

# EST Pipeline System: Detailed and Automated EST Data Processing and Mining

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**Expressed sequence tags (ESTs) are widely used in gene survey research these years. The EST Pipeline System, software developed by Hangzhou Genomics Institute (HGI), can automatically analyze different scalar EST sequences by suitable methods. All the analysis reports, including those of vector masking, sequence assembly, gene annotation, Gene Ontology classification, and some other analyses, can be browsed and searched as well as downloaded in the Excel format from the web interface, saving research efforts from routine data processing for biological rules embedded in the data.**

**Key words:** EST, pipeline, data mining, relational database, Java/J2EE

## Introduction

Accompanied with the increased EST sequences in recent years, many bioinformatical analysis tools were designed for various purposes. Here comes a problem that most biologists would encounter when facing these tools: how to use them? Recently, some research groups have published their automated or semi-automated procedures for EST data analysis, such as ESTAP (1), and some other web-based systems (2). However, the graphical view, the well organized and connected list views, the output capability, and the job logging systems make our EST Pipeline System more effective and user-friendly. The system was initially developed in 2001 by Hangzhou Genomics Institute (HGI), and its software register number was 2002SR2503 issued by National Copyright Administration of P. R. China in 2002. A new version, EST Pipeline System 2.0, is under its finish phase. This paper mainly describes the feature and function of the version 1.0.

The EST Pipeline System is designed to solve some problems for scientists who are not familiar with those software tools. The system combines bioinformatics tools like BLAST (3, 4), Phred (5, 6), Pfam

(7), Crossmatch, Phrap (Phil Green, unpublished), Cap3 (8), and scripts of its own to make sure that the system can do a mining job in EST sequences automatically. Scientists who use this system only need to choose analysis tools and parameters, and then the Pipeline will do all the rest work and present the detailed and well organized information for users, so that scientists could focus on the biological aspect of their projects, saving time from routine data processing work.

## Features of the EST Pipeline System

The EST Pipeline System is composed of web interface, Perl script, third-party bioinformatics software and database. It is easy to operate on the web interface for submitting jobs, selecting result formats, as well as searching the information. Jobs are executed by Java EJBs, which embed some third-party software like BLAST, Phred, Pfam, Crossmatch, Phrap, Cap3, and the raw results are parsed by Perl scripts to be loaded into the Mysql or Oracle relational database. The web interface uses JSP scripts to communicate with EJB and database. Because most of the programming languages we used are platform independent, such as JAVA and Perl, the EST Pipeline System could be executed under most operating systems, including Windows, AIX, Linux, Solaris and so on.

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## Job submission

The process of EST sequence analyses is a pipeline that goes through analysis modules systematically. The pipeline provides a detailed job-submitting page showing the default parameters first. All the parameters of analysis tools are designed in web interface and could be changed easily by users if necessary. Each library has its job logging system that shows what analyses in the pipeline have been done. The default data flow goes through the SequenceStat module for sequence data integrity check, the AssembleStat module for assembly and chimeric contig check, the Lable module for annotation and the GOTREE module for gene function classification.

## Processing of EST sequence raw data

The first analysis after job submission by users is to check the sequence input. The pipeline accepts three kinds of input. The first kind is chromat-files; the second kind is sequence files plus quality files; and the third kind is sequence files only. The SequenceStat module will check sequence name duplication, and the consistence between the sequence file and the quality file. CROSSMATCH (Phil Green, unpublished, <http://bozeman.mbt.washington.edu/phrap.docs/phrap.html>) is used to mask vector sequences into "X". Other masked sequences such as the *E. coli* genome sequence and simple repeat database are provided as an option. Users can also define their own screening sequences. Then the report of the masked sequences will be imported into the database by the SequenceStat module. The last step is to filter sequences that are shorter than 100 bp (by default) after trim cut-off and vector masking. Users are able to change the length threshold of filtered sequences. Only the cleansed sequence data will go on to the assembly module.

## Sequence assembly

The AssembleStat module calls PHRAP (Phil Green, unpublished, <http://bozeman.mbt.washington.edu/phrap.docs/phrap.html>) or CAP3 to assemble the EST sequences into consensi (contigs) according to the user preference, and distills the assembly information. This module is also able to check the quality of each contig, by comparing its member ESTs to its consensus sequence. Contigs suspected to be chimerics will be re-assembled.

## Gene annotation

The Pipeline firstly uses similarity search tools such as BLAST to find homology for the checked contigs in the NCBI non-redundant protein and nucleotide databases (9) and the SWISS-PROT protein database (10). Then the Pipeline uses HMMPFAM (11) to search protein domains in each contig. The BLAST and HMMPFAM E-values can be adjusted by users. According to the homology information, the species, the gene description, E-values, and bit scores will be taken into account to define the final annotation by the Lable module. Notably, there are two user-definable similarity searches using databases of special interest.

## Gene classification

The Gene Ontology is composed of networked key words describing the molecular functions, biological processes, and cellular components property of genes (12). The GOTREE module draws a tree view of the contigs according to their annotation and GO ID assignment. Each GOTREE branch will hierarchically indicate the function of the annotated contigs.

## Database

The EST Pipeline System uses Oracle or MySQL relational database, which users could choose between the advantage of reliability, or speed. Perl modules import the parsed results into database automatically.

## Web Interface of the EST Pipeline System

Every user has a unique ID to enter the pipeline system. After logging in, the index page shown in Figure 1 will introduce the main report pages in the pipeline, which include the Library View, Contig View, Sequence View, and Gene Catalogue View.

### Library View

The Library View shows the information about all the libraries belonging to a user. It includes the summary of EST sequences' number, unique gene number, and some other descriptive information about the organism, tissue, period, *etc.* of each library (Figure 2).

**EST Analysis Pipeline**

Welcome to EST sequence analysis pipeline system!

**What's in Library View?**

We list statistical information of all EST libraries that have been submitted to date.

With Library View, we can:

- Get the statistical information of all libraries submitted to date;
- Manage your libraries by User Annotation;
- Draw comparisons among different libraries.

**What's in Contig View?**

Contig view shows the detail information of contigs in each library.

With Contig View, we can:

- Execute BLASTN/Basic Local Alignment compared with NCBI nucleic acid database) and manage results;
- Execute BLASTX/Basic Local Alignment compared with SwissProt protein database) and manage results;
- Draw comparisons between BLASTN and BLASTX results;
- View contig detail information in graph;
- List the details of consensus of each contig.

Input contig ID, space out with ","

**What's in Tree View?**

In Tree View, we provide you with intuitionistic method to show the classification results of genes in each library according to different rules as Go-Tree, G-Swissprot-Tree and PathWay-Tree.

With Tree View, we can:

- Get Functional, metabolize classification statistical results of each library;
- View statistical results of contigs in graph;
- Get contig details information via hyperlink to related website.

**What's in Job View?**

Job View indicates the current progress of the project. For managers, it's a helpful toolkit to control the running of the whole project.

With Job View, we can:

- See what's going on for the time being;
- Set the important parameters of software packages running in the pipeline.

ESTs are now widely used throughout the genomics and molecular biology communities for gene discovery, mapping, polymorphism analysis, expression studies, and gene prediction.

EST Analysis Pipeline System is a general EST analysis system we've developed. It provides you with integrated software packages which contain the most popular biology softwares on EST analysis.

More information

Current version: 1.0  
Browser required:  
- IE 4.0 or higher  
- Netscape 6.0 or higher

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Fig. 1 The index page of the EST Pipeline System. Users can get concise information of each view.

**EST Analysis Pipeline**

LibraryView | SequencesView | ContigsView | TreeView

All Libraries

**ALL LIBRARIES THAT CAN BE ATTAINED!**

Total 27records pages | PageNo: 1 | GO TO PAGE: 00

ID	LibraryName	Sequences	Contig	Single	Species	Period	Tissue	Proven	Interest	Organ	Contigs	Sequences	Job	Detail
3	rice	14436	8210	4159	null	null	全株	null	null	rice				
4	rice1	231	216	201	0. sativa Indica	null	null	null	null	China rice				
5	rice_A	117	108	101	0. sativa Indica	null	null	null	null	China rice				
6	rice_B	6378	846	2072	0. sativa Indica	trifol	leaf	null	时空表达	China rice				
7	rice_C	4563	569	1712	0. sativa Indica	none	whole plant	null	时空表达	China rice				
8	rice_D	6057	777	2390	0. sativa Indica	trifol	whole plant	null	时空表达	null				
10	rice_F	8942	1222	3864	0. sativa Indica	heading/flowering	panicle	HL	光温敏不育	China rice				
11	rice_G	6756	826	3045	0. sativa Indica	stealing	whole plant	null	时空表达	null				
12	rice_H	5606	859	2795	0. sativa Indica	heading/flowering	panicle	HS	光温敏不育	null				
13	rice_K	11787	1775	4470	0. sativa Indica	heading/flowering	panicle	HS	光温敏不育	China rice				
14	rice_M	9565	1347	3785	0. sativa Indica	heading/flowering	whole plant	HL	光温敏不育	China rice				
15	rice_N	9296	1400	3830	0. sativa Indica	heading/flowering	whole plant	null	null	China rice				
21	NipponbareRice	85284	17574	8824	Nipponbare rice	null	null	null	null	null				
58	rice_B	7074	4369	3569	null	null	null	null	null	null				
59	rice_D	7682	4402	2462	null	null	null	null	null	null				
60	rice_E	9795	5761	4395	null	null	null	null	null	null				
61	rice_F	9483	6045	5032	null	null	null	null	null	null				
62	rice_G	8190	5418	4403	null	null	null	null	null	null				
63	rice_H	10003	6924	5869	null	null	null	null	null	null				
64	rice_K	12053	7270	5443	null	null	null	null	null	null				
65	rice_M	12708	7744	5796	null	null	null	null	null	null				
66	rice_N	9148	5779	4393	null	null	null	null	null	null				

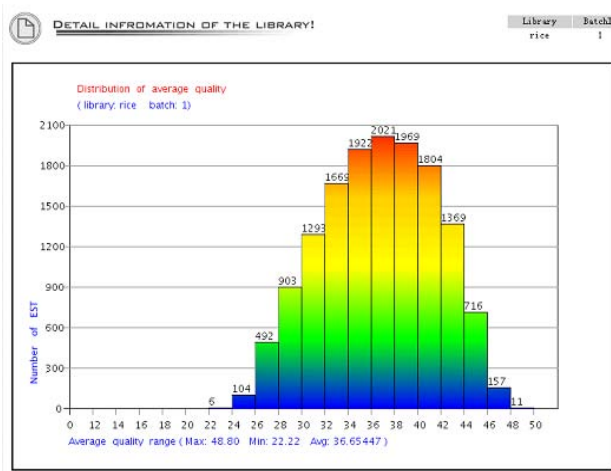
Total 27 records pages PageNo: 1

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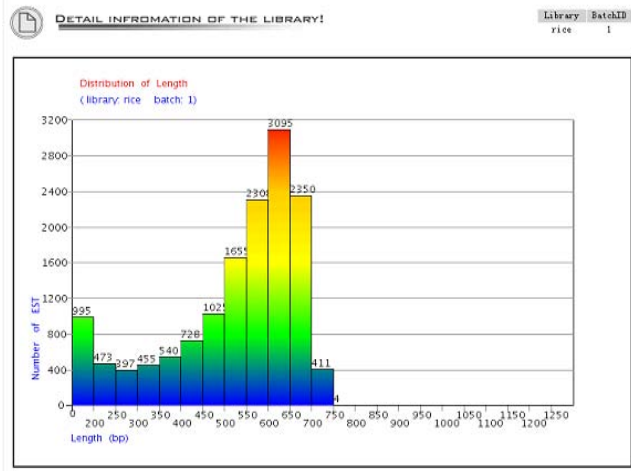
Fig. 2 The Library View. We used the rice EST project as an example. There are two species, *indica* and *nipponbare*, in this project. We could easily tell the information of each library from this view, and then choose the library which we are interested in to view more detailed results in detailed library view, sequence view and contig view.

The detailed library view shows up when the ‘detail’ button is clicked, which includes plots of distribution of the average sequence quality (Figure 3), dis-

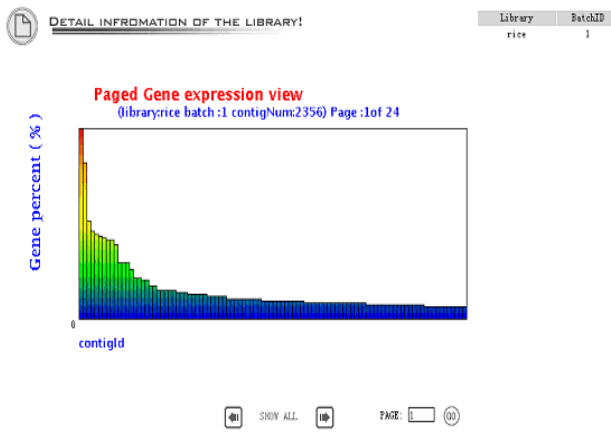
tribution of the sequence length (Figure 4), the gene expression view (Figure 5), and the GC Content view (Figure 6).



**Fig. 3** The distribution of average sequence quality. The X-axis is the quality from 0 to 50. This figure shows that all the quality of the sequences is above 20 because the system cuts off the low-quality bases, which is re-definable during base-calling. The Y-axis is the number of sequence in each range of the average quality.



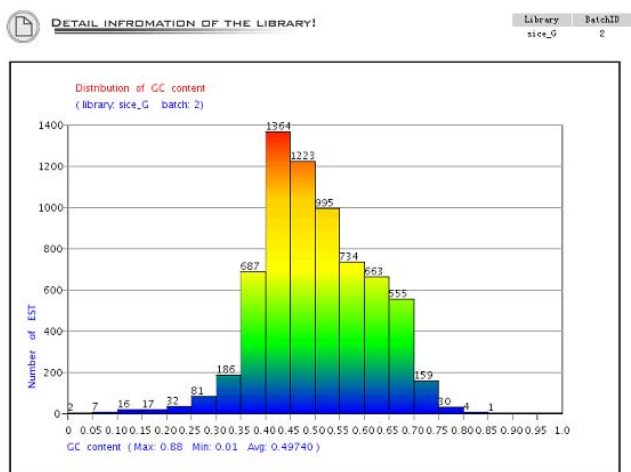
**Fig. 4** The distribution of sequence length. The X-axis is the sequence length and the Y-axis is the number of the sequence within the range of sequence length.



**Fig. 5** Gene expression view is an overview of the gene expression profile in the library. The gene abundance means the contig size divided by the total EST number in the library.

### Sequence View

The Sequence View describes detailed information about the EST sequences. Columns listed in the view show the length, quality, GC content, and other detailed information of every EST sequences. The sequence length includes raw length and trimmed length



**Fig. 6** The distribution of the GC content. The X-axis is the GC content and the Y-axis is the sequence number of the GC content.

(or effective length). The former is the length from base-calling, and the later means the sequence length after ignoring “X” and “N” in masked result from CROSSMATCH. All the sequences could be searched and sorted in the filter on the left of the screen (Figure 7).

Contig Grouped Sequences

Library ID:

Batch ID:

Contig ID:

Sequence ID:

Raw Length:

Trimmed Length:

Quality:

Quality OK:

Order By:

SequenceID

\* You can make any field blank, the search will work!

ALL SEQUENCES THAT CAN BE ATTAINED!

Library BatchID Contig Download  
size\_F 2 All contigs!

Total: 852 records 29 pages | Page 1 | PREVIOUS NEXT | GO TO PAGE:

SequenceID	SequenceName	ContigID	RawLength	TrimmedLength	Quality	GCContent	QualityOK	Detail
85883	rsicef_5807.yl.abd	44765	119	0	27.76	0.83	76	<input type="button" value="Detail"/>
85889	rsicef_5367.yl.abd	44781	278	0	29.29	0.86	132	<input type="button" value="Detail"/>
85897	rsicef_5340.yl.abd	44789	367	0	29.43	0.56	235	<input type="button" value="Detail"/>
85843	rsicef_5316.yl.abd	44817	328	0	24.51	0.5	99	<input type="button" value="Detail"/>
85836	rsicef_5301.yl.abd	44836	425	0	30.45	0.42	334	<input type="button" value="Detail"/>
85832	rsicef_4990.yl.abd	44842	405	0	30.99	0.46	301	<input type="button" value="Detail"/>
85824	rsicef_4980.yl.abd	44845	503	0	32.09	0.67	362	<input type="button" value="Detail"/>
85820	rsicef_4976.yl.abd	44847	324	0	32.51	0.66	227	<input type="button" value="Detail"/>
85803	rsicef_4954.yl.abd	44878	498	0	33.13	0.56	418	<input type="button" value="Detail"/>
85791	rsicef_4937.yl.abd	44887	421	0	33	0.67	281	<input type="button" value="Detail"/>
85789	rsicef_4935.yl.abd	44890	335	0	31.55	0.67	213	<input type="button" value="Detail"/>
85786	rsicef_4932.yl.abd	44899	456	0	26.88	0.59	248	<input type="button" value="Detail"/>
85785	rsicef_4929.yl.abd	44904	233	0	29.4	0.69	141	<input type="button" value="Detail"/>
85769	rsicef_4903.yl.abd	44930	500	0	35.06	0.43	361	<input type="button" value="Detail"/>
85761	rsicef_4909.yl.abd	44947	527	0	43.0	0.63	510	<input type="button" value="Detail"/>
85747	rsicef_4972.yl.abd	44960	566	0	44.01	0.54	825	<input type="button" value="Detail"/>
85743	rsicef_4966.yl.abd	44973	336	0	34.79	0.65	254	<input type="button" value="Detail"/>
85733	rsicef_4954.yl.abd	44980	566	0	41.14	0.6	511	<input type="button" value="Detail"/>
85699	rsicef_4915.yl.abd	45013	341	0	27.06	0.56	133	<input type="button" value="Detail"/>
85693	rsicef_4909.yl.abd	45020	485	0	36.24	0.73	462	<input type="button" value="Detail"/>
85690	rsicef_4905.yl.abd	45023	467	0	31.34	0.48	351	<input type="button" value="Detail"/>
85683	rsicef_4492.yl.abd	45042	477	0	32.0	0.37	381	<input type="button" value="Detail"/>
85631	rsicef_4432.yl.abd	45080	266	0	32.80	0.50	216	<input type="button" value="Detail"/>
85627	rsicef_4428.yl.abd	45100	622	0	44.04	0.4	530	<input type="button" value="Detail"/>
85625	rsicef_4428.yl.abd	45102	579	0	41.64	0.66	551	<input type="button" value="Detail"/>
85615	rsicef_4416.yl.abd	45114	531	0	39.26	0.43	460	<input type="button" value="Detail"/>
85612	rsicef_4412.yl.abd	45121	366	0	37.27	0.53	333	<input type="button" value="Detail"/>
85608	rsicef_4408.yl.abd	45124	618	0	37.97	0.16	537	<input type="button" value="Detail"/>
85590	rsicef_4333.yl.abd	45167	429	0	38.56	0.59	383	<input type="button" value="Detail"/>
85546	rsicef_4328.yl.abd	45170	251	0	28.89	0.42	138	<input type="button" value="Detail"/>

Total: 852 records 29 pages | Page 1 | PREVIOUS NEXT

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**Fig. 7** The Sequence View shows the basic information about each EST sequence in the library. It will be helpful for users who are interested in some special sequences. On the left of the page there are filters for users to search sequences by Contig ID, Sequence ID, Raw length, Trimmed length, and Quality, *etc.*

## Contig View

The Contig View (Figure 8) is one of the most important views in the system. Contig size means how many EST sequences have been assembled into the contig, which is an indicator of gene expression level. If a contig contains only one EST sequence, it is called a singleton. The column BlastN Annotation is the result of BLAST search from NCBI non-redundant database chosen by the Lable module. The Lable module not only considers the best hit from the Blast result but also take organism information into account, and filter out BAC or EST hits (details are discussed in our former publication, ref. 13), so it will be able to assign a more reasonable annotation to the contigs. Users could see all the BLAST alignment information including hit score, E-value, and orientation by clicking the arrowhead button. The next column BlastX Annotation is the search result from SWISS-PROT protein database. All its information is similar to the BlastN Annotation but the annotation is taken from the best hit of BlastX result. Classification is a hotspot with mouse-over popup information for gene classification information, which will be ex-

tiated in detail at the Gene Catalogue View. Clicking the “detail” button in the Contig View will display the graphic view and list view of BLAST alignment details (Figure 9).

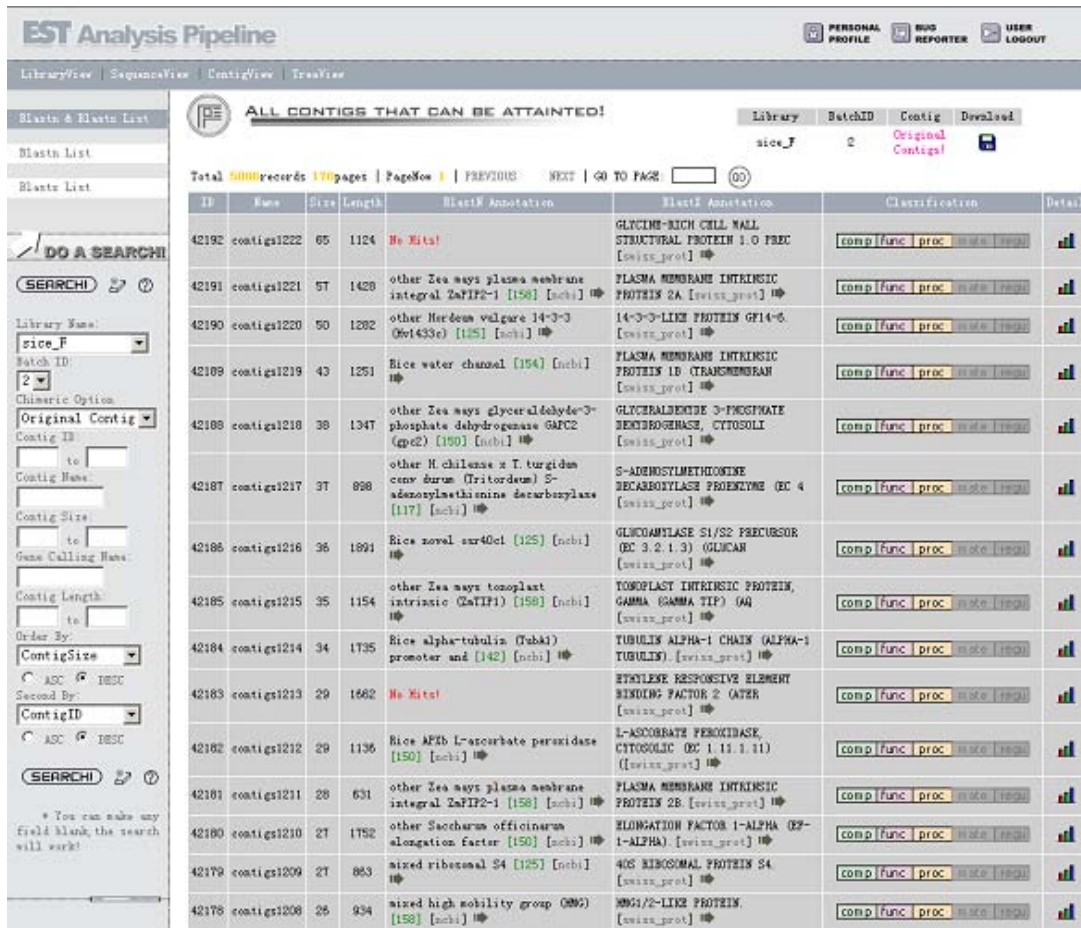
## Gene Catalogue View

Gene Ontology is developed for consistent descriptions of gene products in different databases (12). We can classify the annotated genes into cellular component, molecular function and biological process categories according to their accession numbers in SWISS-PROT Protein Knowledgebase or NCBI protein database. The classification could help a lot on the understanding of gene function (Figure 10).

## Conclusion

The EST Pipeline System is a highly automatic analysis pipeline for EST projects. What users need to do is to upload the library sequences and select parameters for the tools, and the system will complete all the base-calling, screening, assembly, annotation, and functional classification work. Therefore, the re-

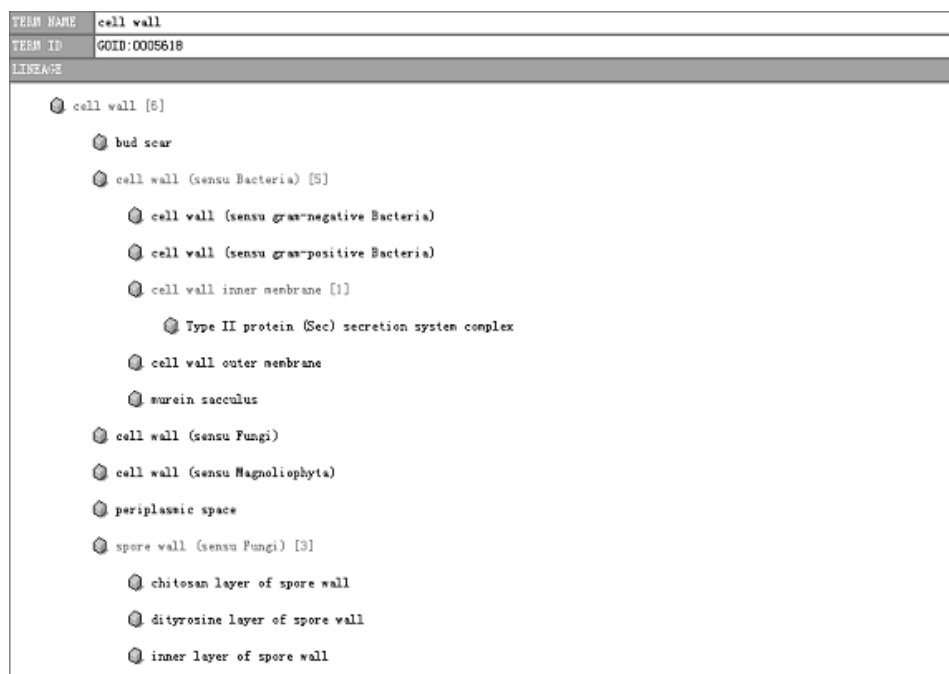




**Fig. 8** The Contig View. Contig size is one of the most important properties of a contig to define the expressing level of the gene. The columns BlastN Annotation and BlastX Annotation list the taken annotation from NCBI non-redundant and SWISS-PROT database, respectively. Different colors are used to indicate the cellular component, molecular function and biological process aspect of Gene Ontology classification. Detailed graphical view and list view are available by clicking the “detail” button.



**Fig. 9** Graphical detail-alignment view. This view shows directly the alignment result between contigs and BLAST database hits. Each line means one hit and each arrowed line indicates an HSP with its orientation. The mouse over event would bring up detailed text boxes for the information of score, length, start, end, etc. of each hits or HSP.



**Fig. 10** A part of the tree view. The number beside the cell wall indicates there are six contigs classified into this functional category, and branches below show the detailed functional category under the father category.

searchers could focus on the biological aspect of those well organized and representative analysis results, and quickly penetrate the biological meaning embedded in the data.

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