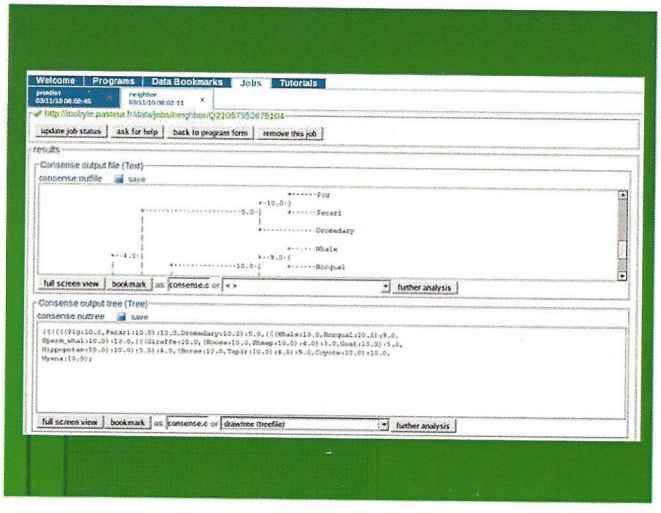
10.)


Initial Alignment
Column 1 2 3 4 5 6 7 8 9
seq1 A B C D E F G H I
seq2 A A B B C B A C A
seq3 C C A C B A C A B
Bootstrap Alignment 1
1 1 8 1 2 5 1 8 2
A A H A B E A H B
A A C A B C A C A
C C A C C B C A C
Bootstrap Alignment 2
1 4 5 6 6 3 4 1 7
A D E F F C D A G
A B B C C B B A A
C C B A A A C C C
The purpose of all this is to check whether all the columns in your initial alignment tell a similar evolutionary story

11.)


Phylip protdist
Reset
Compute distance matrix from protein sequences ?
Run
Help Pages
Alignment File (Protein Alignment) ?
Paste
File
clear data
select
Distance model (P) Jones-Taylor-Thornton matrix
Gamma distribution of rates among positions (G)
No
Yes
Gamma+Invariant
Coefficient of variation of substitution rate among positions (must be positive) ?
Fraction of invariant positions
Bootstrap options
Perform a bootstrap before analysis ?
Resampling methods (J) ? Bootstrap
Random number seed (must be odd) 3
How many replicates (R)? 100

12.)


Welcome
Programs
Data Bookmarks
Jobs
Tutorials
update job status
ask for help
back to program form
remove this job
results
Consense output file (Text)
consense outfile
save
full screen view
bookmark
as
further analysis
Consense output tree (Tree)
consense outtree
save
full screen view
bookmark
as
drawtree (treefile)
further analysis

PROGRAM DETAILS FOR THE NATIONAL WORKSHOP ON

'Use of Bioinformatics in Agriculture & Plant Sciences'

12-13th March 2010

DAY 01 (12th March 2010)

	INAUGURAL SESSION	
9:30 am	REGISTRATION	Reception, NIPGR
10:00 am	WELCOME ADDRESS	Dr. G. Yadav, Coordinator, Sub-Dic
10:05 am	KEYNOTE ADDRESS	Dr. T. Madhan Mohan, DBT
10:10 am	INAUGURAL ADDRESS	Prof. R Geeta, University of Delhi
11:00 am	VOTE OF THANKS	Coordinator, Sub-DIC
11:05 am	HIGH TEA	
	WORKSHOP SESSION - I	
11:30 am	BIOINFORMATICS IN AGRICULTURE	Dr. G. Yadav, NIPGR
12:15 pm	BIOLOGICAL DATA RETRIEVAL & ANALYSIS: DNA	Sachin Pundhir
14:00 pm	LUNCH	
	WORKSHOP SESSION - II	
14:30 pm	PROTEIN SEQUENCE ANALYSIS: WHEAT PROTEIN	Smriti Shridhar
15:45 pm	TEA	
16:00 pm	BIOINFORMATICS & THE PEDAGOGY OF PLANT SCIENCES	Dr. S.M. Leighton, University of Delhi

DAY 02 (13th March 2010)

	WORKSHOP SESSION - III	
9:30 am	METHODS FOR ANALYSIS OF EST DATA	Sachin Pundhir
11:00 am	TEA	
11:15 am	NEXT GEN SEQUENCING & APPLICATIONS	Dr. D. Chattopadhyay, NIPGR
13:00 pm	LUNCH	
	WORKSHOP SESSION - IV	
14:00 pm	3-D STRUCTURAL ANALYSIS OF PROTEINS	Daljit Singh
15:45 pm	TEA	
16:00 pm	PROTEIN FAMILY ANALYSIS & PHYLOGENETICS	Smriti Shridhar
	VALEDICTORY FUNCTION	
17:30 pm	CERTIFICATE DISTRIBUTION	Prof. A.K Tyagi, DIRECTOR, NIPGR
17:45 pm	CLOSING CEREMONY	

PARTICIPANTS OF THE NATIONAL WORKSHOP ON

'Use of Bioinformatics in Agriculture & Plant Sciences'

12-13th March 2010

	Name of Participant	Affiliation
1	Ravi Kant	Haryana Agricultural University
2	Poonam Sharma	CCS Haryana Agricultural University
3	Harmeet Kaur	NIPGR
4	Dr. Neelam R. Yadav	CCS Haryana Agricultural University
5	Rehna Augustine	NIPGR
6	Pooja Verma	NIPGR
7	Rahul Gautam	National Institute of Technology
8	Renu Kumari	NIPGR
9	Swati Chaudhary	NIPGR
10	Ashutosh Pandey	Shobhit University
11	Anurag Srivastava	Shobhit University
12	Abhay Pratap	Shobhit University
13	Pritika Singh	GNDU
14	Dr Parveen Chhuneja	Punjab Agricultural University
15	Khagendra Kumar	National Institute of Technology
16	Praveena K.	NIPGR
17	Meenu	NIPGR
18	Dr. Sridhar Gutam	Indian Agricultural Research Institute
19	Bhanu Prakash Petla	NIPGR
20	Tanima Datta	GNDU
21	Harsimran Kaur	GNDU

THE NATIONAL WORKSHOP ON

'Use of Bioinformatics in Agriculture & Plant Sciences'

12-13th March 2010

Organisers

Dr. Gitanjali Yadav	Coordinator, NIPGR
Sachin Pundhir	NIPGR
Smriti Shridhar	NIPGR
Subhasish Mondal	NIPGR

Speakers

Prof. R. Geeta	University of Delhi
Dr. Sudeshna M. Leighton	University of Delhi
Dr. Gitanjali Yadav	Coordinator, NIPGR
Dr. Debasis Chattopadhyay	NIPGR