fusion antibodies

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BeSC
Belfast e-Science Centre

GeneGrid: Grid Service Based Virtual Bioinformatics Laboratory

P.V. Jithesh

Bioinformatics – Data Driven

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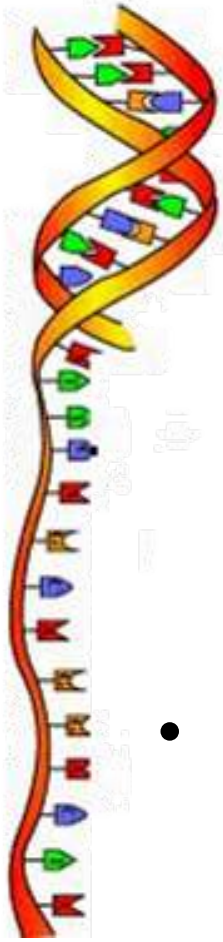
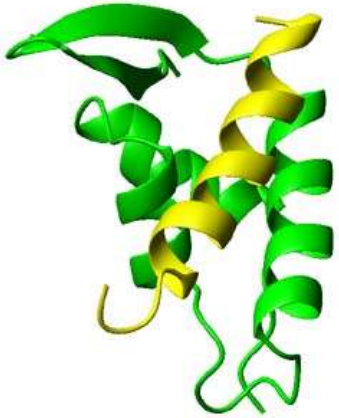
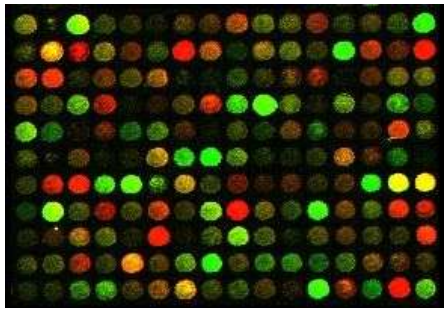


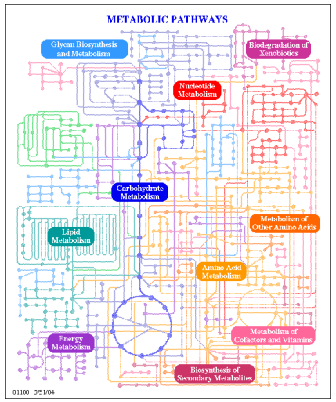
- Genome Sequencing Projects
  - 266 published complete genomes
  - 730 prokaryotic ongoing
  - 496 eukaryotic ongoing
    - http://www.genomesonline.org/
    - 21-06-2005
- Macromolecular Structure Elucidation



- Gene Expression Analysis



- Metabolic pathways



Databases, Tools, Servers

BeSC
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- 719 databases (171 more than 2004 issue)
  - Nucleic Acids Research, 2005, Vol. 33 (Database issue)
- Algorithms and tools for analysis - plenty
- Most tools available through web servers
- 137 web servers
  - Nucleic Acids Research 2004, Vol. 32 (Web Server issue)

GeneGrid: Background

BeSC
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- Workflow Based Grid Computing project
- Initiated by Belfast e-Science Centre
- Commercial partners

- Antibody target discovery
- Genetic disease markers for New diagnostics
- Cancer and Immunology

fusion antibodies

- Potential Products from Molecular Mining
- Epilepsy

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GeneGrid: Objectives

BeSC
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- Grid Based Framework for Bioinformatics Analysis
- Integration of Existing Technologies & Data Sets
- Production of a ‘Virtual Bioinformatics Laboratory’
- Platform for scientists to access collective skills and experiences in a secure, reliable and scalable manner
- *in silico* knowledge discovery

GeneGrid: Components

BeSC
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- Application Integration & Management
- Data Access, Integration & Storage
- Resource Monitoring & Service Discovery
- Workflow Management
- Portal

Application Management

BeSC
Belfast e-Science Centre

- Integrates with GeneGrid
  - Bioinformatics Applications
    - BLAST
    - TMHMM
    - SignalP
    - Primer3
    - HMMER
    - EMBOSS
    - …
  - Utility Programs
- Highly extensible
- Two types of GT3 based Grid Services
  - Factory
    - Persistent, Generic
    - Discoverable by other services through Registry service
  - Instance
    - Transient, Specific to task requested
    - Execution of tasks and updation of results

Data Access, Integration and Storage

BeSC
Belfast e-Science Centre

- Integrates with GeneGrid
  - Public biological databases
    - EMBL
    - SwissProt
    - …
  - Private databases
- Manages GeneGrid specific databases
  - GeneGrid Workflow Definition Database (GWDD)
  - GeneGrid Status Tracking, Result & Input Parameter Database (GSTRIP)
- Based on OGSA-DAI
  - Replicates Data Manager Service Factory and Data Manager Service
  - Extended to support flat files

Resource Monitoring & Service Discovery

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- GeneGrid Application & Resources Registry (GARR)
  - Central registry service - GT3 based
  - Receives data about resources & services, Stores in database
  - Provides interface to query the data
- Node Monitors
  - Present on all resources
  - Transmits resource status & service availability to GARR

Workflow Management

- GeneGrid Workflow Manager - roles
  - Processing of workflows
  - Resource identification
  - Task dispatch
  - Task status update
- GT3 based services
  - Factory
    - Persistent
    - Discoverable
  - Instance
    - Transient
    - Specific to one workflow

Portal

- User interface
- Creation and validation of workflows
- Query and display of results
- Conceals the complexity of Grid from the user
- Relies on data from 2 databases
  - GeneGrid Workflow Definition Database (GWDD)
    - Master Workflow Definition - XML
  - GeneGrid Status Tracking, Results & Input Parameters Database (GSTRIP)
    - Input files and parameters
    - Results and metadata
- Based on GridSphere
  - JSR 168 Compliant Portlets
    - Creation & Submission of workflows
    - Querying workflow status
    - Display of results
    - Administration

Architecture

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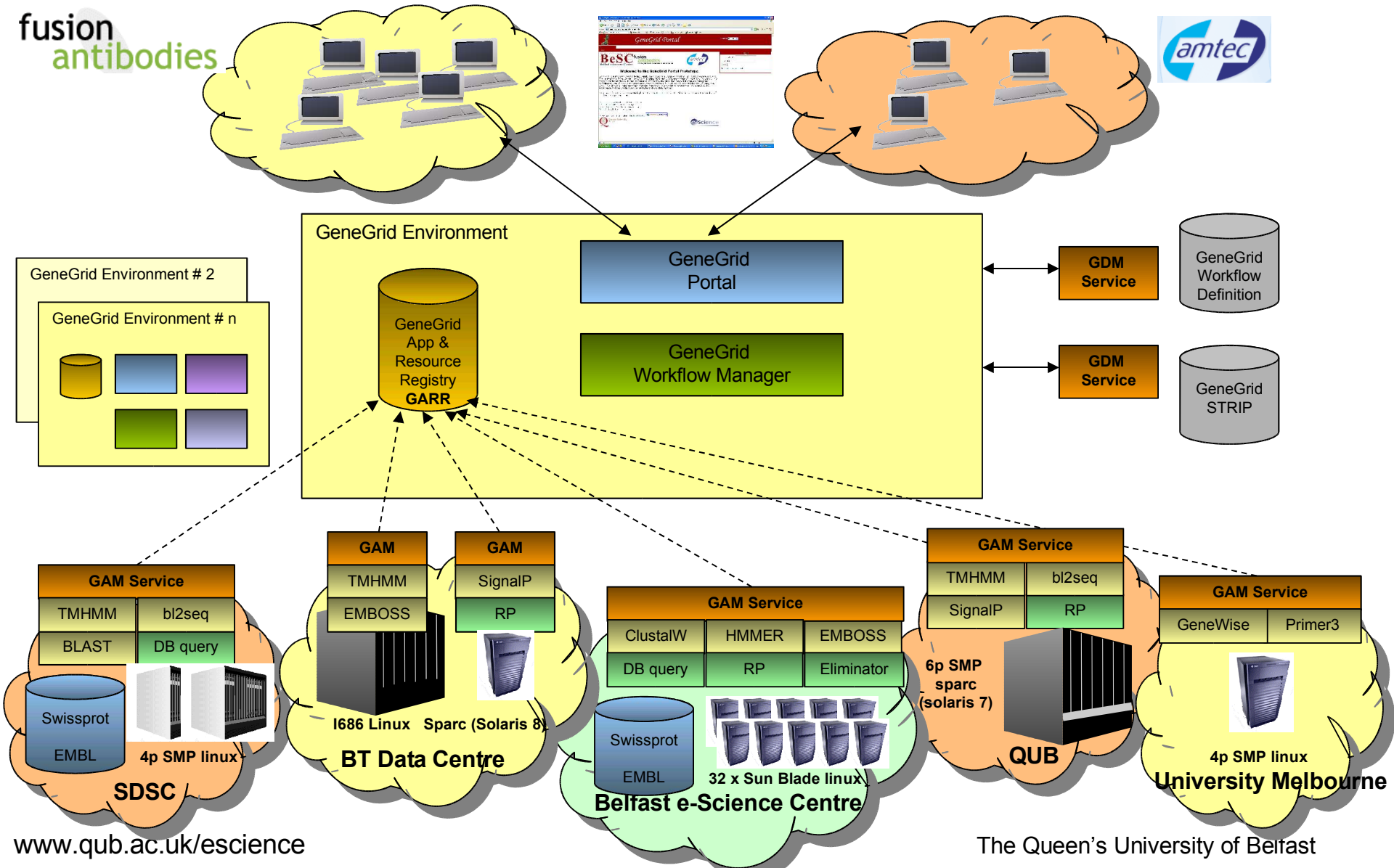

Use Cases

- A - Identification of Novel Protein Family Members
- B – Automated Antigenic Region Detection

A - Identification of Novel Protein Family Members

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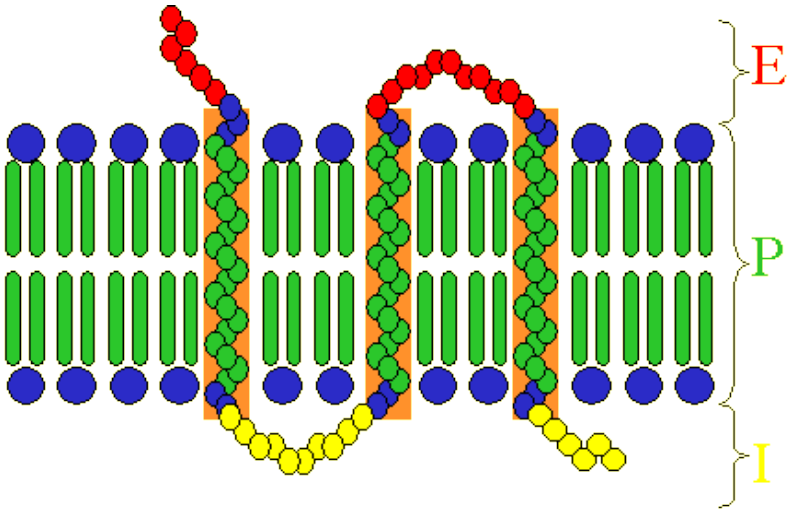
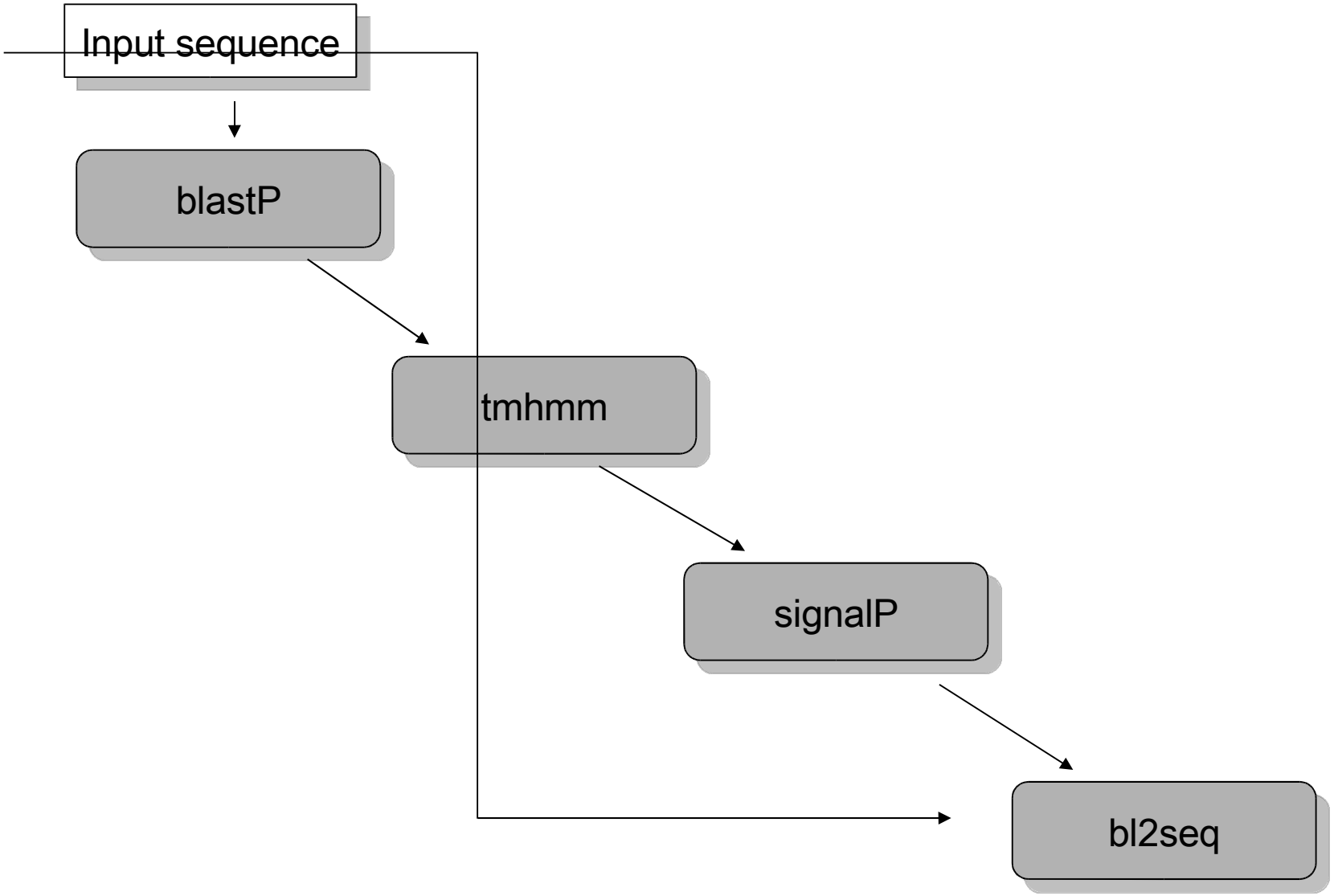
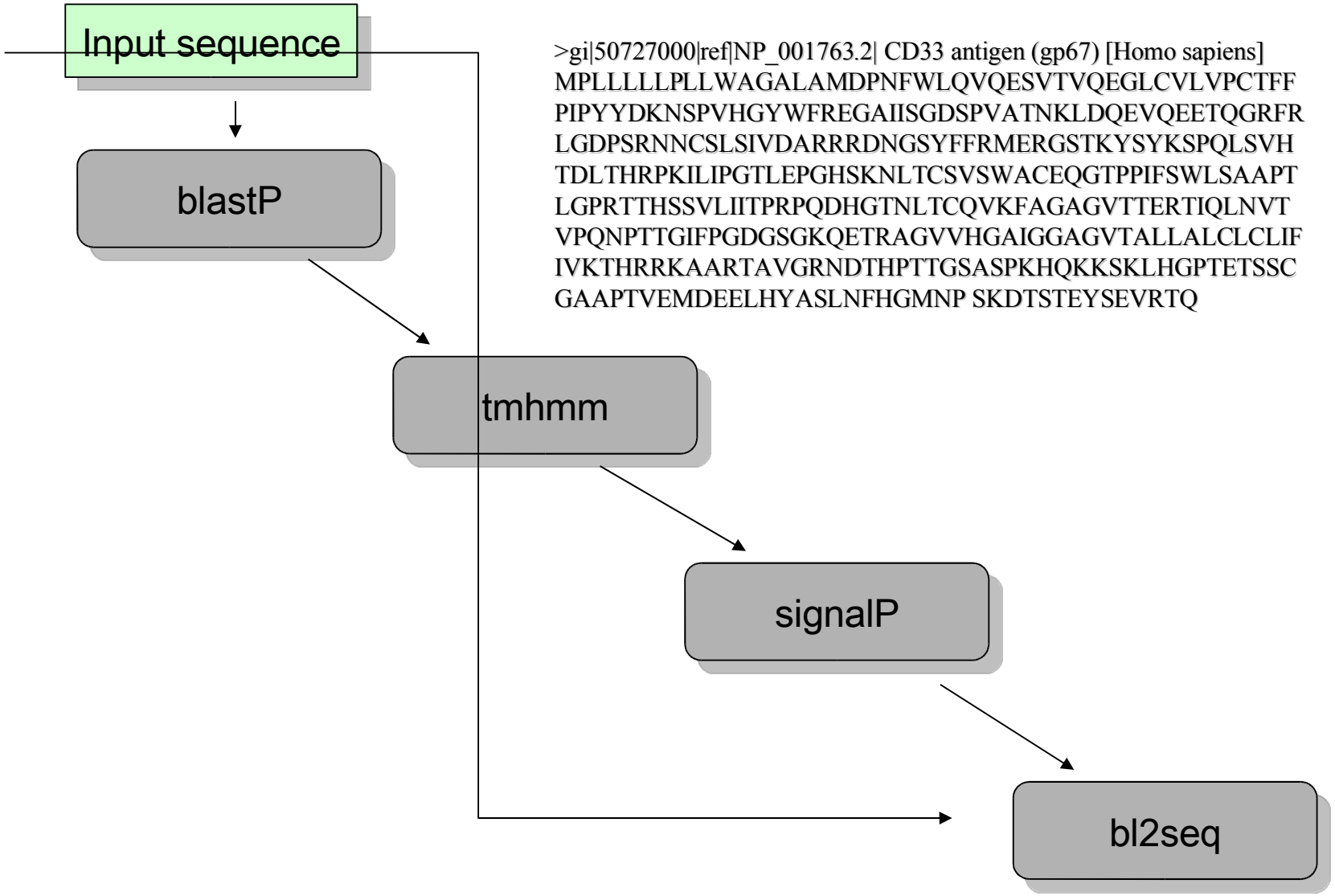
- Identify novel proteins of a family
- Cell surface proteins usually targets for the action of drugs
- Sialic acid binding Immunoglobulin-like lectins (Siglec) family



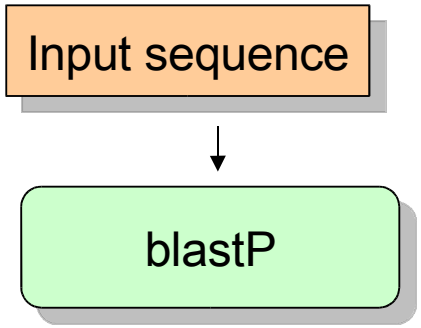
A- Workflow



A- Workflow

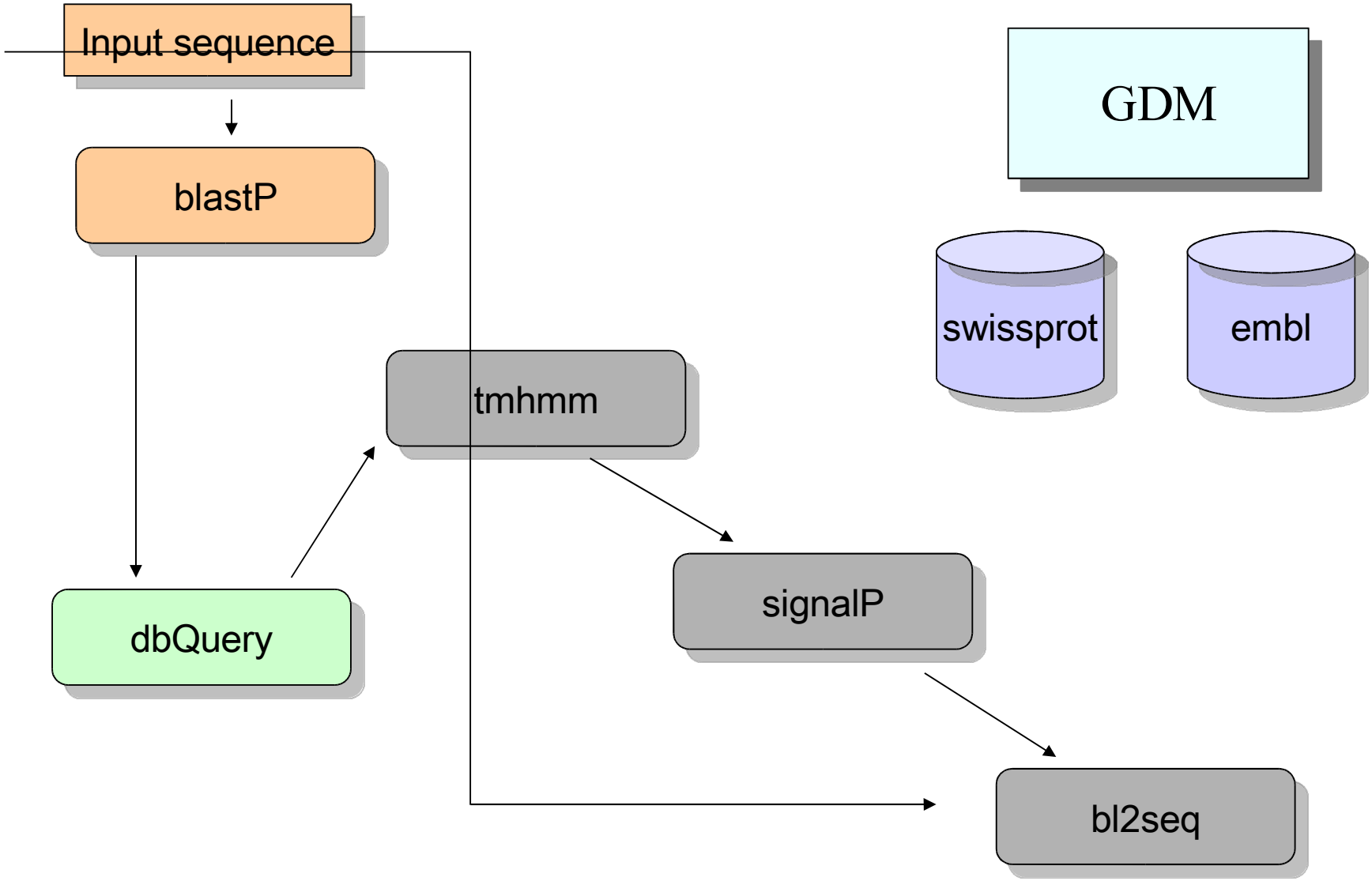

Input sequence
blastP
tmhmm
signalP
bl2seq
>gi|50727000|ref|NP_001763.2| CD33 antigen (gp67) [Homo sapiens]
MPLLLLLPLLWAGALAMDPNFWLQVQESVTVQEGLCVLVPCTFF
PIPYYDKNSPVHGYWFREGAIISGDSPVATNKLDQEVQEETQGRFR
LGDPSRNNCSLSIVDARRRDNGSYFFRMERGSTKYSYKSPQLSVH
TDLTHRPKILIPGTLEPGHSKNLTCSVSWACEQGTPPIFSWLSAAPT
LGPRTTHSSVLIITPRPQDHGTNLTCQVKFAGAGVTTERTIQLNVT
VPQNPTTGIFPGDGSGKQETRAGVVHGAIGGAGVTALLALCLCLIF
IVKTHRRKAARTAVGRNDTHPTTGSASPKHQKKSKLHGPTETSSC
GAAPTVEMDEELHYASLNFHGMNP SKDTSTEYSEVRTQ

A- Workflow

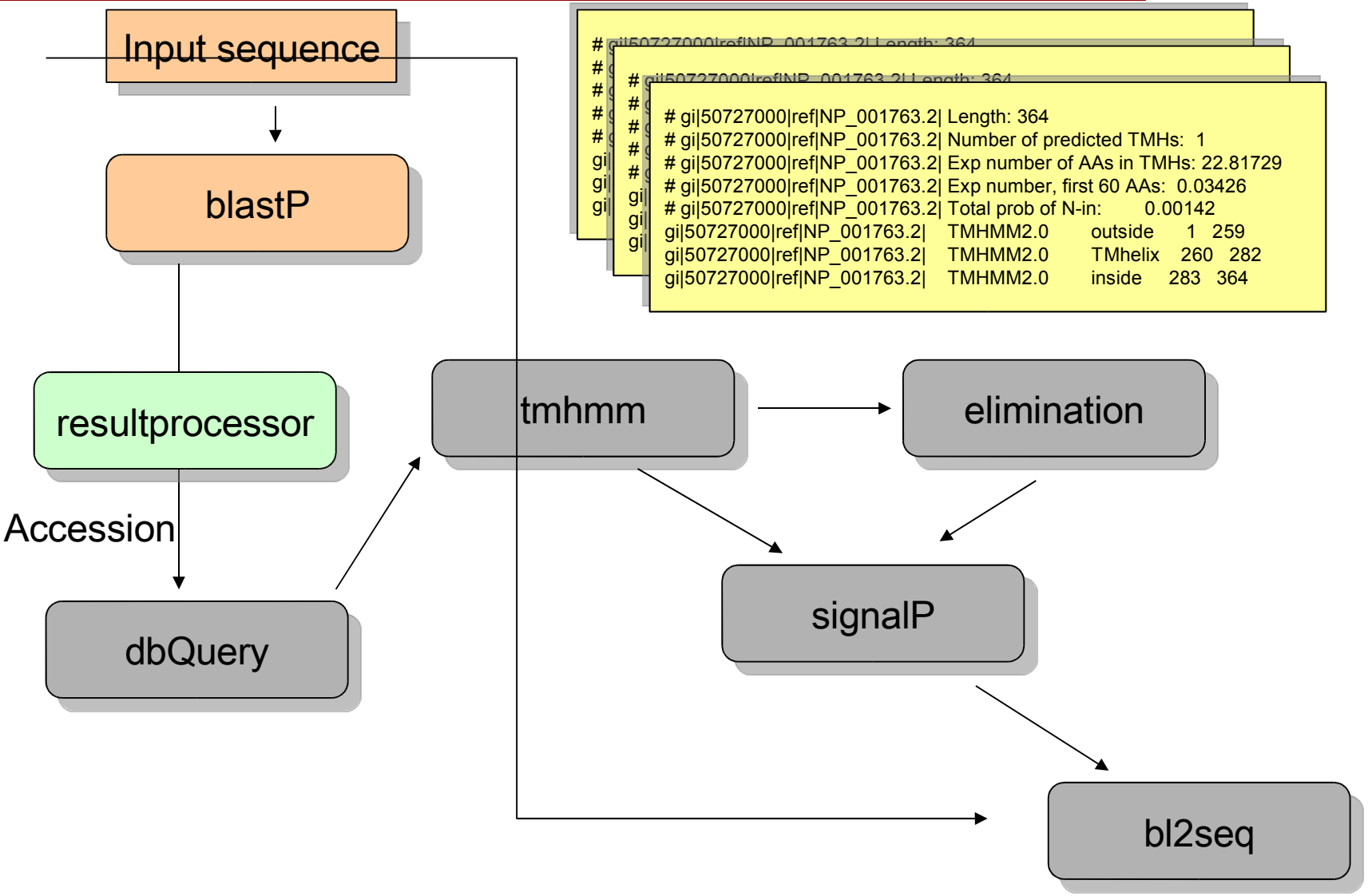



```
BLASTP 2.2.9 [May-01-2004]

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= gi|50727000|ref|NP_001763.2| CD33 antigen (gp67) [Homo sapiens]
       (364 letters)

Database: swissprot
           154,145 sequences; 56,721,989 total letters

Searching.....................................................done

                                                          Score    E
Sequences producing significant alignments:                (bits) Value

sp|P20138|CD33_HUMAN Myeloid cell surface antigen CD33 precursor...   675   0.0
sp|O43699|SIL6_HUMAN Sialic acid binding Ig-like lectin 6 precur...   313   4e-85
sp|Q9NYZ4|SIL8_HUMAN Sialic acid binding Ig-like lectin 8 precur...   295   1e-79
sp|Q95LH0|SILL_PANTR Sialic acid binding Ig-like lectin-like 1 p...   287   3e-77
sp|Q9Y336|SIL9_HUMAN Sialic acid-binding Ig-like lectin 9 precur...   286   4e-77
sp|Q9Y286|SIL7_HUMAN Sialic acid binding Ig-like lectin 7 precur...   286   5e-77
sp|Q96PQ1|SILL_HUMAN Sialic acid binding Ig-like lectin-like 1 p...   285   1e-76
sp|Q63994|CD33_MOUSE Myeloid cell surface antigen CD33 precursor...   266   8e-71
sp|Q920G3|SILF_MOUSE Sialic acid binding Ig-like lectin-F precur...   253   4e-67
sp|O15389|SIL5_HUMAN Sialic acid binding Ig-like lectin 5 precur...   248   2e-65
……
…….
>sp|P20138|CD33_HUMAN Myeloid cell surface antigen CD33 precursor (gp67) (Siglec-3)
          Length = 364

 Score =  675 bits (1742), Expect = 0.0
 Identities = 328/354 (92%), Positives = 328/354 (92%)

Query: 11  WAGALAMDPNFWLQVQESVTVQEGLCVLVPCTFFHPIPYYDKNSPVHGYWFREGAIISGD 70
           WAGALAMDPNFWLQVQESVTVQEGLCVLVPCTFFHPIPYYDKNSPVHGYWFREGAIISGD
Sbjct: 11  WAGALAMDPNFWLQVQESVTVQEGLCVLVPCTFFHPIPYYDKNSPVHGYWFREGAIISGD 70

Query: 71  SPVATNKLDQEVQEETQGRFRLLGDPSRNNCSLSIVDARRRDNGSYFFRMERGSTKYSYK 130
           SPVATNKLDQEVQEETQGRFRLLGDPSRNNCSLSIVDARRRDNGSYFFRMERGSTKYSYK
Sbjct: 71  SPVATNKLDQEVQEETQGRFRLLGDPSRNNCSLSIVDARRRDNGSYFFRMERGSTKYSYK 130
```

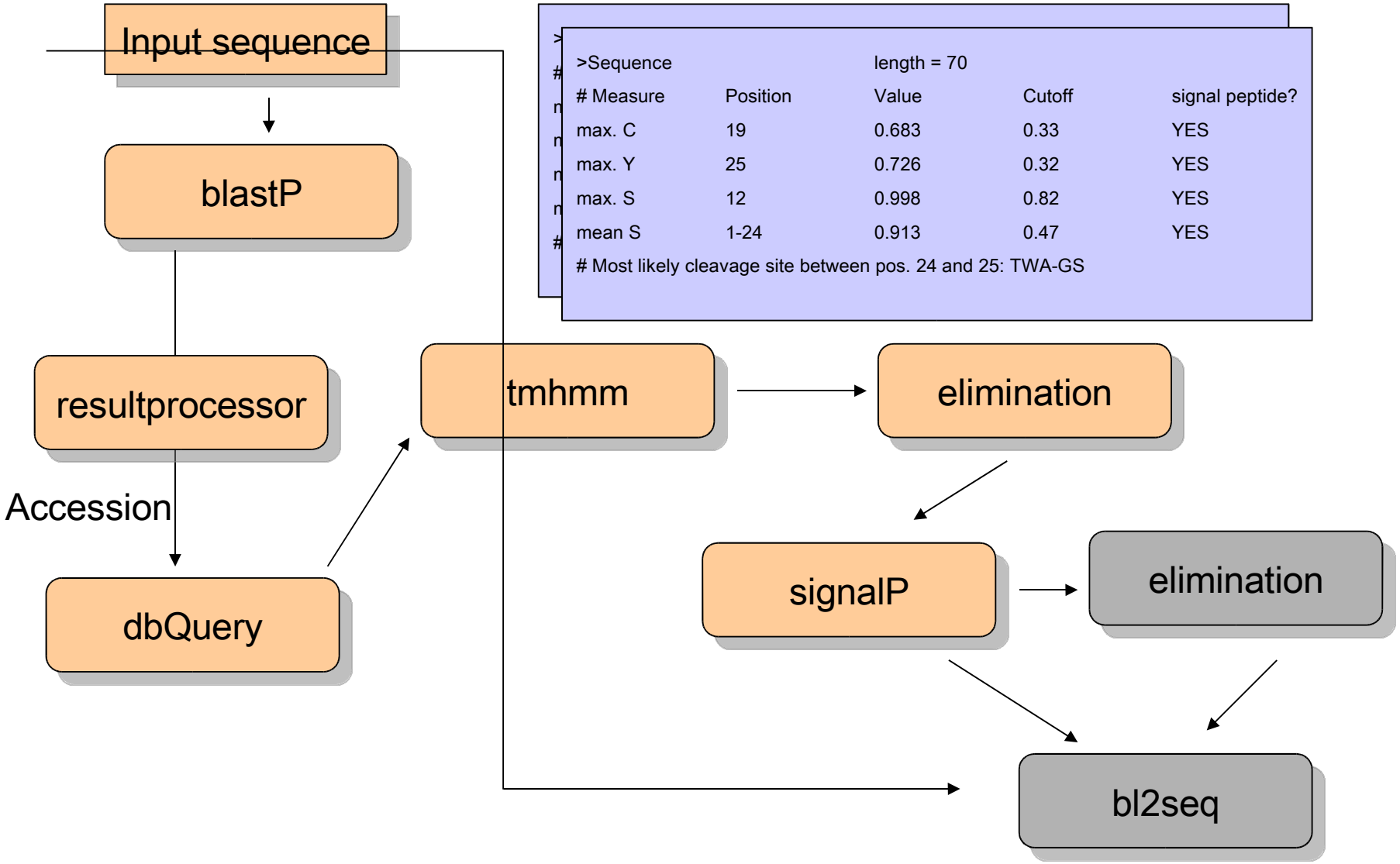
A- Workflow


Input sequence
blastP
GDM
swissprot
embl
tmhmm
dbQuery
signalP
bl2seq

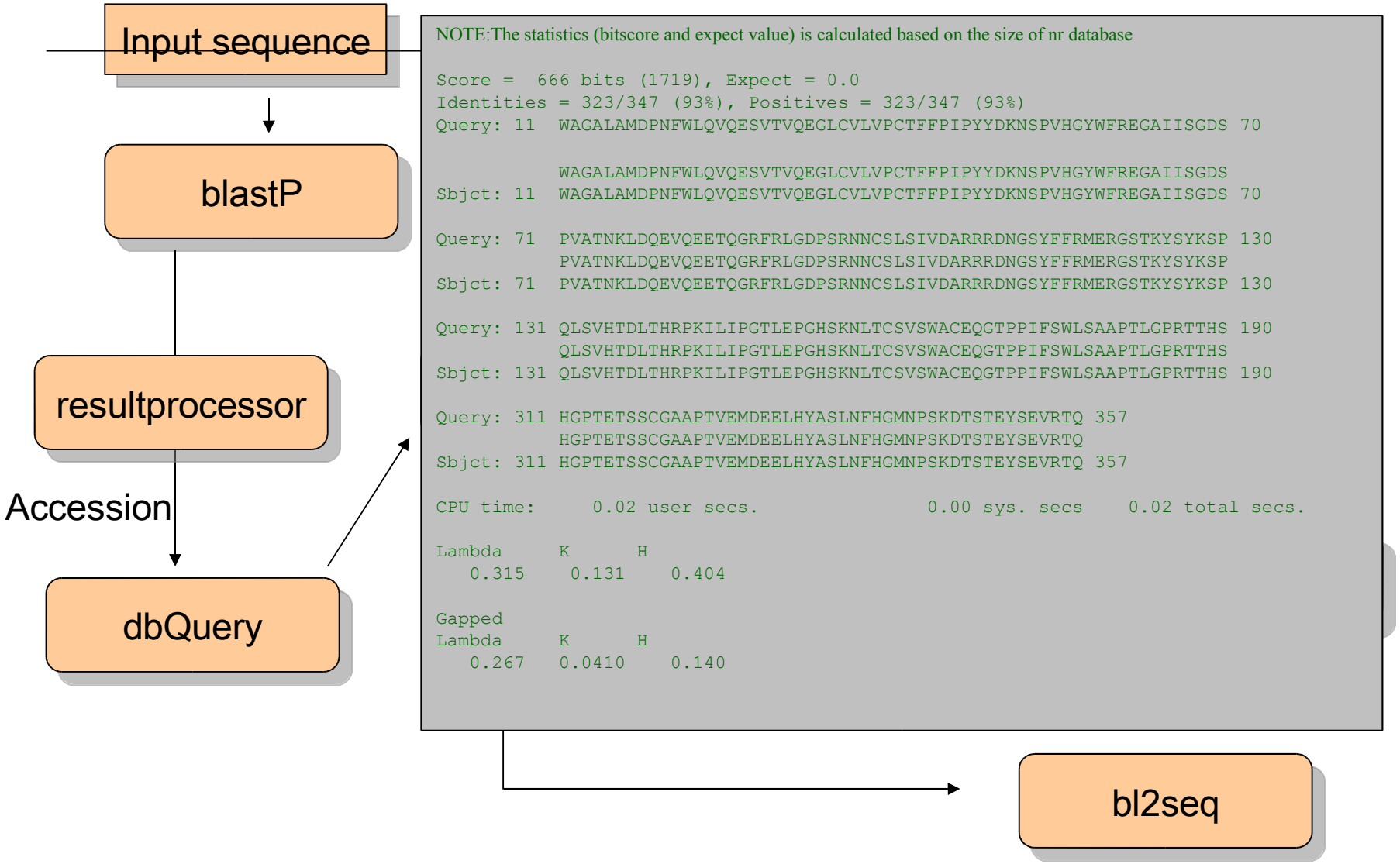
A- Workflow


Input sequence
blastP
resultprocessor
Accession
dbQuery
tmhmm
elimination
signalP
bl2seq
gi|50727000|ref|NP_001763.2| Length: 364
gi|50727000|ref|NP_001763.2| Number of predicted TMHs: 1
gi|50727000|ref|NP_001763.2| Exp number of AAs in TMHs: 22.81729
gi|50727000|ref|NP_001763.2| Exp number, first 60 AAs: 0.03426
gi|50727000|ref|NP_001763.2| Total prob of N-in: 0.00142
gi|50727000|ref|NP_001763.2| TMHMM2.0 outside 1 259
gi|50727000|ref|NP_001763.2| TMHMM2.0 TMhelix 260 282
gi|50727000|ref|NP_001763.2| TMHMM2.0 inside 283 364

A- Workflow


Input sequence
blastP
resultprocessor
Accession
dbQuery
tmhmm
elimination
signalP
elimination
bl2seq
>Sequence length = 70
Measure Position Value Cutoff signal peptide?
max. C 19 0.683 0.33 YES
max. Y 25 0.726 0.32 YES
max. S 12 0.998 0.82 YES
mean S 1-24 0.913 0.47 YES
Most likely cleavage site between pos. 24 and 25: TWA-GS

A- Workflow


Input sequence
blastP
resultprocessor
Accession
dbQuery
NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database
Score = 666 bits (1719), Expect = 0.0
Identities = 323/347 (93%), Positives = 323/347 (93%)
Query: 11 WAGALAMDPNFWLQVQESVTVQEGLCVLVPCTFFPIPYYDKNSPVHGYWFREGAIISGDS 70
WAGALAMDPNFWLQVQESVTVQEGLCVLVPCTFFPIPYYDKNSPVHGYWFREGAIISGDS
Sbjct: 11 WAGALAMDPNFWLQVQESVTVQEGLCVLVPCTFFPIPYYDKNSPVHGYWFREGAIISGDS 70
Query: 71 PVATNKLDQEVQEETQGRFRLGDPSRNNCSLSIVDARRRDNGSYFFRMERGSTKYSYKSP 130
PVATNKLDQEVQEETQGRFRLGDPSRNNCSLSIVDARRRDNGSYFFRMERGSTKYSYKSP
Sbjct: 71 PVATNKLDQEVQEETQGRFRLGDPSRNNCSLSIVDARRRDNGSYFFRMERGSTKYSYKSP 130
Query: 131 QLSVHTDLTHRPKILIPGTLEPGHSKNLTCSVSWACEQGTPPIFSWLSAAPTLGPRTTHS 190
QLSVHTDLTHRPKILIPGTLEPGHSKNLTCSVSWACEQGTPPIFSWLSAAPTLGPRTTHS
Sbjct: 131 QLSVHTDLTHRPKILIPGTLEPGHSKNLTCSVSWACEQGTPPIFSWLSAAPTLGPRTTHS 190
Query: 311 HGPTETSSCGAAPTVEMDEELHYASLNFHGMNPSKDTSTEYSEVRTQ 357
HGPTETSSCGAAPTVEMDEELHYASLNFHGMNPSKDTSTEYSEVRTQ
Sbjct: 311 HGPTETSSCGAAPTVEMDEELHYASLNFHGMNPSKDTSTEYSEVRTQ 357
CPU time: 0.02 user secs. 0.00 sys. secs 0.02 total secs.
Lambda K H
0.315 0.131 0.404
Gapped
Lambda K H
0.267 0.0410 0.140
bl2seq

Use Case A - Results

BeSC
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- 6 Uncharacterised and potentially new siglecs
- Current experiment execution time: 1 day
- GeneGrid – 20 mins
- Different applications were accessed from different resources
  - BLAST – Linux Cluster at BeSC
  - TMHMM – Linux Cluster at SDSC
  - SignalP – Sun SMP machine at QUB

Use Case A - Results

BeSC
Belfast e-Science Centre

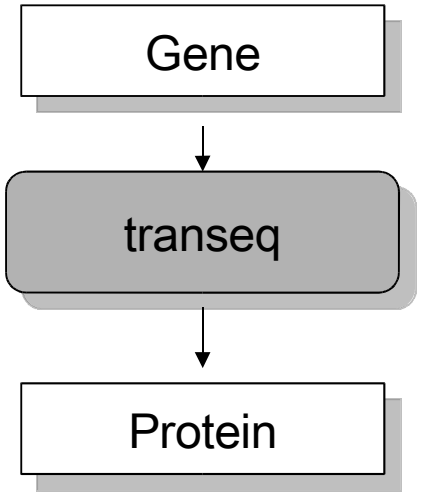
- Extended workflow involves beginning with a number of characterised sequences from a family
- Multiple sequence alignment and Profile generation (clustalW, hmmer etc.)
- Profile search against databases for sensitivity
- Finding whether the selected genes are actually transcribed (est database etc.)
- Phylogenetic analysis by dendrogram generation (Pileup etc.)
- Looking for characteristic domains of the family (rpsblast x CDD)

B - Automated Antigenic Region Detection

BeSC
Belfast e-Science Centre

- Identification of Antigenic regions in proteins starting from the genes
- Routine Bioinformatics procedure in partner company for clients & in-house
- More than 100 genes at a time to be examined using a number of tools
  - 30-60 mins per gene
- GeneGrid allows automated detection of antigenic regions from genes

B - Workflow




```
   1  atggccgtca tggcgccccg aaccctcctc ctgctactct cgggggccct ggccctgacc
  61 cagacctggg cgggctccca ctccatgagg tatttcttca catccgtgtc ccggcccggc
 121 cgcggggagc cccgcttcat cgccgtgggc tacgtggacg acacgcagtt cgtgcggttc
 181 gacagcgacg ccgcgagcca gaggatggag ccgcgggcgc cgtggataga gcaggagggg
 241 ccggagtatt gggaccagga gacacggaat gtgaaggccc agtcacagac tgaccgagtg
 301 gacctgggga ccctgcgcgg ctactacaac cagagcgagg ccggttctca caccatccag
 361 ataatgtatg gctgcgacgt ggggtcggac gggcgcttcc tccgcgggta ccggcaggac
 421 gcctacgacg gcaaggatta catcgccctg aacgaggacc tgcgctcttg gaccgcggcg
 481 gacatggcgg ctcagatcac caagcgcaag tgggaggcgg cccatgaggc ggagcagttg
 541 agagcctacc tggatggcac gtgcgtggag tggctccgca gatacctgga gaacgggaag
 601 gagacgctgc agcgcacgga ccccccaag acacatatga cccaccaccc catctctgac
 661 catgaggcca ccctgaggtg ctgggccctg ggcttctacc ctgcggagat cacactgacc
 721 tggcagcggg atggggagga ccagacccag gacacggagc tcgtggagac caggcctgca
 781 ggggatggaa ccttccagaa gtgggcggct gtggtggtgc cttctggaga ggagcagaga
 841 tacacctgcc atgtgcagca tgagggtctg cccaagcccc tcaccctgag atgggagctg
 901 tcttcccagc ccaccatccc catcgtgggc atcattgctg gcctggttct ccttggagct
 961 gtgatcactg gagctgtggt cgctgccgtg atgtggagga ggaagagctc agatagaaaa
1021 ggagggagtt acactcaggc tgcaagcagt gacagtgccc agggctctga tgtgtccctc
1081 acagcttgta aagtgtga
```

```
MAVMAPRTLLLLLSGALALTQTWAGSHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRF
DSDAASQRMEPRAPWIEQEGPEYWDQETRNVKAQSQTDRVDLGTLRGYYNQSEAGSHTIQ
IMYGCDVGSDGRFLRGYRQDAYDGKDYIALNEDLRSWTAADMAAQITKRKWEAAHEAEQL
RAYLDGTCVEWLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLT
WQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEL
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TACKV
```
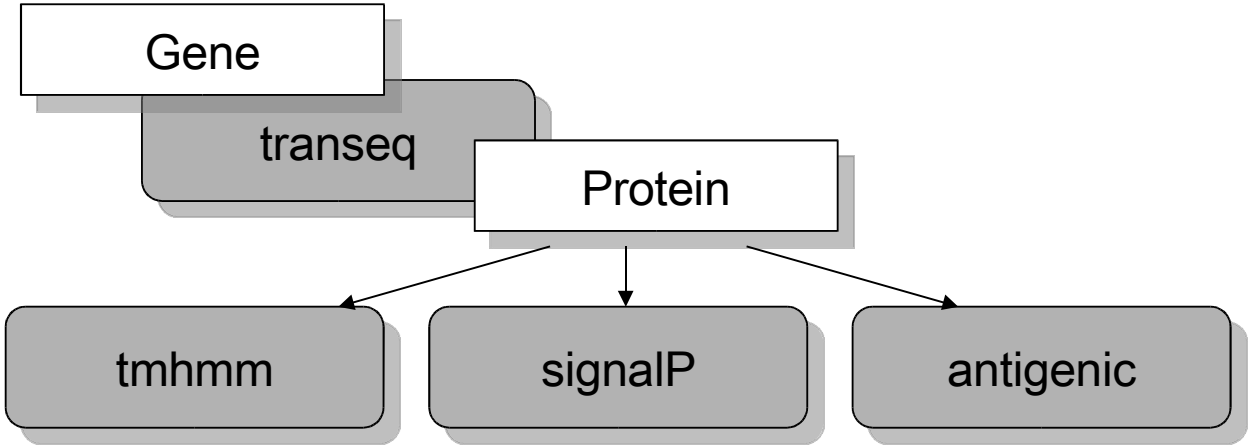
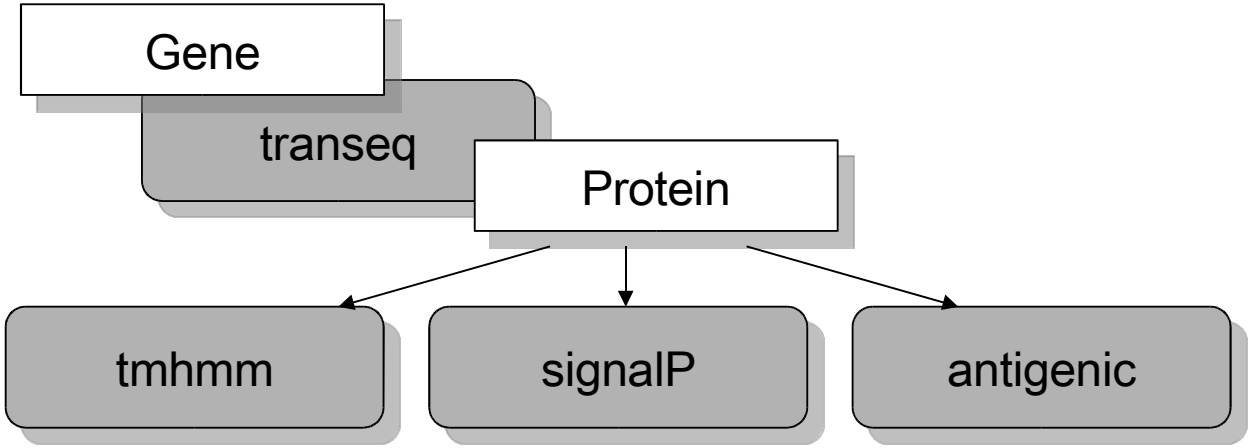

B - Workflow




```
# Sequence Length: 365
# Sequence Number of predicted TMHs: 1
# Sequence Exp number of AAs in TMHs: 30.43917
# Sequence Exp number, first 60 AAs: 7.38298
# Sequence Total prob of N-in: 0.37875
Sequence    TMHMM2.0    outside     1    307
Sequence    TMHMM2.0    TMhelix     308  330
Sequence    TMHMM2.0    inside      331  365
```

B - Workflow

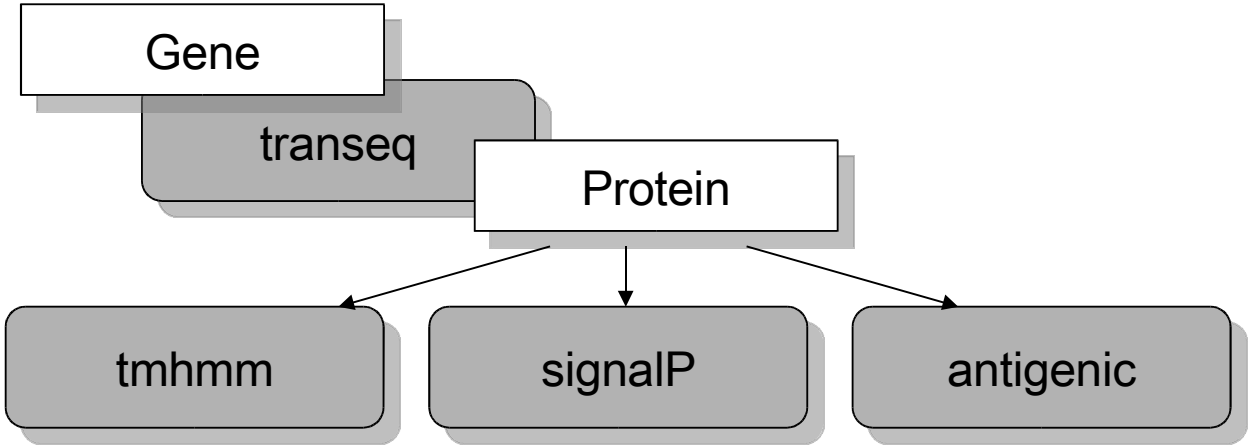


>Sequence length = 70

# Measure	Position	Value	Cutoff	signal peptide?
max. C	19	0.683	0.33	YES
max. Y	25	0.726	0.32	YES
max. S	12	0.998	0.82	YES
mean S	1-24	0.913	0.47	YES

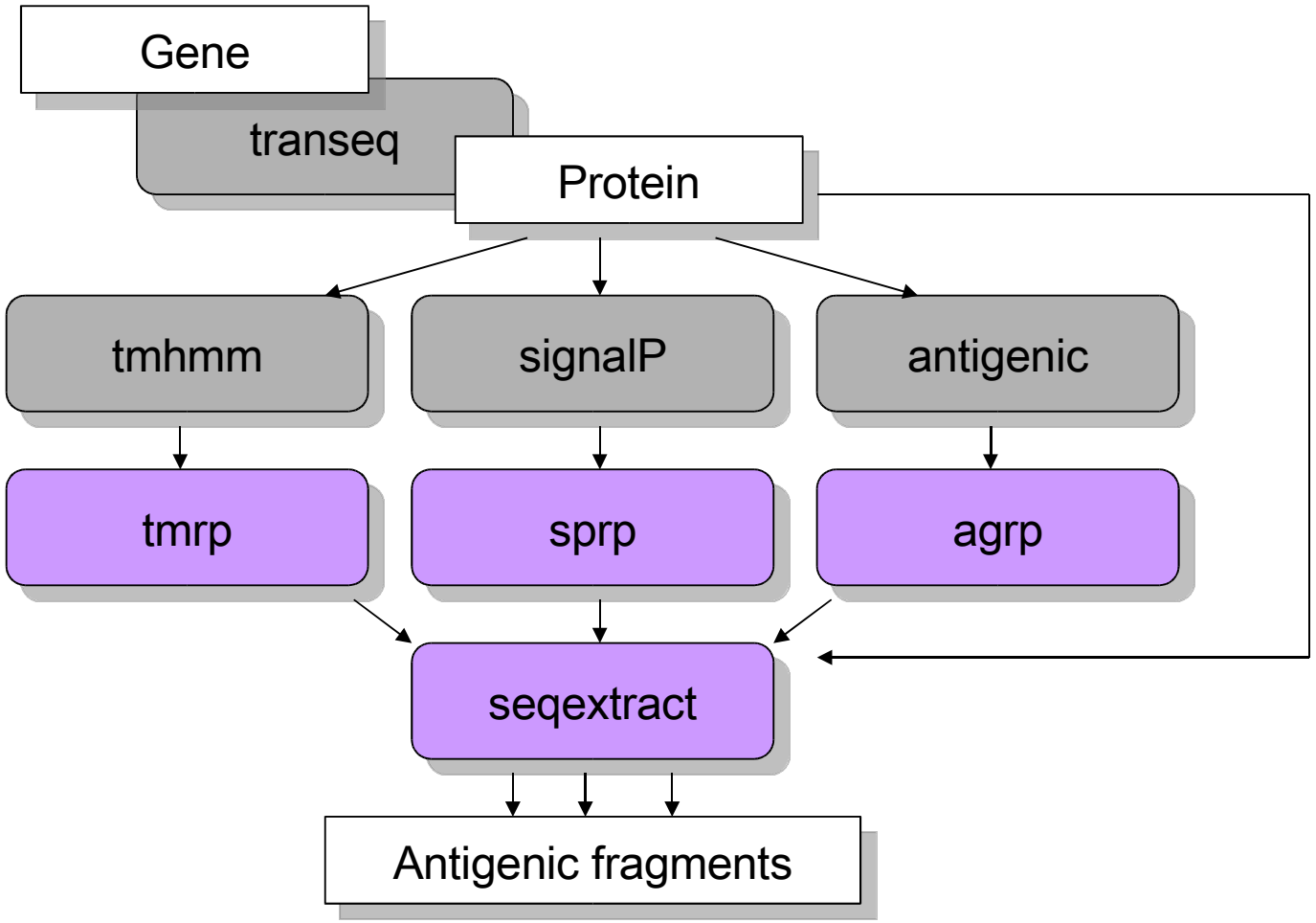
Most likely cleavage site between pos. 24 and 25: TWA-GS

B - Workflow



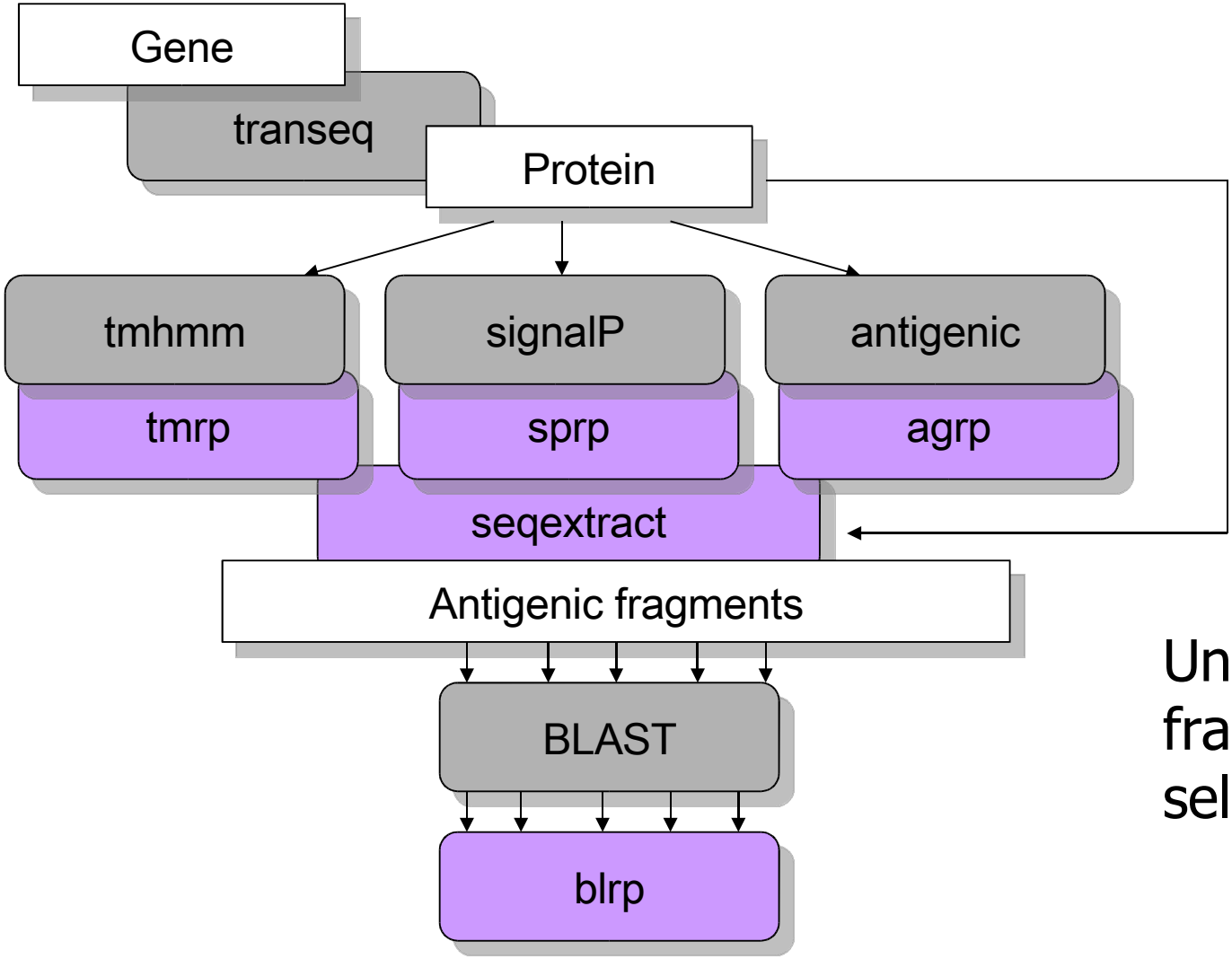

```
#=======================================
# Sequence:      from: 1    to: 365
# HitCount: 2
#=======================================
Max_score_pos at "*"
(1) Score 1.208 length 30 at residues 301->330
                            *
 Sequence: SSQPTIPIVGIIAGLVLLGAVITGAVVAAV
           |                            |
         301                          330
(2) Score 1.156 length 20 at residues 280->299
                 *
 Sequence: RYTCHVQHEGLPKPLTLRWE
           |                  |
         280                299
```

B - Workflow



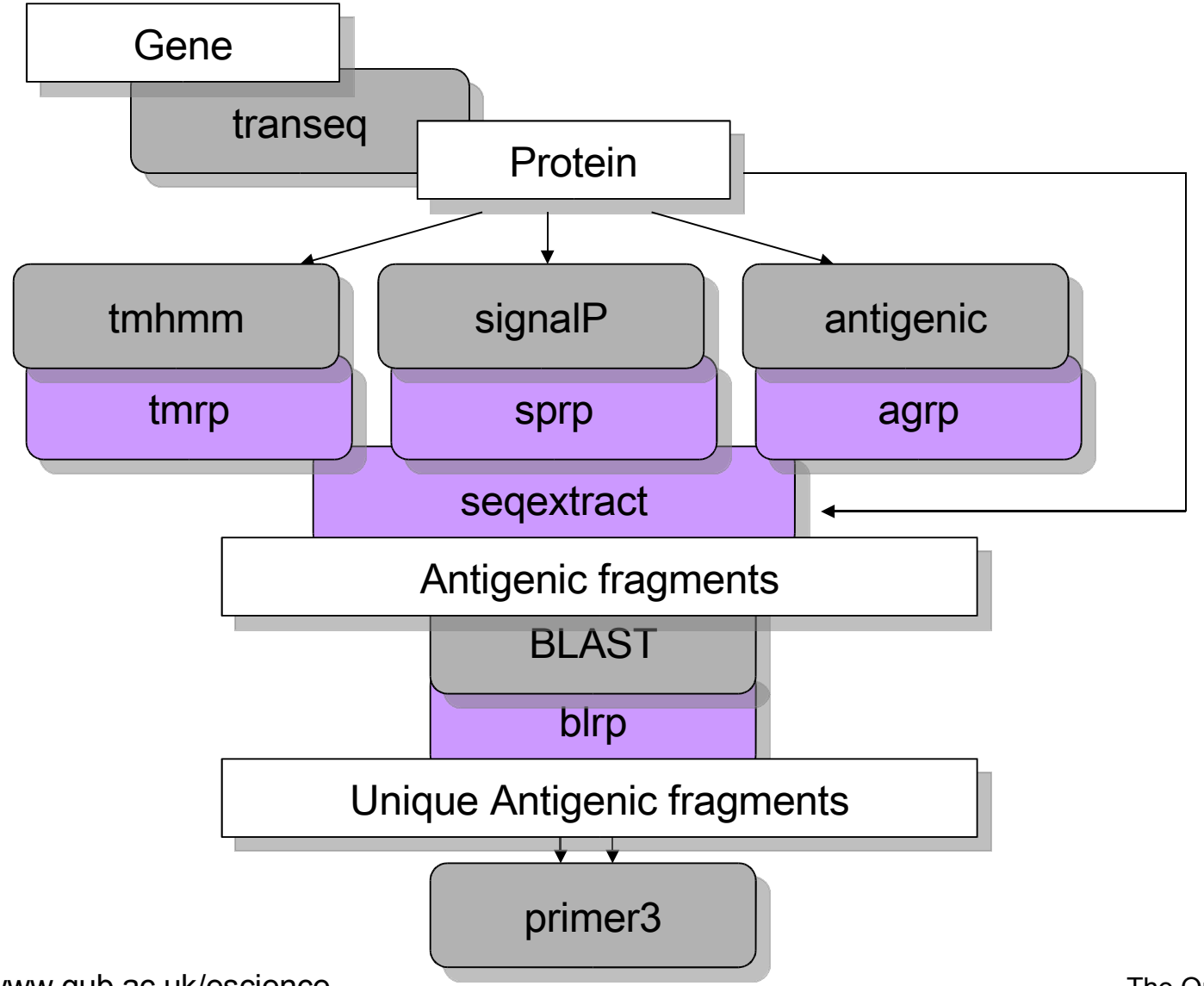
Antigenic fragment selection

B - Workflow



Unique fragment selection

B - Workflow



Select Primer sequences for PCR

Use Case B - Results

- Pre GeneGrid – 30-60 min per gene
- GeneGrid – 90 mins for 100 genes
- Resources used
  - BeSC, BT Datacentre, Uni Melbourne, SDSC
- Automation of time consuming routine bioinformatics tasks
- Individual task execution and overall experiment execution times reduced
- High throughput analysis of genes for potential antigenic regions

BeSC Belfast e-Science Centre

GeneGrid

Queen's University Belfast

English

GridSphere

Home

fusion antibodies
from genes to proteins to antibodies

amtec

Login

User Name

Password

Remember my login

Login

Welcome to the GeneGrid Portal Prototype - Release 0.5

This is the **GeneGrid Test Bed** release 0.5 managed by the Belfast e-Science Centre, utilising resources in BeSC, Queen's University of Belfast, Melbourne University, BT and the San Diego Super Computing Centre.

What's new in Release 0.5...

- More robust and reliable Workflow Definition Database.
- Additional functionality added to existing portlets.
- Utility options added
- Experiment templates introduced.
- New Portlets for using experiment templates.
- New Admin Portlets added.
- GARR extended to support resource information from Sun Solaris 8 & 9 OS.
- All services based on GT3.2.1.
- Support for new Applications.
- Enhancements made to GSTRIP database

Users are limited to selected staff of both commercial partners - Fusion Antibodies, Amtec Medical - and the Belfast e-Science Centre. To obtain a user account, please contact the appropriate representative - Noel Kelly (BeSC), Mark McCurley (Fusion) or Dr. Shane McKee (Amtec). Authorized users will be provided with a username and password by BeSC.

All users are requested to subscribe to the **GeneGrid mailing list** and to use it for directing queries etc. Mail GeneGrid, and place the word "subscribe" (without the quotes) in the message body.

For more on the GeneGrid project, please click here.

e-Science

GeneGrid New Experiment

To create a new experiment, select a task from the list below

Tasks	Category	Description
BLAST	Sequence Analysis	Basic Local Alignment Search Tool
Bl2seq	Sequence Analysis	Align two sequences with blast
TMHMM	Protein Characterisation	Predict Transmembrane regions in proteins
SignalP	Protein Characterisation	Predict Signal Regions in Proteins
ClustalW	Sequence Analysis	Multiple Sequence Alignment
HMMBuild	Sequence Analysis	Build Profile HMM from Multiple Sequence Alignment
HMMCalibrate	Sequence Analysis	Calibrate the Profile HMM
HMMSearch	Sequence Analysis	Search Database with Profile HMM
Transeq	Sequence Analysis	translate nucleic acid sequences
BackTranseq	Sequence Analysis	Back translate a protein sequence
Antigenic	Protein Characterisation	Find antigenic sites in proteins
ePrimer3	Sequence Analysis	Picks PCR primers and hybridization oligos
Database Query	Sequence Retrieval	Retrieve sequence(s) from the EMBL or SwissProt databases

GeneGrid Utilities

Utilities	Category	Description
Blast Processor	Sequence Analysis	Retrieve accession numbers or hit sequence from a blast output file
Eliminator	Protein Characterization	Retain only sequences of interest from TMHHM/SignalP
TmRP	Protein Characterisation	Get the sequence range with TMRegions
SpRP	Protein Characterisation	Get the sequence range with signal Regions
AgRP	Protein Characterisation	Get the sequence range with antigenic Regions
BlRP	Sequence Analysis	Parse BLAST output to check highly homologous hits
SeqExtract	Sequence Analysis	Extract sequence fragments into files based on range supplied in files
SeqExtractR	Sequence Analysis	Extract sequence fragments into files based on range supplied as parameter

Refresh

Selected Task Overview...

Name:	BLAST
Id:	GeneGrid:20050302121914807 1
Category:	Sequence Analysis
Description:	BLAST :
Status:	SUCCESS
Processing Started:	Wed, 2 March, 2005 at 1:08 PM
Completion Date:	Wed, 2 March, 2005 at 1:08 PM

Result Information

File Id:	GeneGrid:20050302130818913
File Format:	text
File Structure:	blast

Data:

```
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= test start sequence
         (463 letters)

Database: swissprot
           154,145 sequences; 56,721,989 total letters

Searching.................................................done

                                                           Score    E
Sequences producing significant alignments:                (bits) Value

sp|Q9Y336|SIL9_HUMAN Sialic acid-binding Ig-like lectin 9 precur...   852   0.0
sp|Q9Y286|SIL7_HUMAN Sialic acid binding Ig-like lectin 7 precur...   615   e-176
sp|Q9NYZ4|SIL8_HUMAN Sialic acid binding Ig-like lectin 8 precur...   567   e-161
sp|Q96PQ1|SILL_HUMAN Sialic acid binding Ig-like lectin-like 1 p...   543   e-154
sp|Q95LH0|SILL_PANTR Sialic acid binding Ig-like lectin-like 1 p...   539   e-153
sp|Q91Y57|SIL5_MOUSE Sialic acid binding Ig-like lectin 5 precur...   421   e-117
sp|O43699|SIL6_HUMAN Sialic acid binding Ig-like lectin 6 precur...   369   e-102
sp|O15389|SIL5_HUMAN Sialic acid binding Ig-like lectin 5 precur...   306   9e-83
sp|Q920G3|SILF_MOUSE Sialic acid binding Ig-like lectin-F precur...   297   4e-80
sp|P20138|CD33_HUMAN Myeloid cell surface antigen CD33 precursor...   286   6e-77
```

BeSC Belfast e-Science Centre

GeneGrid

Queen's University Belfast

Logout

Welcome, P.V. Jithesh

Welcome | GeneGrid

New Experiment | My Templates | Common Templates | My Experiments

GeneGrid View Experiments

Selected Experiment Overview...

Identifier:	GeneGrid:20050511162043015
Description:	may 11 1623 hmmer
Status:	SUCCESS
Submission date:	Wed, 11 May, 2005 at 4:21 PM
Completion Date:	Wed, 11 May, 2005 at 4:25 PM

Task Name	Task Description	Status	Results
ClustalW	ClustalW :	SUCCESS	View
HMMBuild	HMMBuild :	SUCCESS	View
HMMCalibrate	HMMCalibrate :	SUCCESS	View
HMMSearch	HMMSearch :	SUCCESS	View

You own the following expeiments currently on record in the GeneGrid Environment

Experiment Identifier	Experiment Description	Status
GeneGrid:20050513193911152		ACTIVE
GeneGrid:20050513193511385	test may 13 1937	SUCCESS
GeneGrid:20050218180113557	test	FAILED
GeneGrid:20050221165545118	new test	FAILED
GeneGrid:20050221182712095	Place Workflow Description here...	FAILED
GeneGrid:20050222101841353	Place Workflow Description here...	FAILED
GeneGrid:20050222155712788	Place Workflow Description here...	FAILED
GeneGrid:20050222163101796	thistest	FAILED
GeneGrid:20050222164009786	Place Workflow Description here...	ACTIVE
GeneGrid:20050222172041144	just checking	SUCCESS
GeneGrid:20050222180044577	this should work	ACTIVE
GeneGrid:20050222180749591	final test	FAILED
GeneGrid:20050222183240515	this will work	SUCCESS

GeneGrid: Status

BeSC
Belfast e-Science Centre

- 30 month project, started in August 2003
- Prototype Releases
  - 0.1 - March 2004
    - Conceptual prototype
  - 0.2 - August 2004
    - Functional prototype
  - 0.3 - October 2004
    - First release for commercial partners' use
  - 0.4 - January 2005
  - 0.5 - June 2005

Thank You!

BeSC
Belfast e-Science Centre

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  - s.wasnik@qub.ac.uk
- Bioinformatician: P.V. Jithesh
  - p.jithesh@qub.ac.uk
- More information:

http://www.qub.ac.uk/escience/projects/genegrid/