LIMS IMPLEMENTATION IN A GENOTYPING STUDY

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Dedicated to my wife Vera, for her commitment, trust and patience

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ABSTRACT

David Opare Kennedy

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Discovery laboratories are dealing with DNA sequencer-based technologies which have seen great advancement over the past decade, resulting in several steps of the genotyping process becoming automated. This, in turn, has led to increased throughput. Laboratory Information Management Systems (LIMS) are needed to organize data flow as large amounts of data are difficult to process by hand. A commercially developed LIMS was implemented at a Clinical Pharmacology Division laboratory of Indiana University, Indianapolis, during a P450 2D6 genotyping study. The LIMS application used was Biotracker™ (Ocimum Biosolutions), and its modular design led users through each step of the genotyping process, from starting an experiment to the storing of output data from the genotype detection step. This ensured that every DNA sample was handled in an identical manner and all the necessary data were captured. The application helped design protocols and experiments, and manage different projects utilizing laboratory resources from the same inventory source, as in any typical laboratory. DNA samples, reagents, instruments, and generated data were also easily recorded and tracked. LIMS provide functions to trace back to protocols, inventories, projects, files or sample source for any genotype data. One of the features of LIMS that is not crucial to academic laboratories but was found useful during this project was the audit trail functionality, which allowed researchers to know who carried out what experiment at what time, and also to track

inventories. Workflows of projects were also designed, and submitted for review and approval. Another aspect of this project was a survey to find out the knowledge and attitudes toward LIMS in academic research. It was observed that most academic researchers are not familiar with the total capabilities of LIMS, defined as special computer software that is used in the laboratory for the management of samples, inventories, laboratory users, instruments, standards and other laboratory functions such as invoicing, plate management, and work flow automation. However, several software technologies are employed but mostly for data storage and instrument integration, which normally come with vendor-specific instruments. Also, most respondents in laboratories conducting genotyping studies and DNA sequencing are more likely to use some form of LIMS. Lack of knowledge was cited as the most prevalent reason for not having used LIMS.

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LIST OF ABBREVIATIONS

ANOVA	Analysis of Variance
ASPE	Allele-Specific Primer Extension
CLIMS	Crystallography Laboratory Information Management Systems
CYP450	Cytochrome P450
DASH	Dynamic Allele-Specific Hybridization
DNA	Deoxyribonucleic acid
ELN	Electronic Laboratory Notebook
LIMS	Laboratory Information Management Systems
MARS	Microarray Analysis and Retrieval System
MIAME	Minimum Information About a Microarray Experiment
MSDS	Material Safety and Data Sheet
PACLIMS	Phenotype Assay Component LIMS
PCR	Polymerase Chain Reaction
SAP	Shrimp Alkaline Phosphatase
SNP	Single Nucleotide Polymorphism
TIMS	TaqMan Information Management System

ACKNOWLEDGEMENT

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Finally, to the God I trust. If it had not been for Him on my side! (Psalm 124)

CHAPTER ONE: INTRODUCTION

1.1. Laboratory Information Management Systems (LIMS)

LIMS were originally developed in-house by organizations to streamline their data throughput and reporting processes. This took considerable time and resources to implement. Custom-built systems were later designed by independent systems development companies to run in specific laboratories, and offered increased flexibility and functionality (Gibbon, 1996). The main function of LIMS is to help to manage laboratory processes workflow precisely. Their use also encourages good laboratory practices by standardizing protocols, recording, and annotating data from every step of the workflow.

A number of LIMS have been developed to meet different needs of commercial as well as academic research laboratories. Among these are Labware (Labware Inc), LabVantage sapphire (Labvantage), Starlims (Starlims Corporation), Corelims (Core Informatics), Biotracker (Ocimum Biosolutions), Sample Manager (Thermo Scientific), and Labworks (Perkin-Elmer). Among LIMS developed to meet the challenges of laboratory workflow in academic research is TaqMan Information Management System (TIMS), a suite of tools written in Visual Basic developed specifically for genotyping laboratories using the Taqman technology for SNP genotyping (Monnier, 2005). It is aimed at improving data workflow, preventing errors linked to managing data by hand, as well as saving time. CLIMS (Crystallography LIMS) was specifically designed to manage protein crystallization workflow and data (Isler, 2004). It features a graphical user interface to a relational database, and assists in all aspects of protein-crystallization projects (protein expression, handling, crystallization optimization, visualization of

results and preliminary diffraction data). Prilusky *et al*. (2005) designed HaIX, an open source LIMS for managing all types of experiments on the way from cloning through to structure determination in a structured manner allowing extensive data mining, and creation of any protocol. It is built around a three-tier architecture model. A web browser on the client's computer, the application and business logic which is PHP based supported by an Apache web-server, and a PostgreSQL to manage the storage and DB-server third tier. This was built for both small and large scale laboratories. A Microarray Analysis and Retrieval System (MARS) provides a comprehensive Minimum Information About a Microarray Experiment (MIAME) supportive suite for storing, retrieving, and analyzing multicolor microarray data, and comprises LIMS, a quality control management, as well as a user management system (Maurer, 2005). A minimal LIMS, called PACLIMS (Phenotype Assay Component LIMS) was developed to record data and track mutants. This system was designed to accommodate the experimental protocol as it evolved and fulfill the role of process control by enforcing the steps of the protocol (Donofrio, 2005). This software reduces laboratory and data entry errors while allowing the data generated at different locations to be entered.

1.2. Single Nucleotide Polymorphisms (SNPs) and genotyping

SNPs are genetic markers used as tools in biological, genetic, medical, and pharmacological applications due to their abundance and slow mutation rate within generations. SNPs occur when a single nucleotide (Adenine-A, Thymine-T, G-Guanine, C-Cytosine) in the DNA sequence in a region of the genome is changed, compared with what is observed in majority of the population. About 99.9% of the DNA sequence of

one individual is identical to that of another, and 80% of the remaining 0.1% will be SNPs. Both versions of the single base substitution of one nucleotide with another in the DNA sequence occur in the general population at a frequency greater than 1% (Venter, 2001; Collins et al, 1998; Gingeras, 2007). In an entire human genome there are approximately 10 to 30 million potential SNPs, many of which have unknown associations. SNPs represent the most frequent form of DNA variation and disease-causing mutations in many genes, and their discovery and mapping involve several strategies that are either experimental or in-silico. Experimental SNP discovery is the most widely used but involves complex processes and is expensive. In-silico discovery makes use and takes advantage of large data sets with potential SNP information that have been generated for other purposes but not yet used as a SNP information source (Useche, 2001). SNPs can change the function or the regulation of a protein, and are also useful as genetic markers that can be used to find the actual DNA sequence variants that cause differences in gene function or regulation which directly contribute to disease processes (Roeder, 2005). Another significant goal of SNP discovery is to identify those that are associated with significant biological effects in response to chemical drugs (Shubbert, 2001; Stamer, 2005; Stamer and Stuber, 2007). A large percentage of people given a drug respond in the intended medically beneficial way, however, some smaller percentage might either have no response or have a life threatening response and death.

SNPs form the basis of genotyping, which is a technique for measuring genetic variations between individuals due to changes in base pairing in the DNA sequence. There are several different SNP genotyping experimental methods and these consist of

various combinations of different allele-discrimination and signal detection methods. Many of these methods have been developed into commercial products with a 96- or 384-well format and automation, such as single-base extension-based SNPStream (Orchid Bioscience), and Pyrosequencing's high throughput system obtaining a throughput of 10000 genotypes a day, Invader (combined with PCR), fluorescent polarization-based methods, and dynamic allele-specific hybridization (DASH). These technologies are capable of tens of thousands of genotypes per day with automation, making large-scale association studies possible (Kwok, 2001; Howard, 1999; Abravaya, 2003; Klito, 2007; Olivier, 2005; Syvanen, 2001; McGuigan, 2002). With the advances in DNA sequencer-based technologies, it has become possible to automate several steps of the genotyping process leading to increased throughput, generating about 10,000 genotypes per day. Recent years have seen many reports in the literature announcing the results of studies linking a gene variant to an increased risk for common diseases such as diabetes (Saxena, 2007), myocardial infarction (Helgadotir, 2007), breast cancer (Easton, 2007; Hunter, 2007; Shen, 2006; Santella, 2005; Kennedy, 2005), as well as factors associated with drug metabolism (Borges, 2007; Lim, 2006; Shubbert, 2001; Stamer and Stuber, 2007; Kircheiner, 2004; Giacomini 2007).

1.3. Cytochromes P450

Cytochromes P450 are a superfamily of heme enzymes present in living things (Nelson, 1996). Currently, the number of P450s with known sequences, either as nucleotide sequences or amino acid sequences are about 8000 (Nelson, 2008). P450s and their respective genes are named with the abbreviation CYP followed by an Arabic

numeral which expresses the family number, e.g. CYP2. This number may be associated with the function of the enzyme, or it may have been chosen rather arbitrarily. A family is divided further to create a subfamily based on higher degree of sequence similarity, and these subfamilies within one family are labeled sequentially as, e.g., CYP2D. Individual members of a family or subfamily are labeled again by Arabic numerals (e.g., CYP2D6). More than 7700 distinct CYP sequences are known. Human CYPs are primarily membrane-associated proteins, located either in the inner membrane of mitochondria or in the endoplasmic reticulum of cells. They are responsible for metabolising thousands of endogenous and exogenous compounds. Most CYPs can metabolize multiple substrates, and many can catalyze multiple reactions. In the liver, these substrates include drugs and toxic compounds as well as metabolic products such as bilirubin (a breakdown product of hemoglobin). In drug metabolism, cytochrome P450 is probably the most important element of oxidative metabolism (a part of phase I metabolism) in humans (metabolism in this context being the chemical modification or degradation of chemicals including drugs and endogenous compounds). P450 are also present in many other tissues of the body including the mucosa of the gastrointestinal tract, and play important roles in hormone synthesis and breakdown, such as in estrogen and testosterone synthesis and metabolism, cholesterol synthesis, and vitamin D metabolism.

The impact of decreased activity of CYP2D6 on drug treatment may be extremely important. Variability of its activities in human liver samples may be ascribed to genetic polymorphism as CYP2D6 is not inducible. It causes the presence of three main phenotypes of oxidative metabolism of drug substrates of this enzyme. These three

phenotypes are classified as the slow metabolizers (with defective CYP2D6 alleles), the extensive (or rapid) metabolizers (with the wild-type allele or with alleles having nucleotide changes not causing altered activity of CYP2D6), and the ultrarapid ones with multiple genes for the functional CYP2D6 enzyme.

CHAPTER TWO: BACKGROUND

2.1. Genotyping and LIMS

A typical genotyping process involves several steps, which can generally be divided into two, sample preparation and allele detection. Sample preparation involves purification of DNA from blood, which is often labor-intensive, time-consuming, and costly and enhances the risk of cross-contamination of samples. Sample preparation steps involve sample collection, sample tracking, DNA extraction and purification, DNA tracking, PCR plate tracking, and use of instruments. A robust system for the management of sample identity and history is therefore required for any high throughput laboratory to document sample ID, date received, and any related information. Every PCR plate must have a reference to a template that details the plate contents and a unique identifier that allows the tracking of specific genotypes back to the plate.

Great advances have been made in allele detection tests because novel technologies for DNA analysis have been developed, and this has led to more data being generated per genotyping. Owing to the multi-step nature of genotyping much planning is needed to streamline an effective workflow. The larger the laboratory or the bigger the genotyping project, the higher the complexity of managing all these resources. A number of data management issues are encountered in high-throughput genotyping for a large disease mapping project. The data management system used must allow the import of raw data from the laboratory as well as the processing of that raw data to generate finished genotypes. Error analysis and correction of the finished data, which requires the ability to trace back to the raw data, the compilation of all data, and export in a finished form to suitable programs for genetic analysis are all important steps. There is therefore a strong

need for a software system that can help with the tracking of samples, capture, and management of data at different steps of the process.

2.2. Current practice in academia

Discovery laboratories like academic laboratories carry out sequencing, genotyping, gene expression, proteomics, metabolomics, cell biology and general life science projects. Traditionally, upon approval of project proposal, the responsible personnel assemble their reagents, labware, and make reservations for instruments. Much time is lost looking for reagents and vendors information, and placing orders for out of stock reagents. Instruments are usually reserved in a notebook or on a sign-up sheet attached to the instrument. Samples are collected, and the experiments are carried out with the aid of protocols from assay kits supplied by a manufacturer or they are downloaded or assembled from a website, or built from scratch with information from literature. This may be typed out and printed for storage and dissemination. Mostly, data is transferred from instruments to an external storage site, usually a computer used only for data processing, resulting in redundancy in datasets scattered in different directories. Sometimes, results are printed from instruments to storage in physical files. Other issues are data integrity and accountability, as data management is mostly done by hand, and getting data off instruments into a storage system may not be in a manner that is lossless. Data management by hand presents a situation where it is difficult to link files to experiments and to the original sample. Results are published after data analysis, and the raw data is archived in a random or assigned directory on a computer, diskette or CD, or printed for filling and storage. This may be the end of the data and perhaps the study.

Most often these data cannot be located after several years of storage. During the next project, the whole cycle is repeated, sometimes even subsequent studies which may be similar to a previous one have to go through the whole cycle from the beginning, and investigators have to assemble all the logistics all over again. Much time and resources are spent in this repeating cycle. A typical challenge is inventory keeping. At best, reagents are stored in alphabetical order in cabinets or on shelves, but it is always difficult to locate or even identify items in refrigerators or freezers. Instrument sharing is also a problem. The major problem is that steps involved in project execution are not linked to a specific workflow but are all segregated.

LIMS have over the past three decades flourished in the commercial sector (Vanderslice, 1990; Cagnd, 2004). Commercial sectors generated large datasets and needed automated processes to assimilate these, whereas in academia the data load generated could be easily managed by modest, conventional means with a spreadsheet application on a less sophisticated and expensive computer. LIMS serve to help manage workflow precisely and also encourage good laboratory practices by standardizing protocols, and recording and annotating data from every step of the workflow. It is also known that government regulatory requirements (Title 21, Code of Federal Regulations: Electronic Records and Electronic Signatures), have necessitated the use of LIMS in the commercial sector (Food and Drug Administration, 2003), but are non-existent in academia. Atrium Research, a market research organization dedicated to scientific informatics in the United States, is one of the few informatics research companies that look at trends and implementations of LIMS, electronic laboratory notebooks (ELNs), and scientific data management systems. However, studies so far have centered on and

targeted the commercial sector. Shankar (2004) demonstrated through an ethnography study the record-keeping attitudes of academic researchers and called for more analysis of recordkeeping as an information infrastructure, and inquiry into the nature of the record in other kinds of knowledge production environments. Some scientists believe that LIMS were initially created, developed, and applied exclusively in the commercial sector. Cost, failed implementation, and general resistance to computerized systems are among the factors that influenced the initial enthusiasm for LIMS usage (Perry, 2002). However, with the decline in the cost of LIMS, smaller commercial companies are able to implement them, and LIMS are appreciated as a valuable and even necessary tool in the commercial laboratory. However, LIMS have very little presence in academia (Viksna, 2007; Steinlechner, 2001; Schreier, 2006; Hendricks, 2003). A few laboratories have created open source software that may run a couple of processes such as high-throughput technologies. The National Cancer Institute started encouraging the use of Labvantage LIMS (Labvantage, 2002) for its cancer research programs. According to Perry (2002), there are two reasons for the difference between the commercial and academic use of LIMS, namely, the history of LIMS development and the special characteristics of academic research and development laboratories. He explained that in the early days, LIMS were custom-designed, labor-intensive applications. They were expensive, took years to implement, and were often unsatisfactory to end-users. However, large organizations wanted automation of routine operations to increase productivity and have used LIMS. The situation in academia was much different. Thus, LIMS implementation was traditionally limited to commercial laboratories that had both the need and the resources to accomplish this.

Furthermore, recent lawsuits regarding proprietary rights to discoveries have also sparked the need for LIMS and ELNs. LIMS have been thought to remain out of the financial reach of academic laboratories, and vendors do not consider them a potential profit-making business. Recently, several LIMS vendors have initiated academic pricing models.

2.3. Proposed project

One of the challenges of high-throughput SNP genotyping is to create an informatics environment that can support such a large data flow efficiently, such as for tracking blood and tissue samples to managing data at different steps of the research process. Owing to this multi-step nature of genotyping much planning is needed to streamline methods, instruments, reagents, and samples to facilitate an effective workflow. Currently, most academic laboratories handle inventorying by hand, using common software such as Microsoft Word and Excel. An efficient tool is also needed to manipulate the large data output for further analyses and final reporting. This project aimed at using a commercially available Biotracker LIMS to manage the entire workflow of a study involving drug metabolism-related P450 genotypes in an academic research laboratory setting, from sample preparation to final report generation. Biotracker architecture has a database management layer written in pure Java that makes it independent of databases, and supports Oracle, MySQL, SQL Server, and Sybase. It can run on any platform such as Windows, Linux, or Solaris. It has several modules which are interdependent and make for a smooth workflow (Figure 1). Biotracker was used at each step of the genotyping process from the start of the study to the storing of output

data to final reporting. This project involved the management of such an academic study usually conducted by scientists at the Clinical Pharmacology Division at Indiana University in Indianapolis, Indiana, without the use of LIMS. This is possibly the most popular cytochrome P450 among physicians and other health professionals, because of its genetic polymorphism.

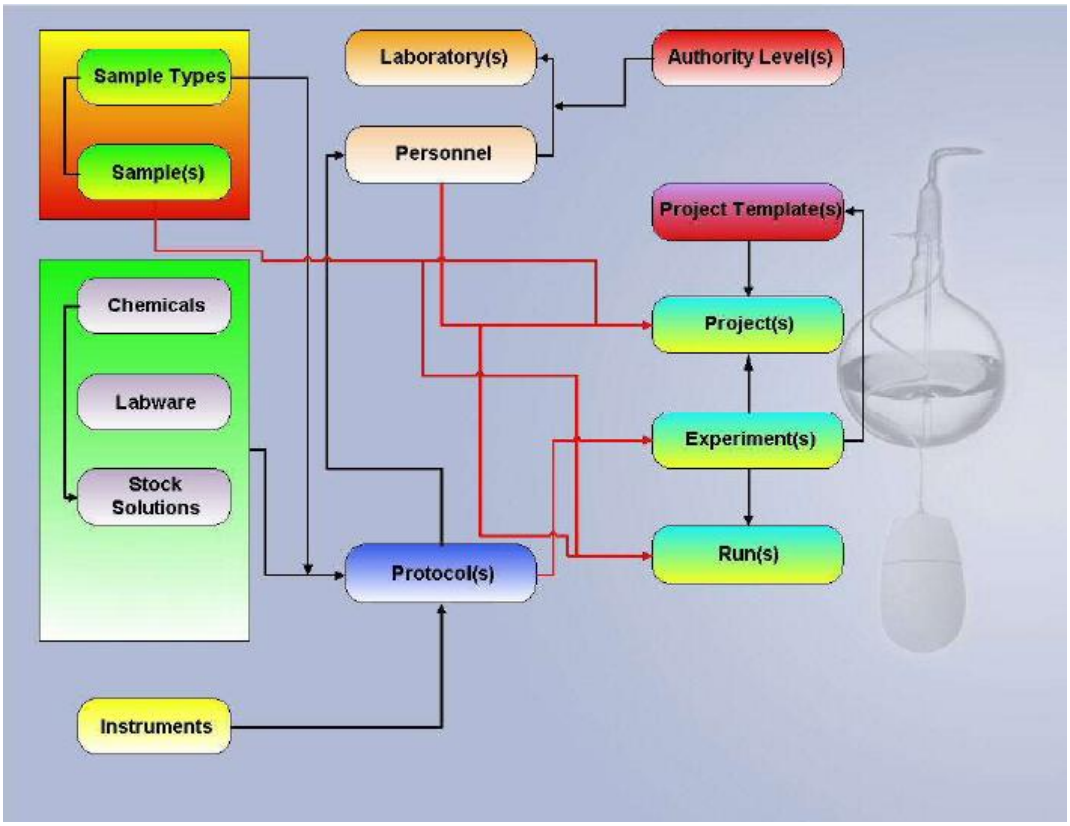


Figure 1: Interdependency of various modules in Biotracker

(Obtained from Biotracker manual)

The use of LIMS in academia is not widespread despite the large number of commercial-off-the-shelf (COTS) systems as well as open source LIMS that are currently

available to universities. As part of this project, a short survey was conducted to assess the factors that may be influencing attitudes towards LIMS implementation in the academic community. This included obtaining responses from experienced scientists, technicians, and postdoctoral fellows. Personal characteristics of respondents examined included age, sex, laboratory information, education, work experience, expertise of the laboratory, working hours, type of institution, instruments available, city or state of research. These were examined to shed light on the nature of the respondents and their work, and to see if any of these factors affected their LIMS usage. Knowledge characteristics looked at knowledge of LIMS. Questions were designed to determine whether respondents had any knowledge of LIMS or had used similar software. Respondents were also asked their reasons for not having used LIMS before.

CHAPTER THREE: METHODOLOGY

3.1. Materials and methods

Biotracker LIMS was obtained from Ocimum Biosolutions, Inc. (Indianapolis, Indiana). It is a multi-platform, multi-user, cost-effective software designed to improve laboratory performance. Biotracker is designed for sequencing, gene expression, genotyping assays, proteomics core labs, and bio-specimen banking facilities. The genotyping assays functionality was used in this project to manage, and track biological samples (blood), reagents, instruments, processes, and results at every stage of the project. Key features of Biotracker, such as integration support for Luminex, Autogenomics, SNP stream, or Illumina instruments, were not available on this student version. The genotyping study was part of an on-going study at the Division of Clinical Pharmacology, Indiana University Medical School. The genotyping method was based on the Taq-It Mutation Detection Kit assay for P450-2D6 (Tm Bioscience Corporation, Toronto, Canada).

3.2. Genotyping method overview

The genotyping work was done in the laboratory of Professor Todd Skaar at the Clinical Pharmacology Division of Indiana University, Indianapolis. The Tag-It^{TM} Mutation Detection Kit for P450-2D6 is designed to simultaneously detect a panel of 12 small nucleotide variants found within the highly genetically polymorphic cytochrome P450-2D6 gene located on chromosome 22. The enzyme product of the P450-2D6 gene is involved in the oxidative metabolism of more than 100 clinically relevant drugs (Abraham, 2001). Enzyme activity varies with the genotype resulting in different drug

metabolism phenotypes (McElroy, 2000). The 12 small nucleotide changes tested for in this kit represent the most prevalent phenotypically-relevant variants within the P450-2D6 gene. Eight blood samples received from Riley Hospital, Indianapolis, were used in this project.

Briefly, a QIAamp DNA blood Mini Kit (Qiagen, Valencia, CA) was used to extract genomic DNA from the leukocyte portion of whole blood. For each genomic sample being tested, two separate PCR reactions were performed (Figure 2). Each PCR reaction required 25 ng genomic DNA (total - 50 ng genomic DNA per sample). The first PCR (PCR-A) produced an alpha fragment (3.8 kb) used to detect the variants, as well as a duplication amplimer (3.2 kb) which indicates the presence of the duplication genotype. The second PCR (PCR-B) produces a beta fragment (2.6 kb) used to detect the variants, as well as a deletion amplimer (3.5 kb) indicative of the deletion genotype. After PCR amplification, the two reactions (PCR-A and PCR-B) were pooled. The pooled PCR product was then treated with Shrimp Alkaline Phosphatase (SAP) to inactivate any remaining nucleotides (particularly dCTP), and with Exonuclease I (EXO) to degrade any primers left over from the PCR reaction. Allele Specific Primer Extension (ASPE) reaction was then carried out using 26 universally-tagged primers supplied in the ASPE primer mix. A 5 uL aliquot of the ASPE reaction was hybridized with the universal array (Bead Mix) in the presence of the hybridization buffer and incubated with Streptavidin, R-Phycoerythrin conjugate (reporter solution). Samples were read on the Luminex® 100 xMAP™ instrument and signal was generated for each of the 12 small nucleotide variants as well as for the duplication and deletion amplimers, if present. These fluorescence values were then analyzed to determine whether the wild-type/mutant allele for each of

the 12 small nucleotide variants had been detected or whether the samples carried an allele(s) with the deletion or duplication. All the steps of the genotyping project and assay were monitored, and the DNA samples, reagents, instruments and workflow were tracked with Biotracker LIMS.

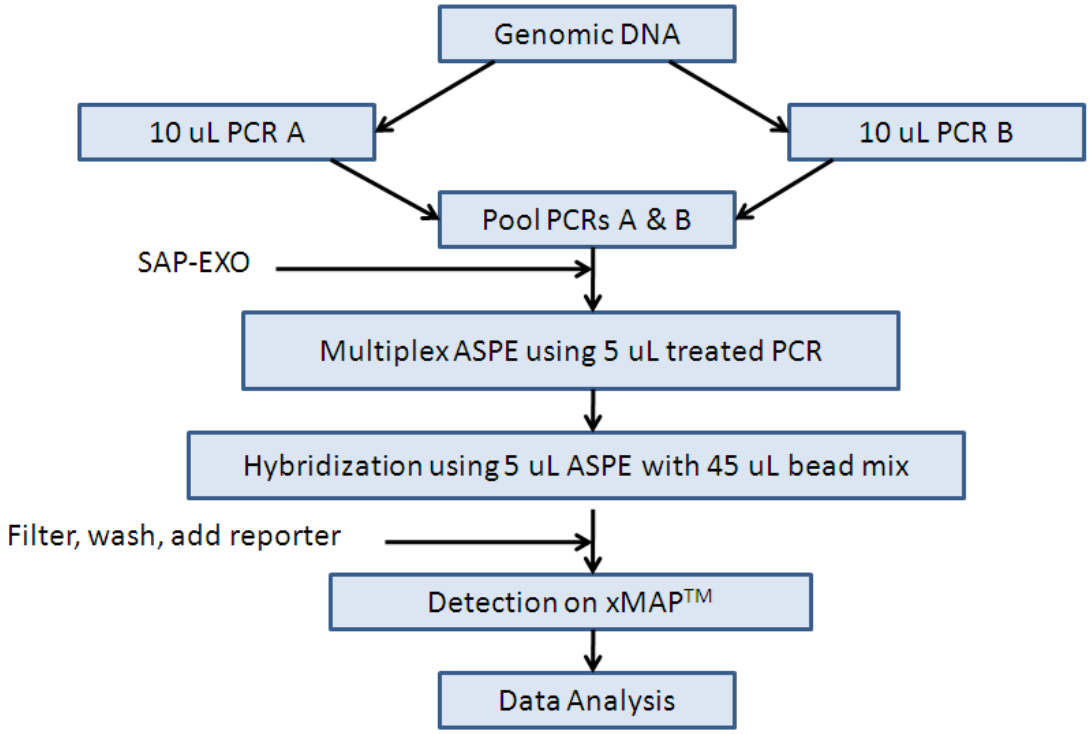


Figure 2: P4502D6 assay overview

3.3. LIMS functionality

3.3.1. Starting Biotracker

The investigator's role was a LIMS administrator and a research scientist in the laboratory on this genotyping project. Initially, the administrator logged in through the window in Figure 3 with a software developer provided ID and password, created a

database server, set the LIMS configuration, and created users and assigned passwords and privileges.

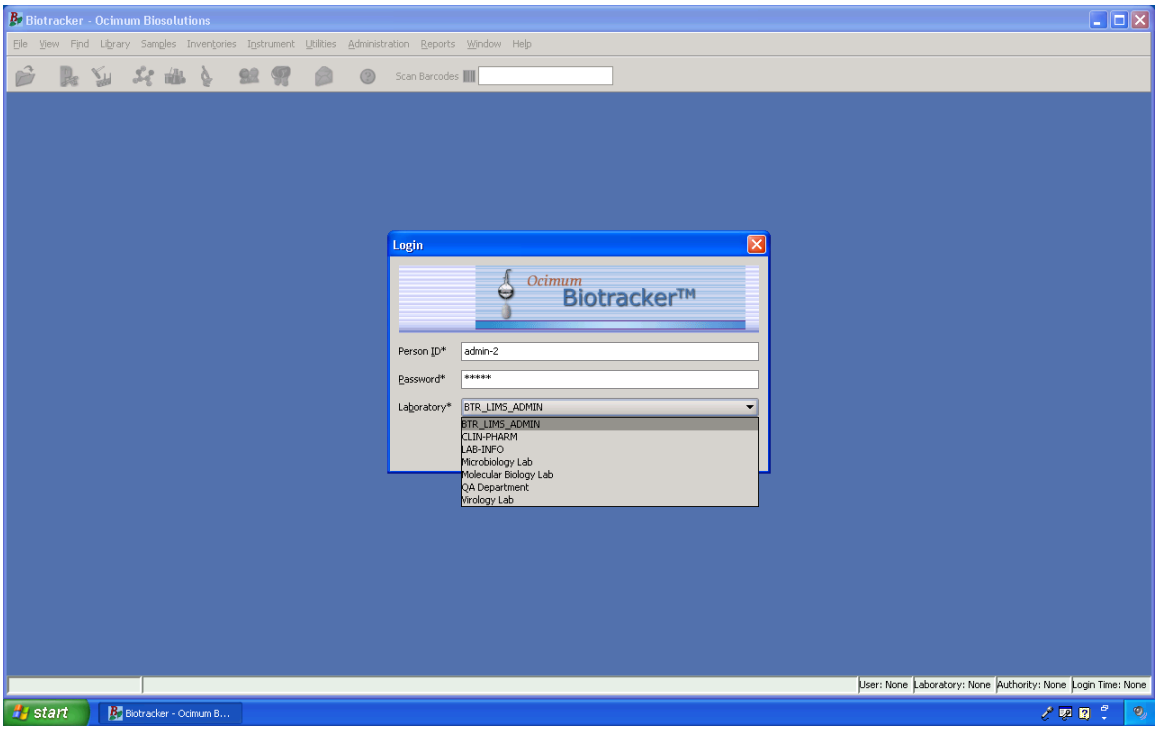


Figure 3: Biotracker LIMS log-in

On entering the software, the LIMS window shows a menu bar (12 items), tool bar (10 iconic items), navigator bar, work area, status bar, and scan barcode window (Figure 4).

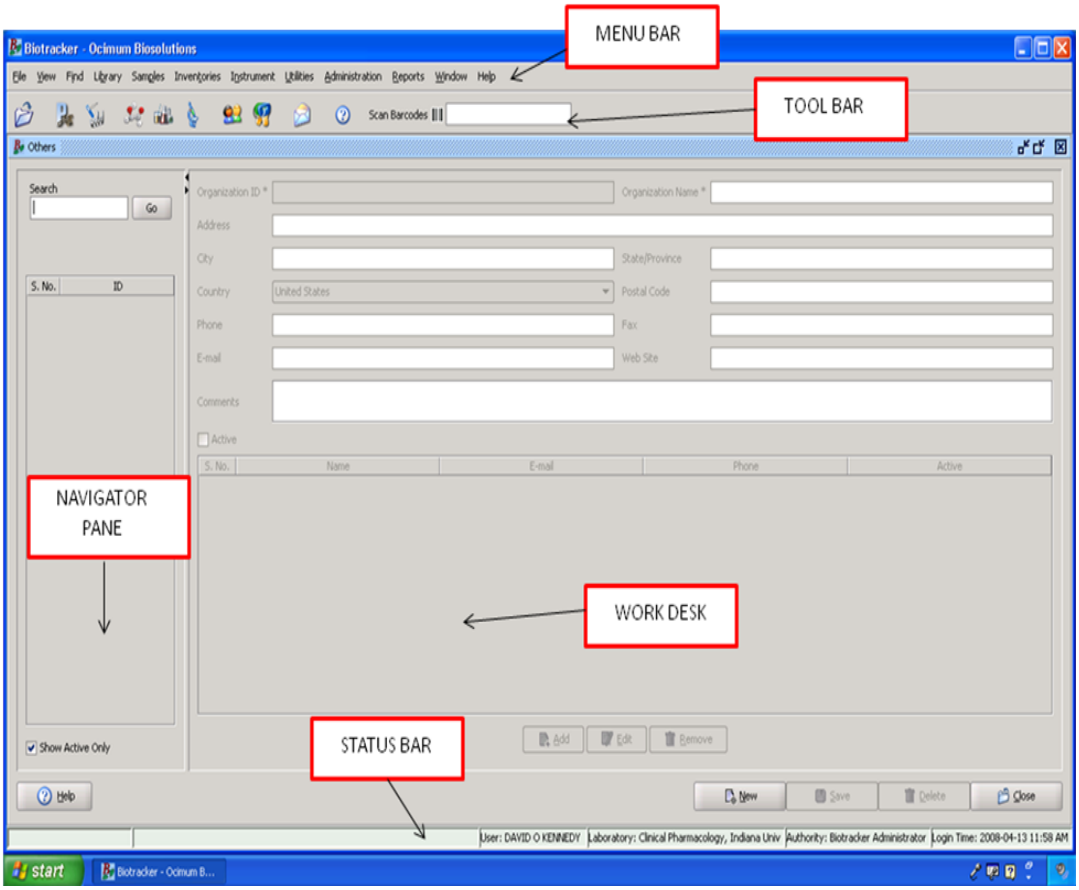


Figure 4: Biotracker window

Through the File menu item, the Administrator set the database connections, since client and server were installed on different machines, as in the window in Figure 5.

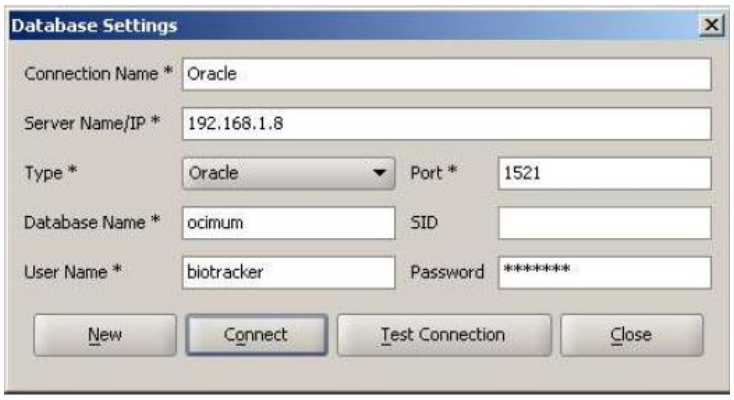


Figure 5: Establishing database settings

3.3.2. System configuration

System configuration was accessed through the File menu as in Figure 6. Configuration involved setting root password, password conditions, precision, and currency, date format, scientific notation for a given range, integration with Google Scholar, entering settings for outgoing (SMTP) mail server and Biotracker email, necessitating authentication from mail server, and selecting mail server requirements.

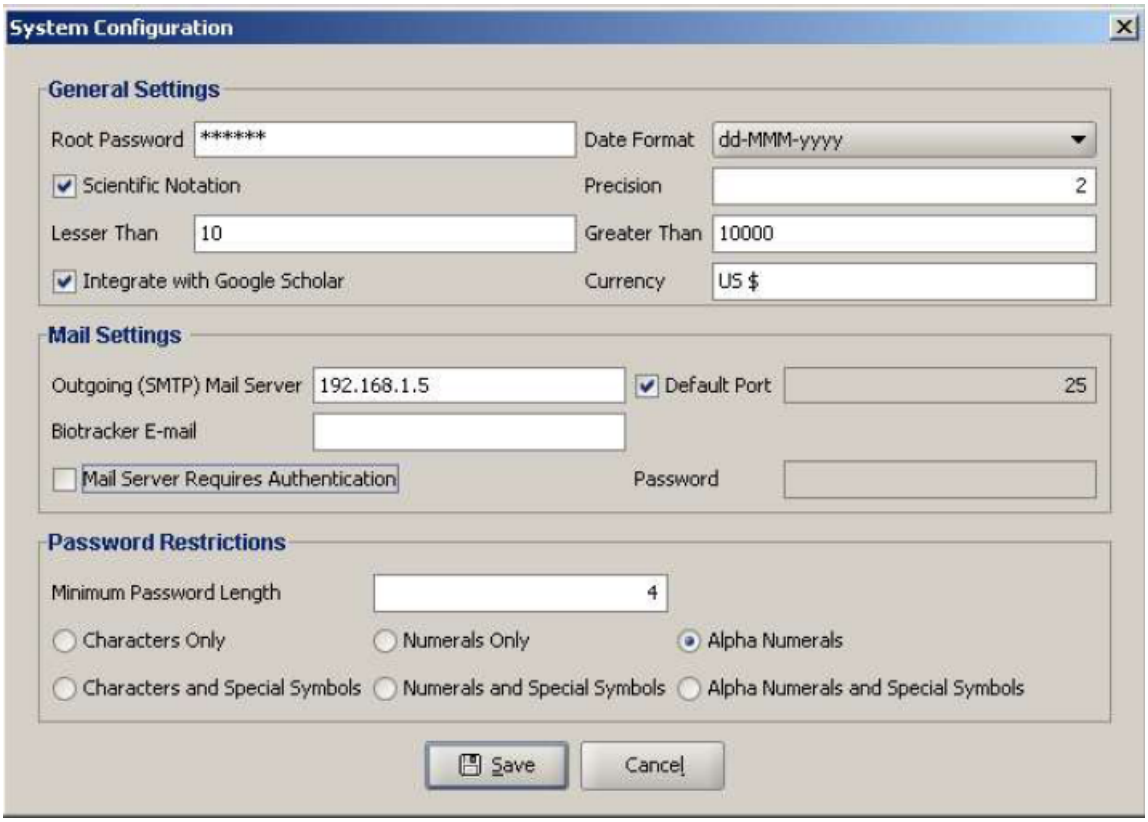


Figure 6: System configuration

Accounts for other users in the laboratory were set up through the Administration module on the menu bar (Figure 7).

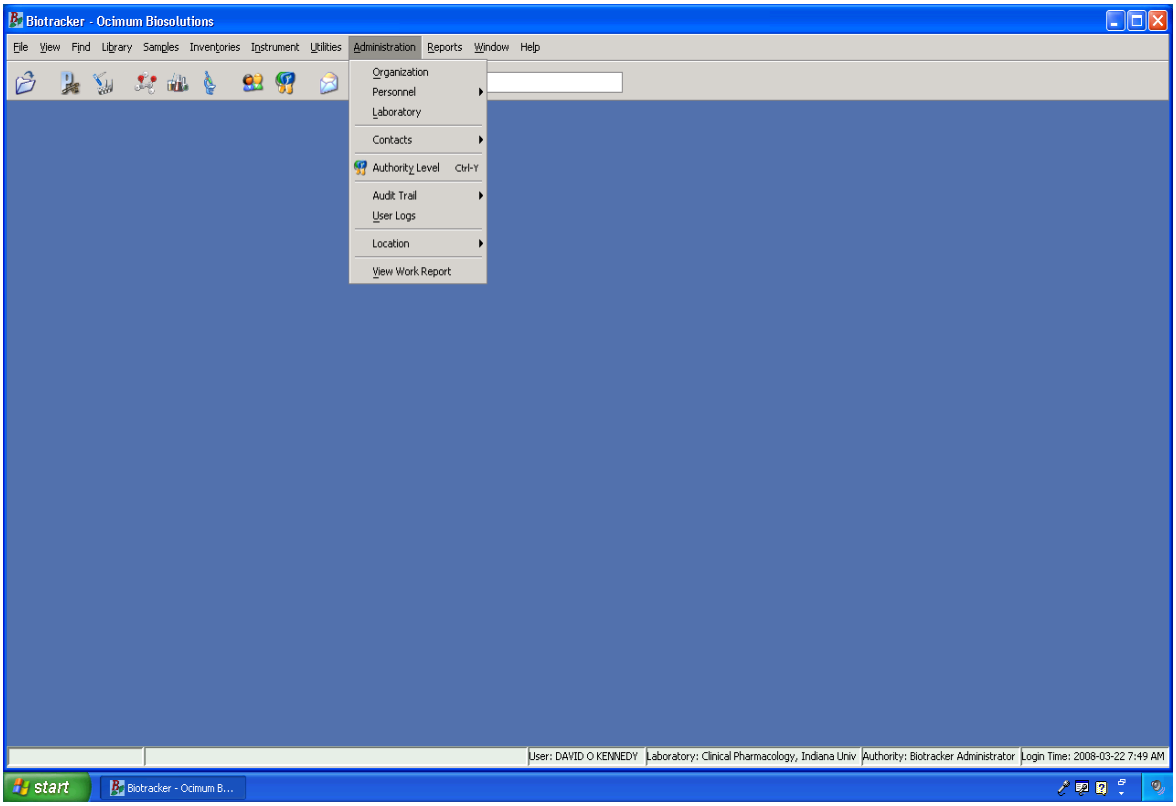


Figure 7: LIMS administration management

3.3.3. Users, laboratories, collaborators, vendor management

Users were created for the Clinical Pharmacology laboratory namely, Professor/Head, Lab Manager, Technicians, and students. An important aspect of Biotracker is that passwords are coupled with assigned laboratories, and together both are needed to login. This allowed the same user to access items in different laboratories. For the genotyping project, three laboratories were set up: Clinical Pharmacology, Laboratory Informatics, and Molecular Biology. Every researcher was assigned to a laboratory.

Authority level has well defined privileges, and each user was assigned levels according to their roles. Vendor and collaboration information included names, addresses, and contacts.

3.3.4. Audit trail and electronic signature

A record of electronic signatures was step up to show the sequence log of activity, various actions taken, the researcher names, time and date, and approval or rejection of data. Actions once performed on the system are logged into a non-editable audit trail. Thus, this module ensures full integrity of data and accountability of user actions (Figure 8).

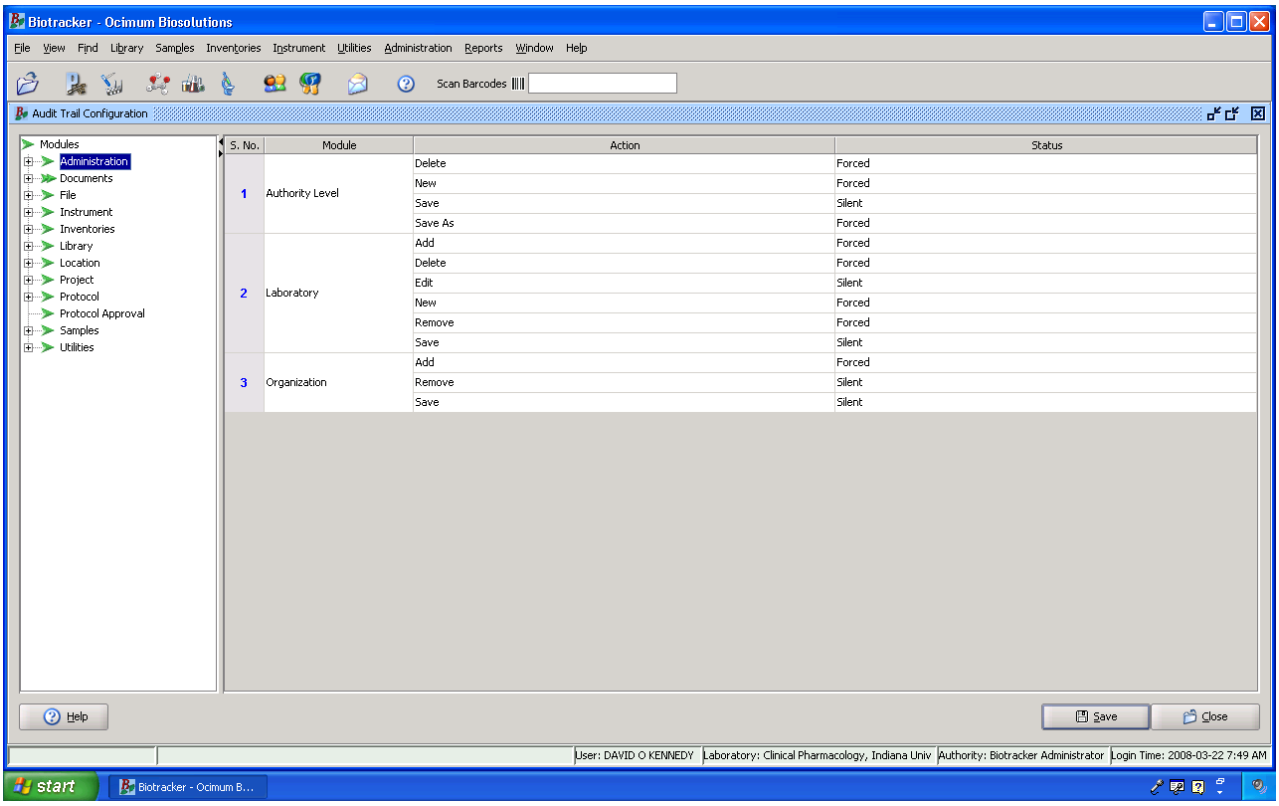


Figure 8: Audit trail configuration

3.3.5. Samples, plates, and inventory management

Types of samples, plates, chemicals, primers, antibodies, and labware according to the manufacturer's instructions for the Tag-It Mutation detection kit for P450 2D6 were set up. This included names, catalogue numbers, prices, volumes or weight of reagents, consumables, and equipments. Access to these items was through the menu bar or the tool bar icons. Inventory Management was used to keep track of chemicals, instruments, glassware, stock solutions and materials in all laboratories (Figure 9). The key features of this utility allowed researchers to catalog various inventory items, provide pertinent information about vendor location, and purchase orders. At this time, automatically updating stocks when they are used in an experiment was also set up. Barcode management allowed barcodes to be set up and used for inventorying (Figure 10). Plate tracking functionality was used to create 96 or 384 well plates. The 96-well plates were later associated to experiments and runs.

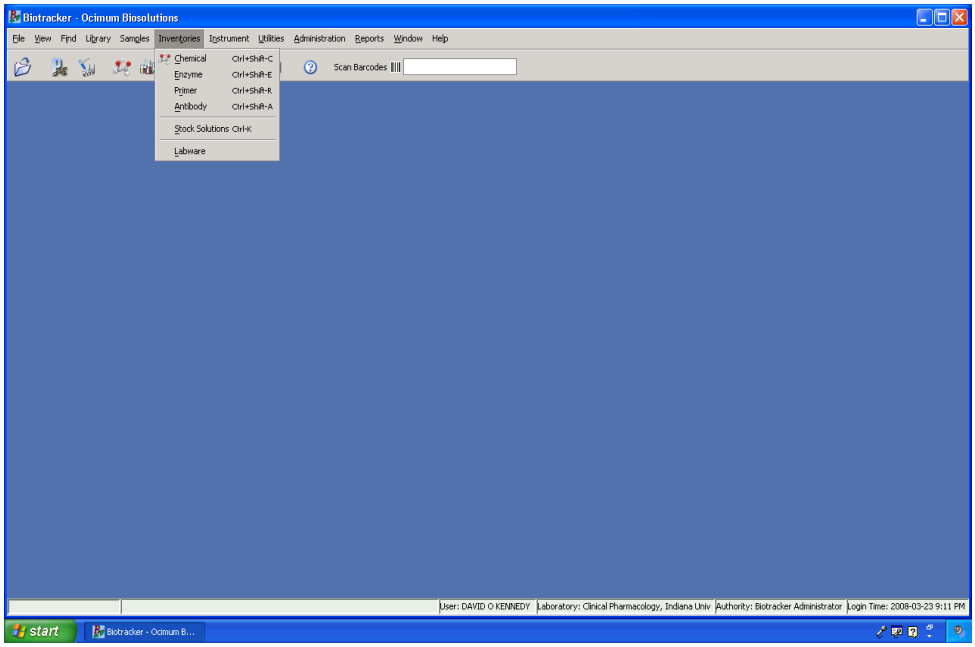


Figure 9: Inventory management

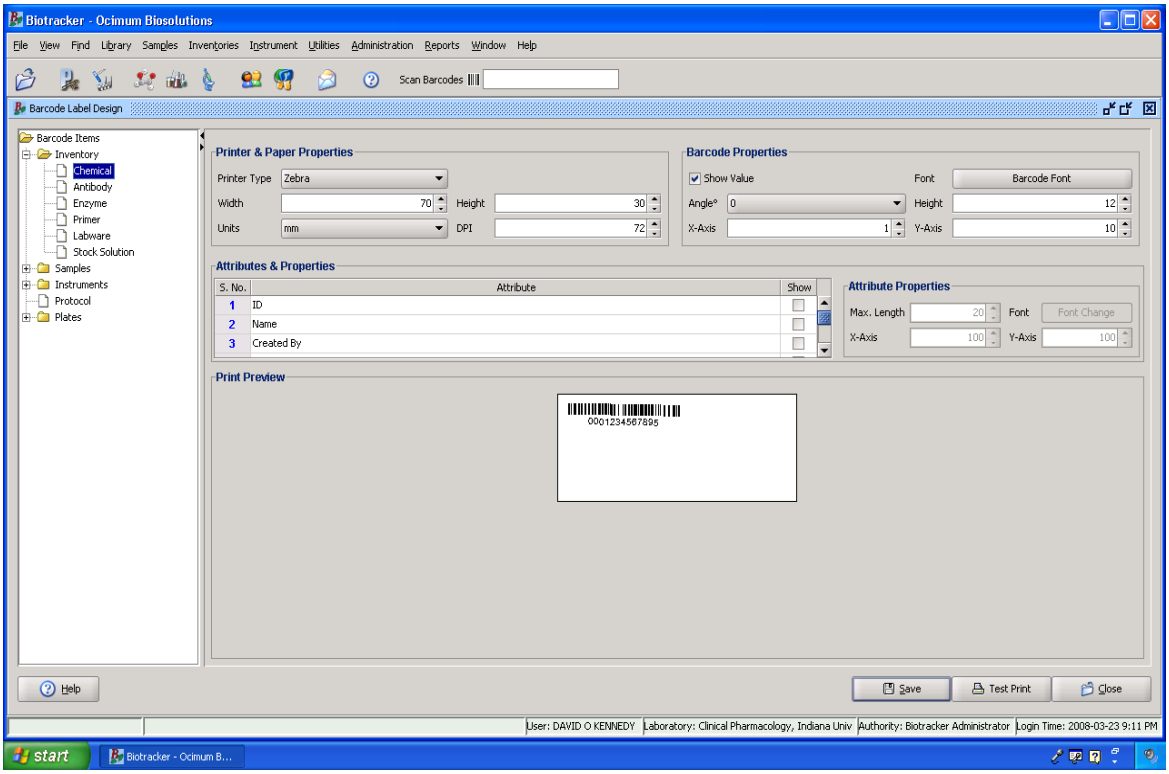


Figure 10: Barcode design management

3.3.6. Units management

Different units of scientific measurements such as weight, volume, and concentration, were created for subsequent use through the Utilities menu.

3.3.7. Experiment and protocol management

From the Library menu, Experiment template was selected and used to create all the experiments according to the manufacturer's instruction for the Tag-It mutation detection assay. The same was done for protocols, which were sent for approval after being designed (Figure 11) before use. Protocols created were for DNA extraction, Sample preparation, Multiplex PCR, Amplicon treatment, Multiplex ASPE, Bead

hybridization, Data acquisition, and Data analysis. These were later used in the genotyping process and were archived for later use. Experiments and workflows were defined in templates, which were stored in a library. These were used to set up projects, and could be used for multiple projects. Workflow tab provided a diagrammatic workflow of the project, and protocols and experiments were added to workflows.

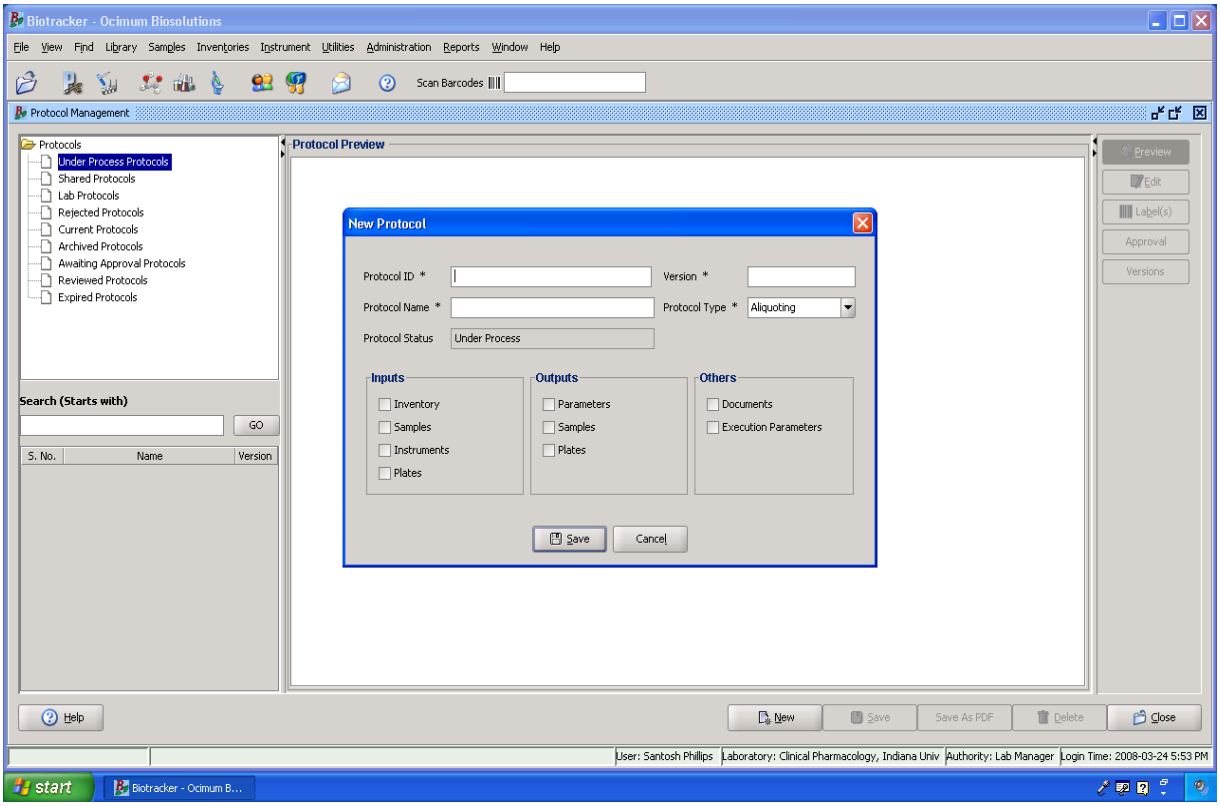


Figure 11: Protocol design

3.3.8. Project management

Project Management module in Biotracker allows a researcher to establish a hierarchical model for project creation. A project in the Biotracker architecture is a combination of experiments in a researcher-defined sequence. Experiments were created earlier with a Tag-It prefix, and stored in a library. Nine experiments were

created from the Tag-It mutation assay steps and used to create the LIMS-genotyping project, namely LIMS_TagIt P450 2D6_SP project. The person in charge of this project was the Lab Manager. A hierarchical system of workflow was created from a library set up with protocols and experiments. This system leads to easy resource appraisals and result validations. Also, researchers get a composite picture of required resources, expected outputs and an approximation of costs involved, which can aid the decision-making process. Once a project was created, samples, personnel, instruments, and other resources were linked to it using the workflow feature. Project-related roles for personnel were managed using Role Management. Each role had well defined privileges. The runs, experiments and the project itself were all set up to be reviewed and approved before execution.

3.3.9. Report management

The Report menu item (Figure 12) was accessed to allow the generation of customized reports of personnel, inventories, experiments, protocols, and projects. Several reports were created to show the overall outcome of the LIMS-genotyping project. The report for LIMS-TagIt P450 2D6 project was generated. Reports can be stored as PDF or printed for dissemination immediately after project completion or at a later time.

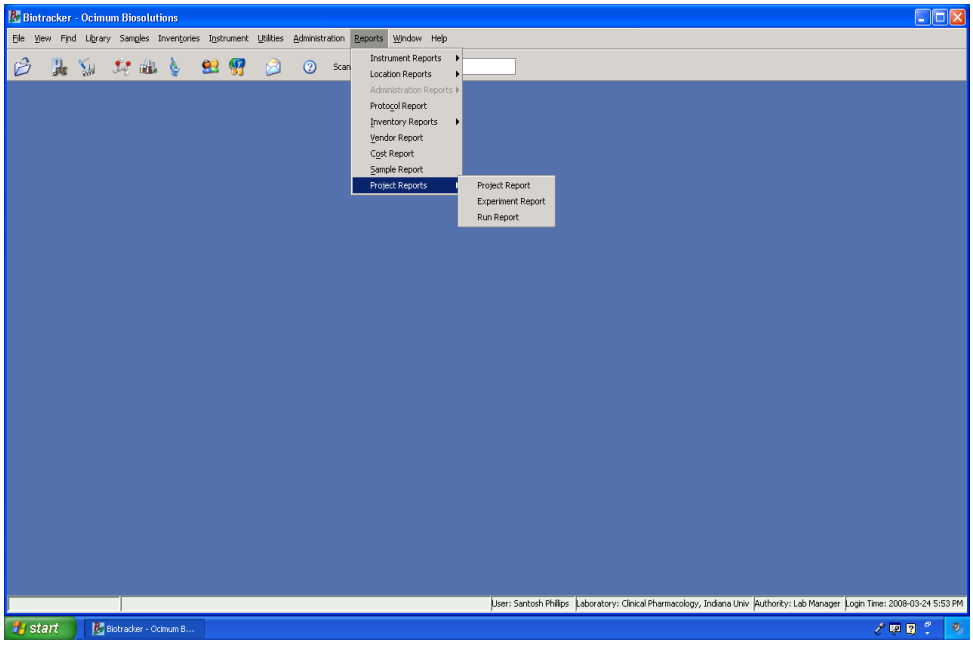


Figure 12: Report management

3.4. LIMS in academia

3.4.1. Research design

Participants in the US were chosen from a list obtained from three scientific journals, namely, Carcinogenesis (Oxford Journals, UK), Science (American Association for the Advancement of Science, Washington, DC, USA), and FASEB journal (Federation of American Societies for Experimental Biology, Maryland, USA). These journals have contributors from a wide variety of research disciplines. A number of participants were selected from Indiana University-Purdue University Indianapolis. The selected participants were contacted by emails and phone. The protocol for this survey was approved by the Institutional Review Board of the Indiana University.

3.4.2. Data collection instruments

The factors that affect the use of LIMS in academia were identified mainly from questionnaires administered to scientists across different disciplines in academic research in the implementation of LIMS in laboratory automation projects. These factors were analyzed in categories relevant to LIMS such as data storage, retrieval, and audit trail, and by subject of research such as sequencing, gene expression, genotyping assays, proteomics, and genomics. The study tool was a questionnaire with two parts, namely, (A) to collect demographic data about researchers, and (B) to ascertain the presence or absence of LIMS in the laboratories after a definition of LIMS had been provided. Factors that affect the usage of LIMS were also investigated. Knowledge of and use of LIMS were also be established.

3.4.3. Demographics

Participants included postdoctoral fellows, technicians and experienced scientists, regardless of age or sex, or region of residence. Scientists from different research disciplines were recruited to eliminate any differences caused by research discipline and use of LIMS.

3.4.4. Analysis of results

Data analysis involved classifying respondents, responses and the items which characterize those responses. After ordering the responses frequencies were generated. Effect sizes and factor analysis were used in developing an index, and regression and Cronbach's alpha (reliability) were used in analyzing the results. ANOVA test was

conducted to test for relationship between variables. Relationships analyzed included use of software technology and actual LIMS use, as well as laboratory experience and subject of research, on LIMS implementation. Respondents were grouped into specific areas of subject of research such as pharmacology, proteomics, genomics, genotyping, and these were correlated with their responses to questions relevant to LIMS use. Attitudes and usage of LIMS, or lack thereof, were analyzed from responses to specific questions administered.

3.5. Project evaluation scheme

The following concerns were addressed to evaluate the project.

1) Was the project smoothly implemented?

2) Did the project meet the overall goal(s)?

3) Did the laboratory personnel see the benefits of the project?

4) Was the outcome worth the use of LIMS?

5) Were the results of the two parts of the project in agreement?

3.6. Expected results

Part 1:

This project was expected to be successful in exposing the benefits of LIMS to researchers in academic laboratories. It was expected that the idea of a central repository for everything to do with the smooth execution of the project would attract scientist to begin to seek to use LIMS in their daily laboratory management.

Part 2:

A large number of scientists were expected to participate in the questionnaire survey. It was expected that the results from this study might shed light on factors that contribute to the 'LIMS-lag' in academia and help software developers meet the challenges of making their products available to academics, which would eventually help academics in making good and informed decisions about conducting research.

CHAPTER FOUR: RESULTS

4.1. General results for LIMS and P450-2D6 genotyping project

In this project a commercially designed LIMS Biotracker was successfully deployed in a genotyping project in a discovery laboratory to achieve the proposed objectives of effectively managing workflow. The project was designed to detect a panel of nucleotide variants found within the highly genetically polymorphic cytochrome P450-2D6 gene, the enzyme product of which is involved in the oxidative metabolism of more than 100 clinically relevant drugs. Biotracker LIMS was used to chart the course of the entire project, and also to manage and track samples, reagents, and inventories such as chemicals, primers, labware, and stock solutions. The work flow component of the LIMS provided a palette containing various user created components to create a work flow linking all the steps of the genotyping process. Personnel and laboratory information, as well as vendor and collaboration information were also managed, as well as secured access into the LIMS by all users.

4.1.1. LIMS administration and project management results

Seven laboratories were created, namely, Biotracker LIMS Administration (BTR_LIMS_ADMIN), Clinical Pharmacology (CLIN-PHARM), Laboratory Informatics (LAB-INFO), Microbiology, Molecular Biology, QA Department, and Virology (Figure 13). Information created included the address of the laboratory, and associated personnel. Of direct interest to this project was the Clinical Pharmacology laboratory, where eight (8) users were created under the category of LIMS administrator,

professor/head of department, lab manager, technician, and student. Information added to user profiles included names, authority level, email addresses, and expiry date in the laboratory. This ensured a centralized repository for personnel information. Only users having the required privilege could access this information in LIMS. Also, any information in LIMS could be accessed from a remote location, one of the great benefits of LIMS.

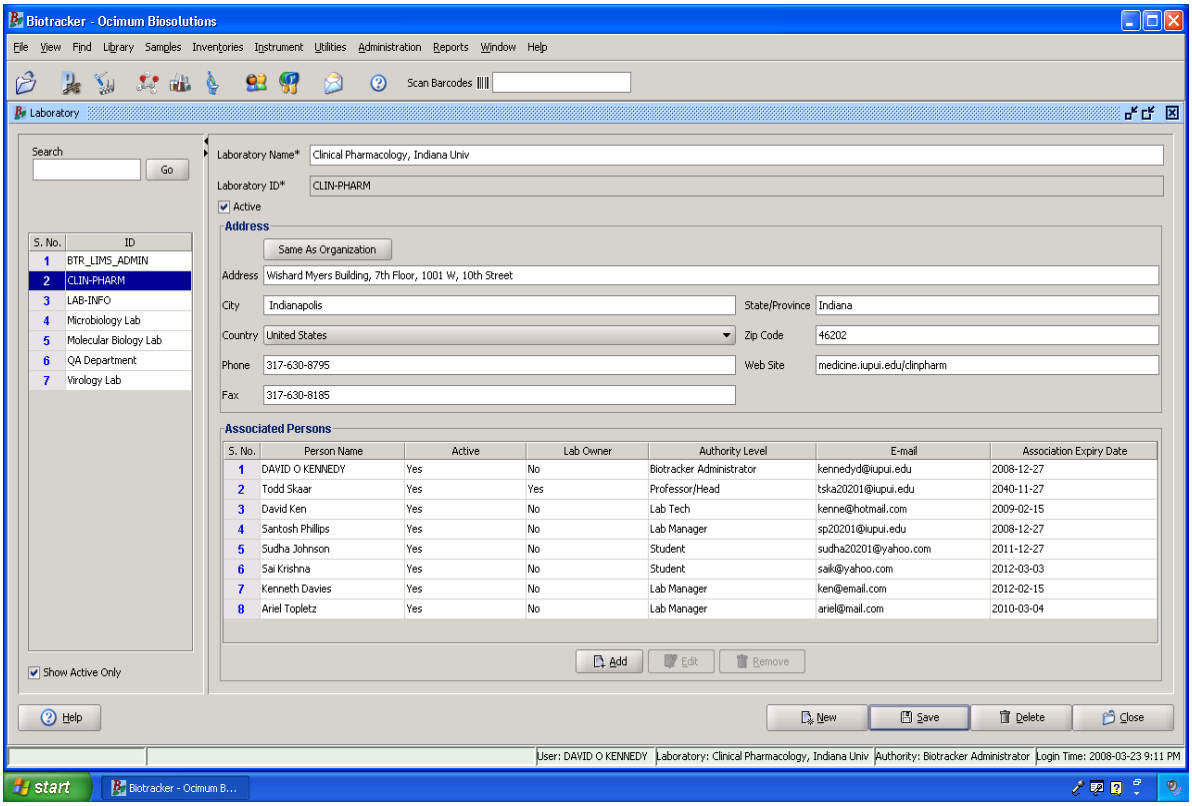


Figure 13: Laboratory management

From the Administration menu information about personnel was created (Figure 14). This included general information, personal information, associated laboratory, images and skills.

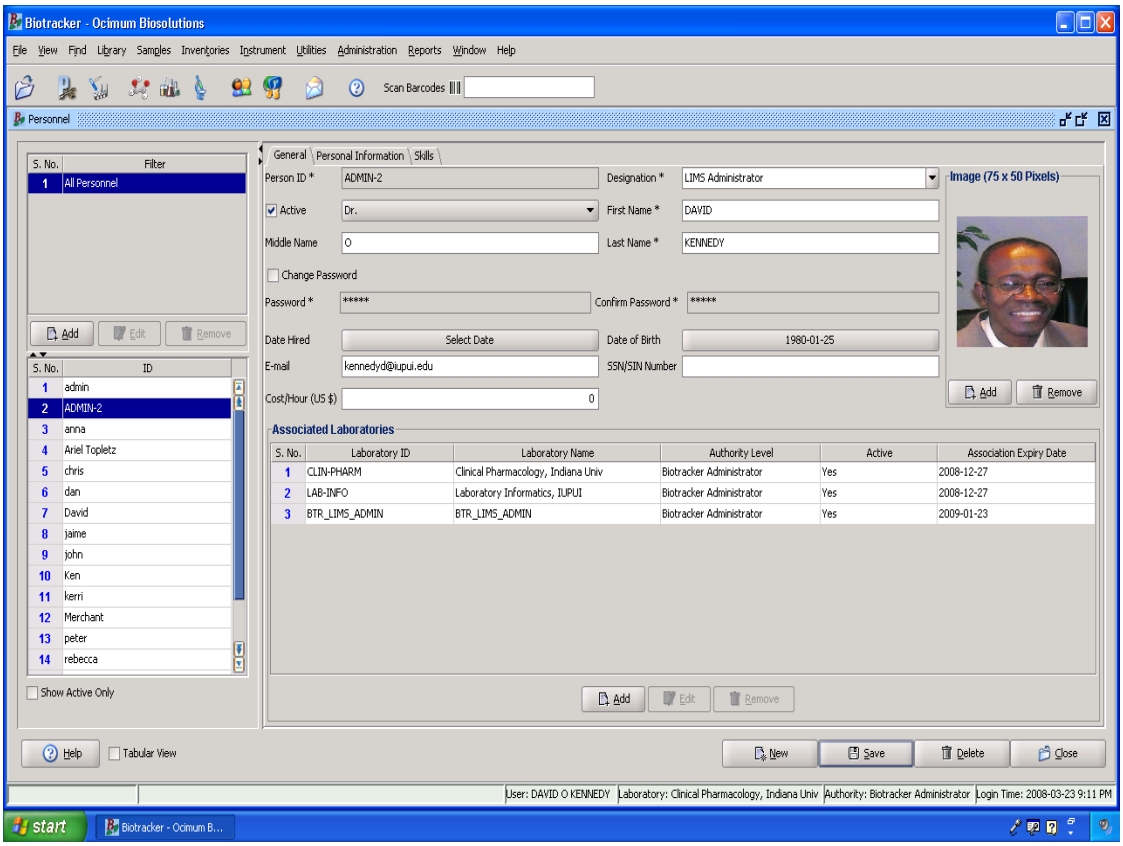


Figure 14: Personnel management

Authority levels were created for all the personnel in the laboratory. In Figure 15 below, the Professor/head designation had access to every aspect of LIMS, except a few configuration system procedures limited to the LIMS administrator. Authority level assignment included ability to view, delete, save, approve, reject, add, or remove a document. Authority level assignment is crucial in the execution of duties or getting

access to any part of the LIMS. This also played a role in LIMS security besides passwords.

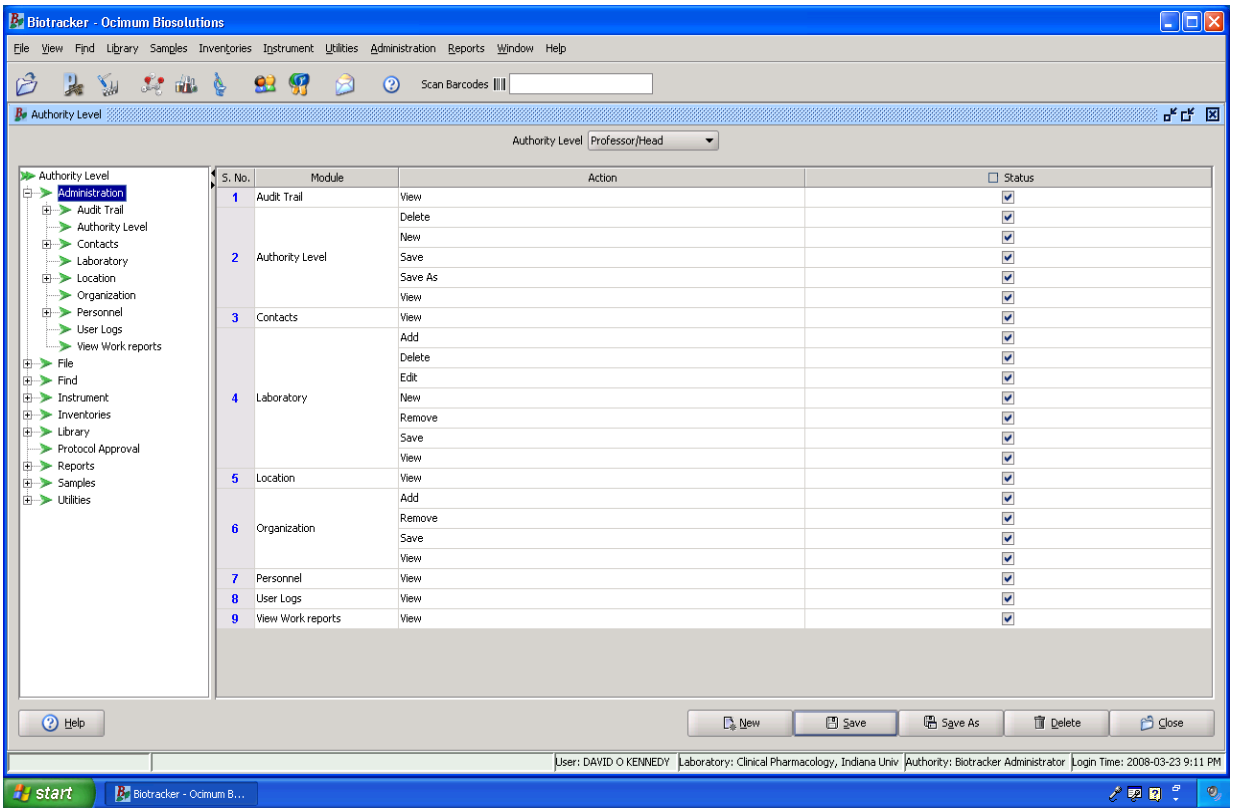


Figure 15: Authority level setup

Most projects are carried out with other institutions. In Biotracker, information about all collaborations was centralized. This included the address and names of members for Johns Hopkins University, Riley Children's Hospital and the School of Informatics, Indiana University (Figure 16), with whom the laboratory had collaborations.

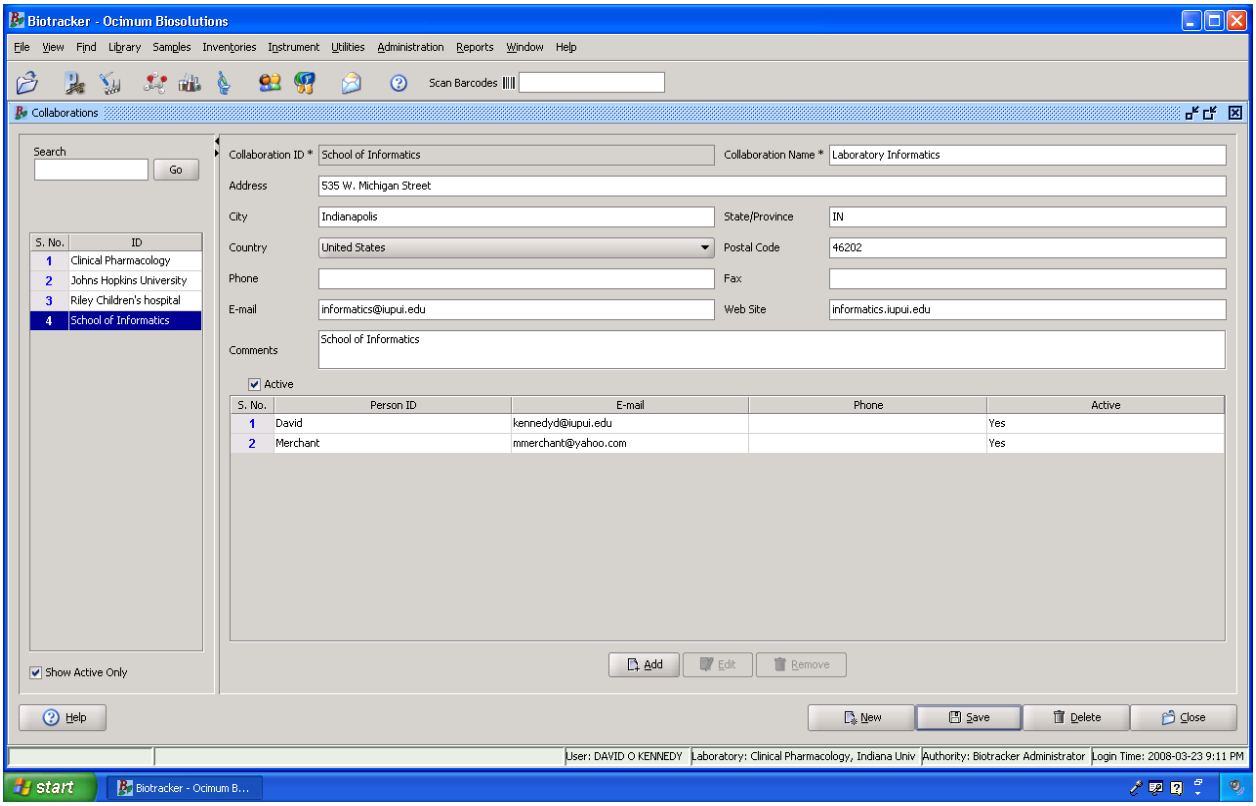


Figure 16: Collaboration management

Most often information about manufacturers and vendors is hidden in large catalogues or online, and much time is lost in searching for information, as well as the products they supply. In Biotracker, all information about vendors associated with the laboratory or the genotyping project was created and stored in LIMS (Figure 17). This provided a quick and easy access to information at any time. A very useful aspect of the vendor information is that all supplies obtained from the vendor including catalogue number and names of contact persons and their contact information were also included. Vendor names appear in the navigation bar and detailed information can be displayed in the work area. Vendors associated with the genotype study were linked to the assay catalogue, where the kit manufacturer had suggested which vendors had the appropriate equipments

and consumables. Detailed information about the particular vendor was then obtained online and then inserted into LIMS. Even though this took some time, it took a one time effort to assemble all the information into a central repository. Manufacturers and vendors included Millipore, Qiagen, Beckman, Corning, and Roche Diagnostics.

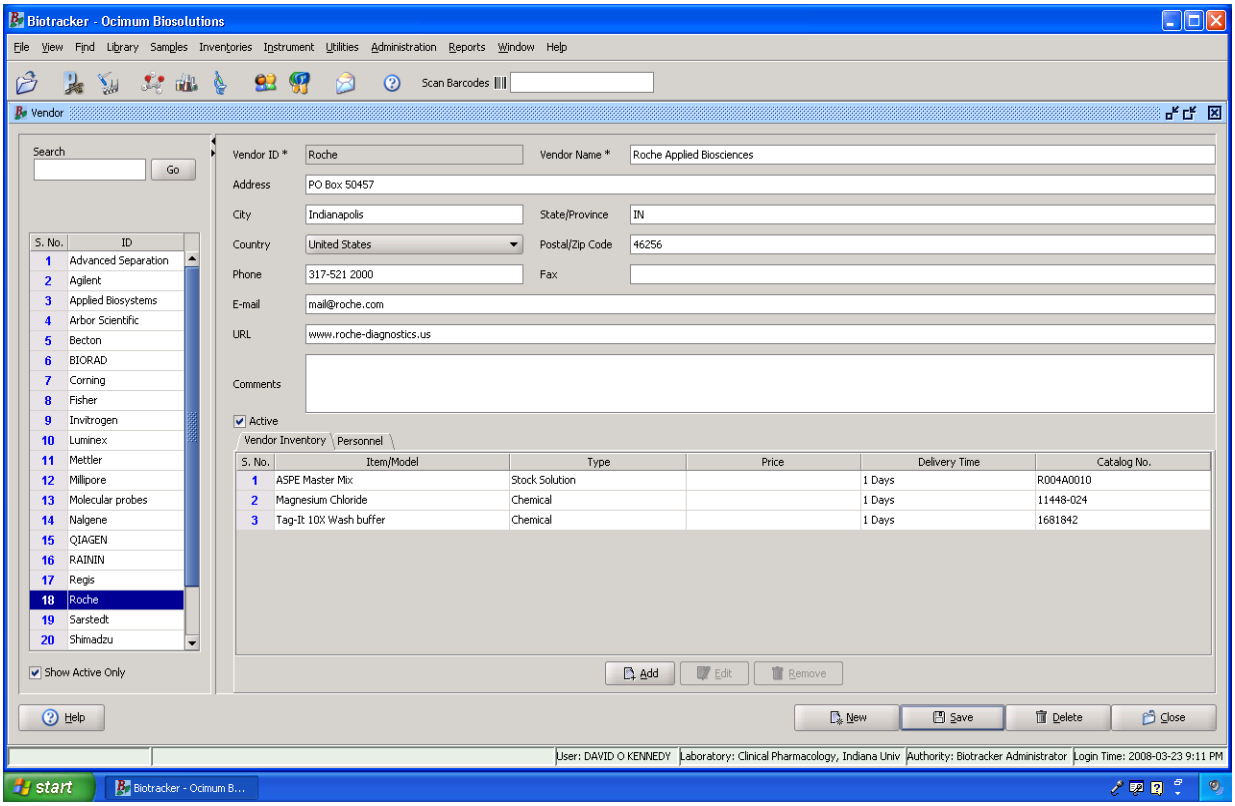


Figure 17: Vendor information management

Locating samples and inventories in any laboratory can be a challenging task. However, Biotracker reduces this time in a very efficient way. Different types of locations were created for the Clinical Pharmacology laboratory (Figure 18). This was based on conditions in the laboratory, and included freezers, refrigerators, cabinets, rooms, and workbenches. Shelves, racks, and boxes were also created. This provided for the minutest

detail of the location of reagents, stock solution, samples, instruments, and labware. Locations were created for chemicals, stock solutions, labware, instruments, primers, and antibodies. Access to locations was also restricted to personnel in a particular laboratory. In the locations window, all other users had security locks on such locations, and could not have access in the folder. The locations window also shows the contents of the location. Items could be searched for in LIMS by name or barcode, and this will lead directly to their location.

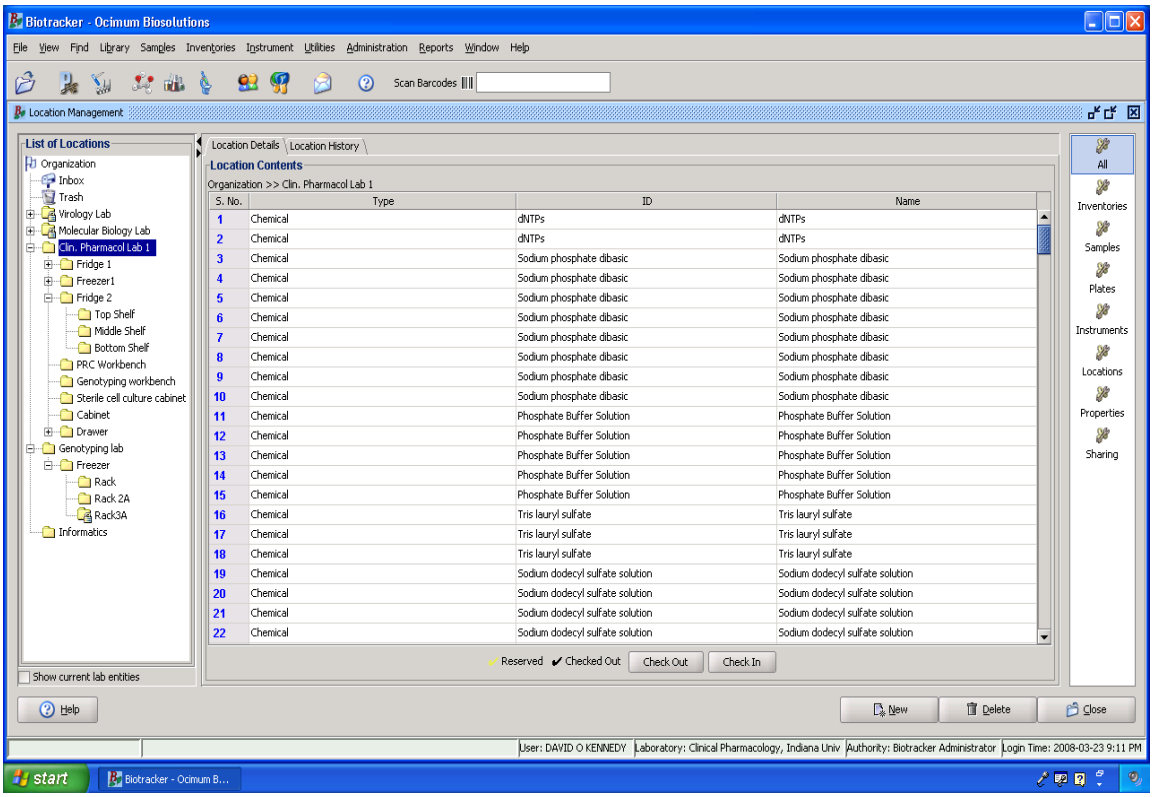


Figure 18: Location management

Figure 19 shows the details of a box created for DNA samples in the laboratory on a rack in a freezer in the Clinical Pharmacology Laboratory room 1.

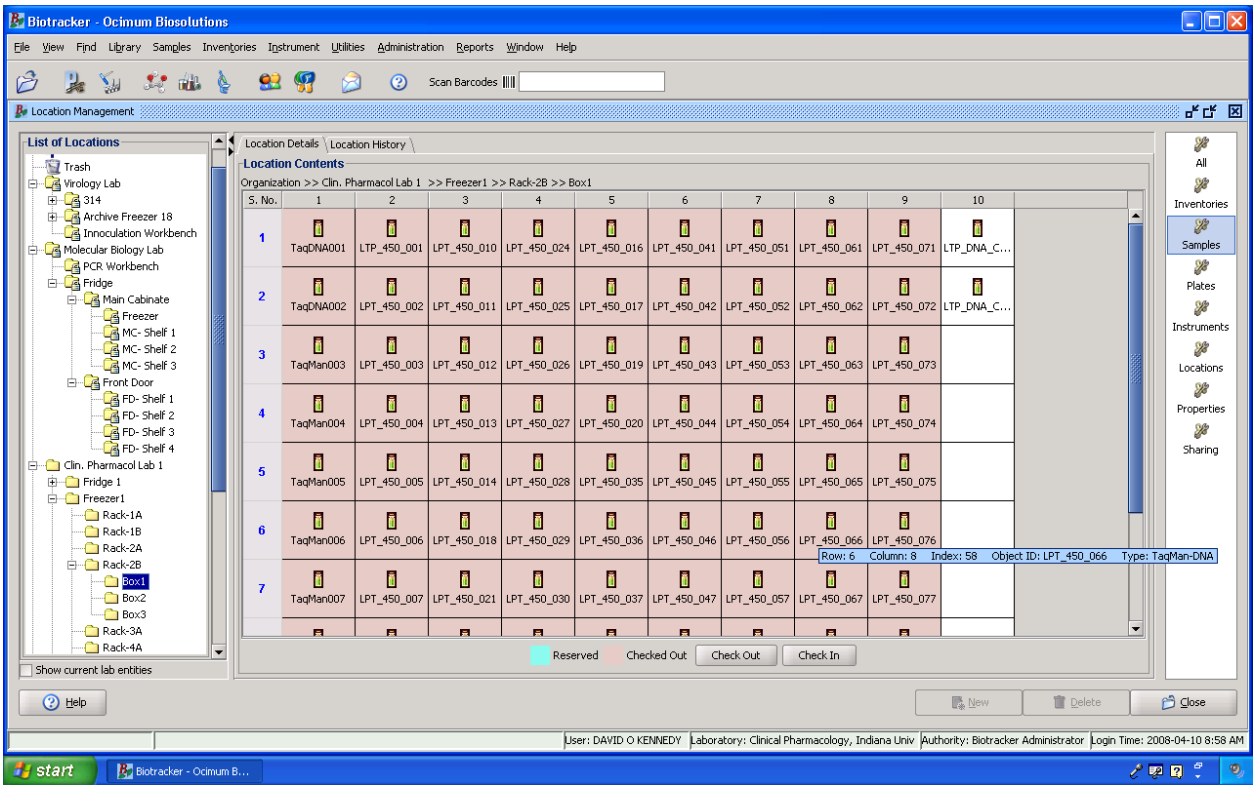


Figure 19: Details of box contents

Details of all chemicals for the project as well as others in the laboratory were all created through the Inventory menu item. The Inventory menu consists of chemicals, primers, antibodies, stock solution, and labware. For instance, clicking on Glycerol in the navigation pane brings up all details in the work station window. Information created included number of containers, physical and chemical properties, storage conditions, vendor, structure (if a compound), material safety data sheets (MSDS), and usage (Figure

20). MSDS information is not readily available in a conventional laboratory and one has to search for such information. However, this can be readily accessed in LIMS.

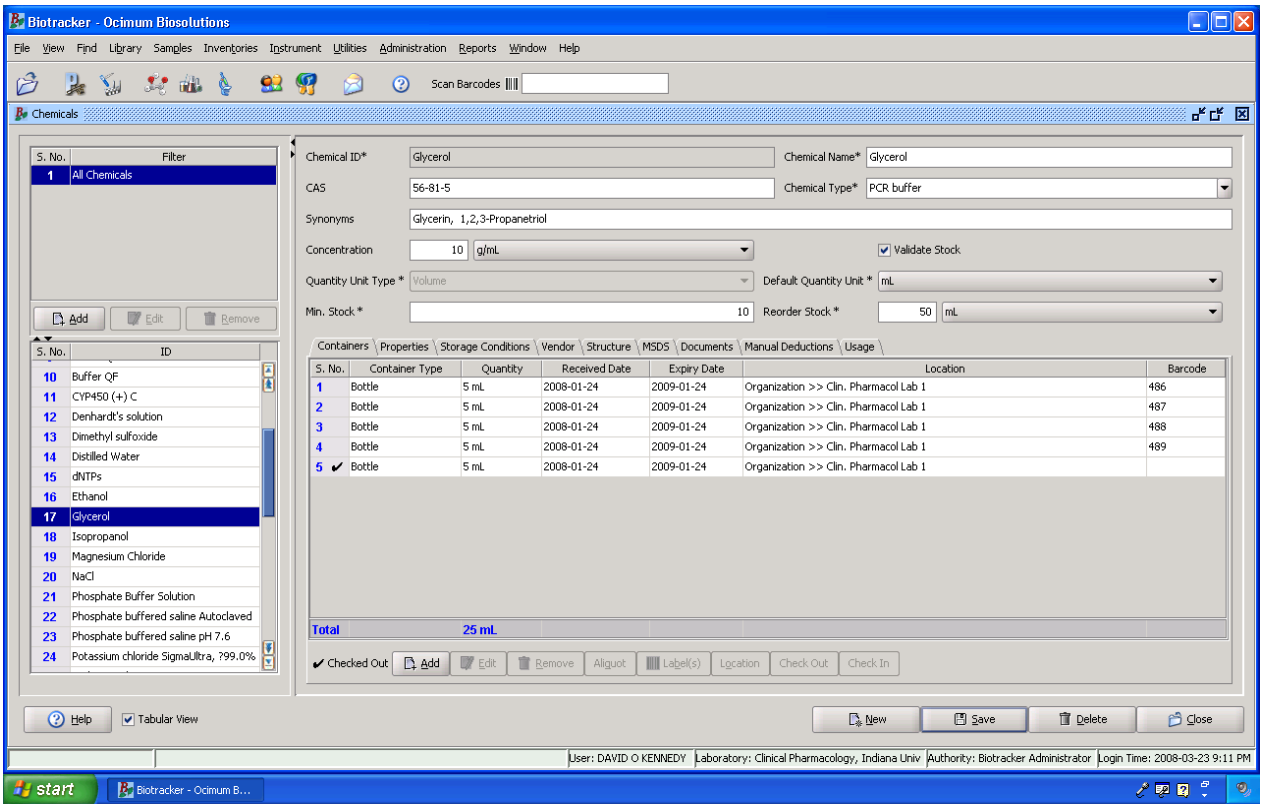


Figure 20: Chemicals management

Information on stock solution preparation was input through the Inventory and Stock Solution menu. Figure 21 shows the preparation of a stock solution of Streptavidin, R-Phycoerythrin (SA-PE) conjugate. This allows anyone in the future who wants to prepare the SA-PE stock solution to have instant access to its constituents and conditions for preparation and storage. Other information created includes number of containers, physical and chemical properties, storage conditions, vendor, MSDS, and usage.

Enabling stock validation ensured that whenever the amount of chemical or other reagents went below a pre-defined level (minimum stock, reorder stock), the item is coded red in the stock overview window.

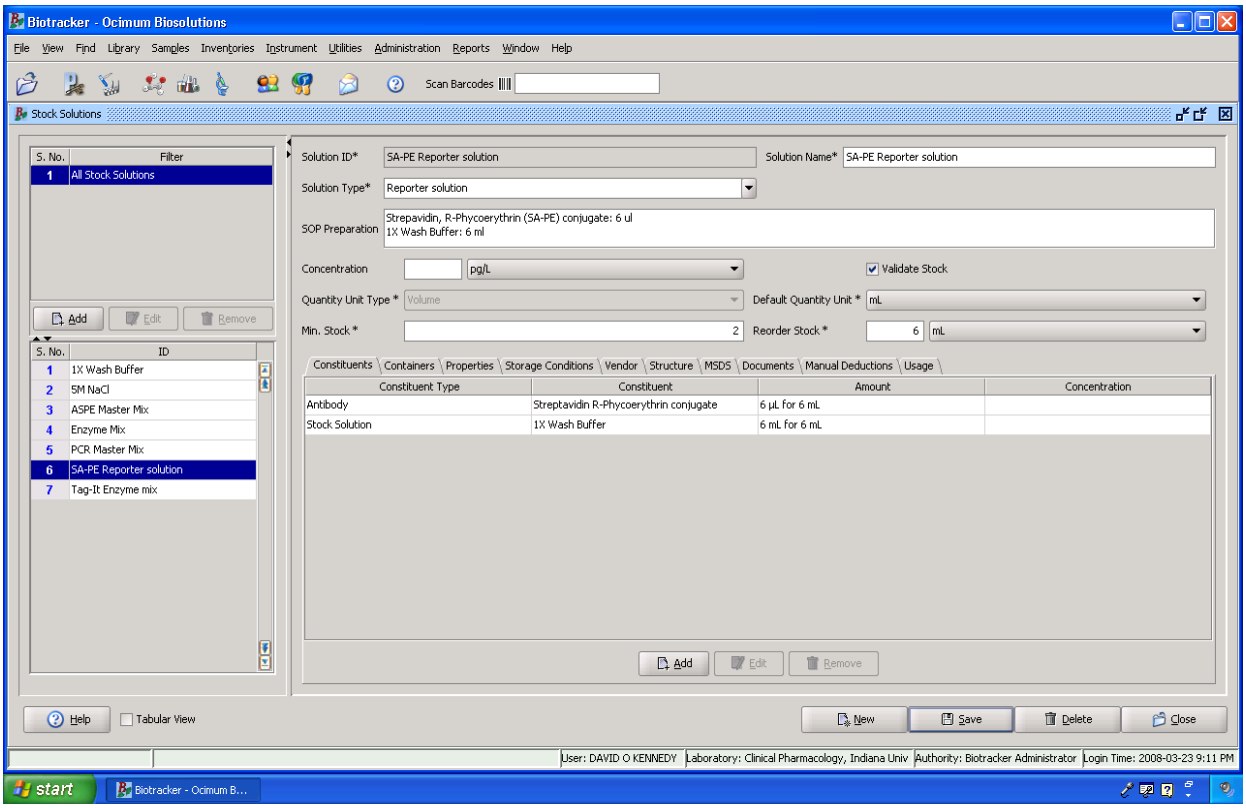


Figure 21: Stock solution management

Information for all primers, including orientation, sequence, complements, complementary sequence, Genebank ID, containers, physical and chemical properties, storage conditions, vendor, MSDS, expiry date, and usage were entered through the Inventory-Primers menu (Figure 22). The validate stock option was enabled to ensure that whenever the amount of primer went below a pre-defined level (minimum stock,

reorder stock) the item is coded red in the stock overview window, and ready for re-stocking.

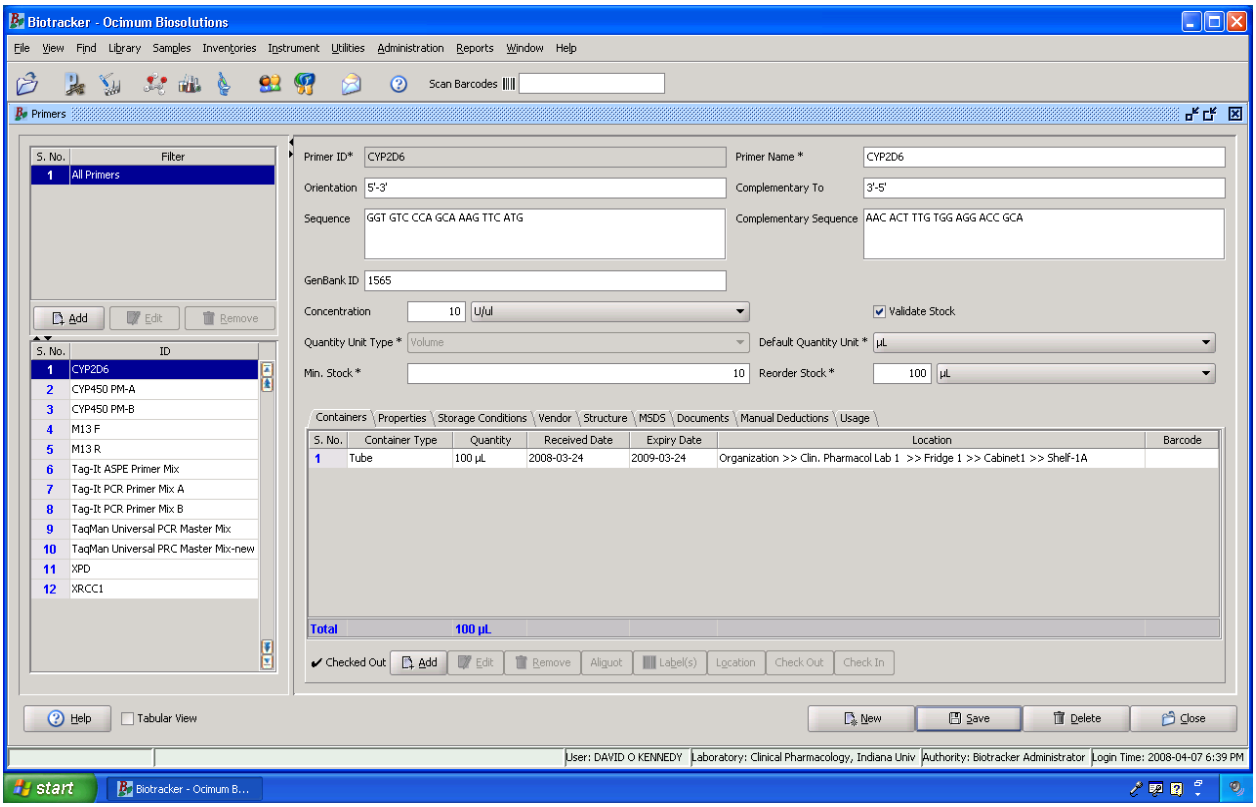


Figure 22: Primers information management

Information for all labware for the project as well as others in the laboratory was stored in Biotracker (Figure 23).

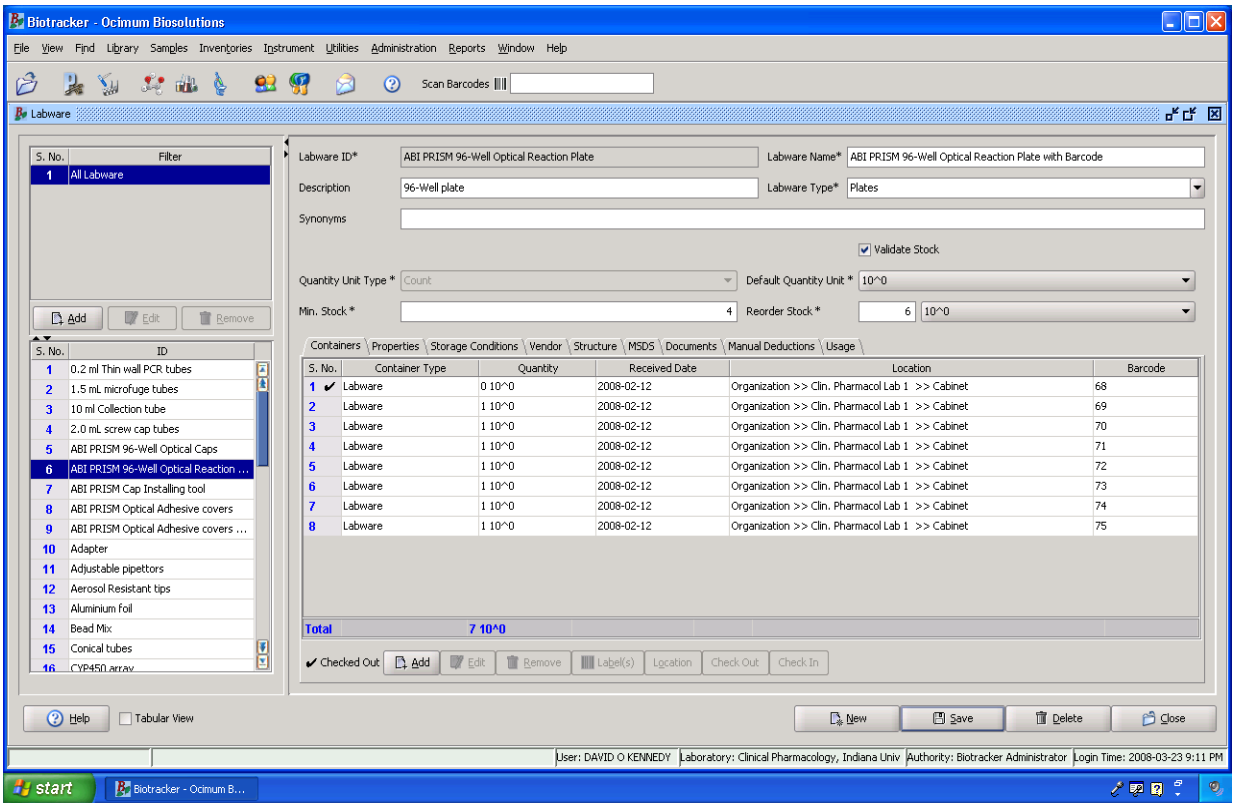


Figure 23: Labware management

This included information about vendors, location, quantity, received date and barcode. The validate stock option was again enabled to ensure that whenever the amount of labware went below a pre-defined level (minimum stock, reorder stock), the item is coded red in the stock overview window. Labware used included 0.2 mL thin wall polypropylene tubes for PCR, 0.5 mL polypropylene microcentrifuge tubes, 1.5 mL polypropylene microcentrifuge tubes, 25 mL pipettes, 50 mL polypropylene conical

tubes, thin-wall polycarbonate 96-well plates, Seal and Sample Aluminum Foil Lids, borosilicate glass tubes (5 or 10 mL), Microseal, and parafilm.

Several sample types were created to identify the various products at the end of each experimental run (Figure 24). Some of these samples were stored overnight and the reactions continued the next day. Therefore, it was necessary to place them in a location for easy access at a later date. Sample types created were whole blood, DNA, end-products from the multiplex PCR, amplicon treatment, multiplex ASPE and bead hybridization steps. These products could be stored at 2 to 8 ^{o}C until ready to use, for a maximum of 48 hours. Information on storage conditions was input as well.

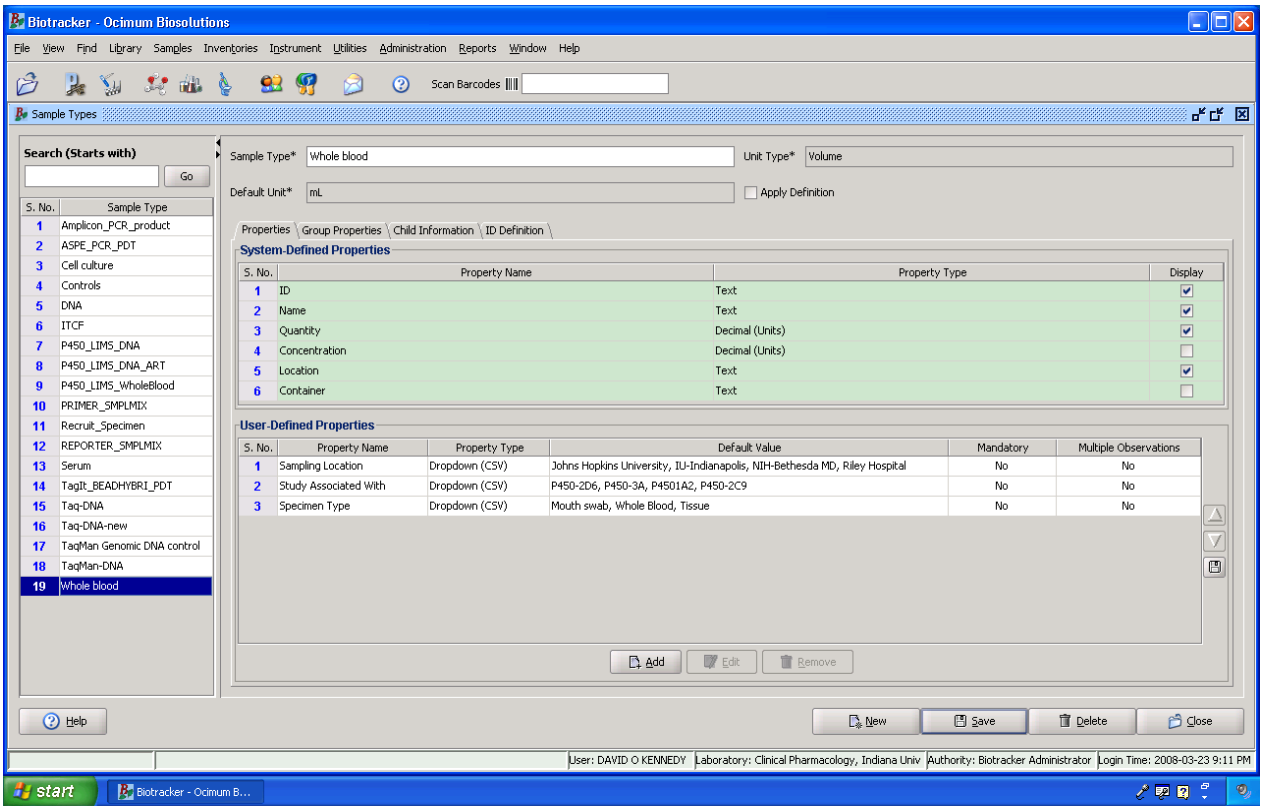


Figure 24: Experiment sample type management

Information for instruments for the project as well as others in the laboratory was stored in LIMS. This included information about manufacturer, purchase date, warranty dates, person-in-charge, vendors, location, quantity, received date and barcode. Also, information about maintenance, validation, contracts, usage and location were stored (Figure 25).

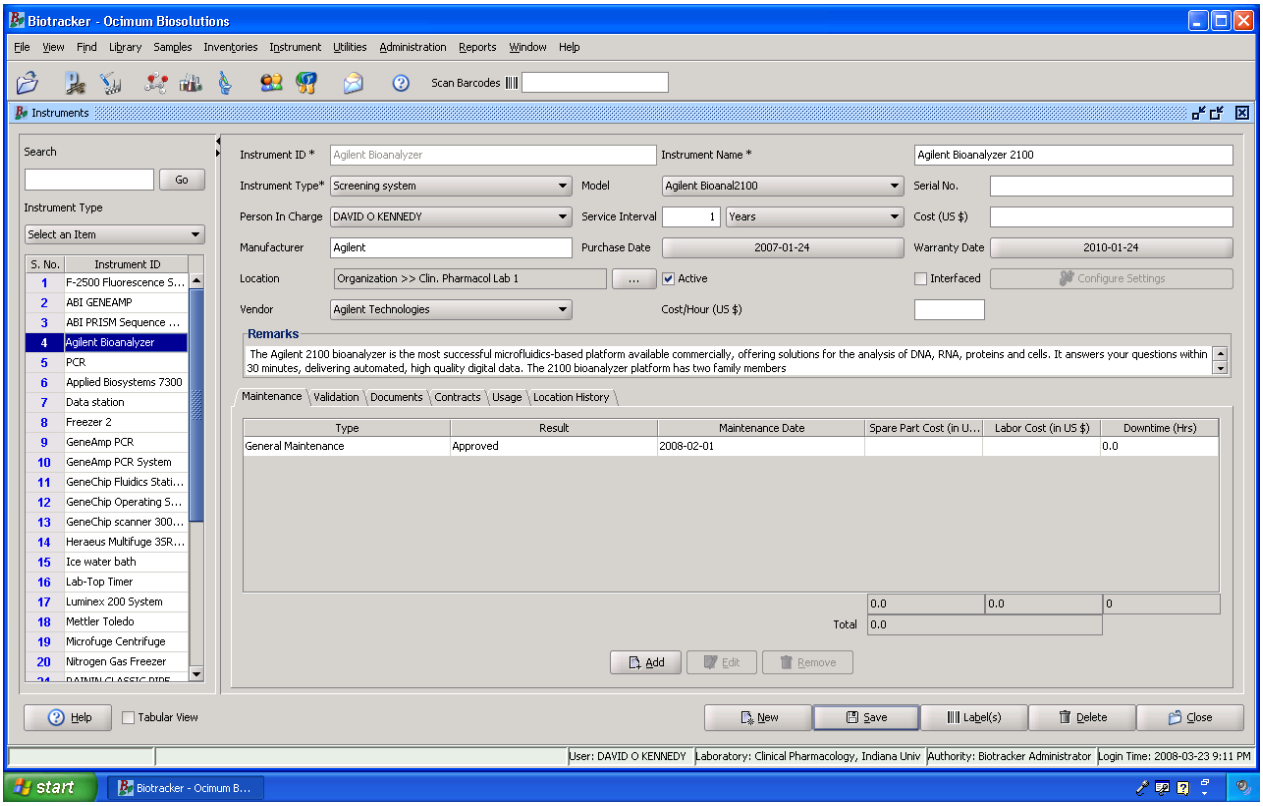


Figure 25: Instrument management

Several protocols were prepared based on the protocols supplied with the Tag-It mutation detection kit for P450 2D6. This was a 12-page manual with 6 different experimental steps. The experimental steps were revised and protocols were generated. This enabled protocols to be used at various steps of the workflow. Since these were stored in LIMS,

they could be viewed on the computer or printed many times for use. Another advantage is the fact that modifications could be made easily at anytime by anyone who is given access to the protocol. Privileges are given for accessing protocols, ensuring proprietary rights at any time. Incomplete protocols are stored as 'under process protocols', laboratory specific protocols are stored as 'Lab protocols', and only personnel from that laboratory can view or use them. Information on any protocol includes name, valid dates, source, and steps for execution. Figure 26 shows an approved laboratory-specific protocol for the Tag-It sample preparation step.

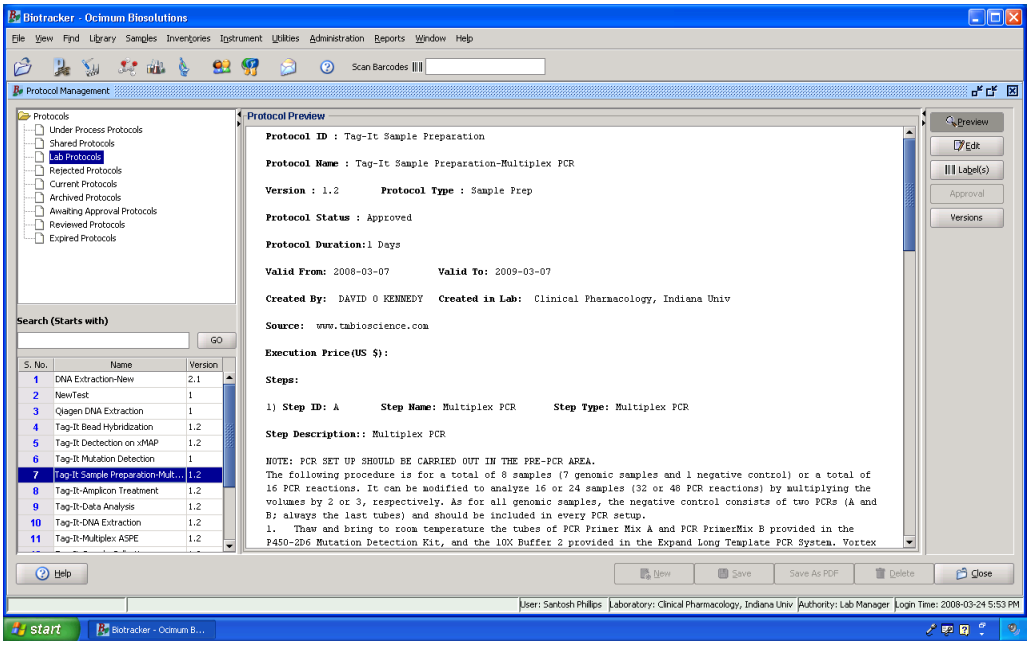


Figure 26: Protocol management

Among the protocols generated were

(1) Tag-It DNA Extraction for DNA extraction based on directions from Qiagen

(2) Tag-It Sample Preparation Multiplex PCR for preparing the PCR primer products

(3) Tag-It Amplicon treatment for the amplicon treatment of the PCR primer products

(4) Tag-It Multiplex ASPE for mixing the PCR amplicons with the ASPE primer mix

(5) Tag-It Bead Hybridization for the hybridization of the products from the ASPE step with the bead mix

(6) Tag-It data acquisition with the Luminex 100 xMAP system

(7) Tag-It data analysis with the Tag-It data Analysis software

Whenever changes are made to an existing protocol, a new version is created. The version number of the new protocol is system generated. Protocols were used to set up the experiment templates for the LIMS_TagIt P450 2D6_SP project, and the experiment templates were used to set up the project. Project Management module in Biotracker allows a researcher to establish a hierarchical model for project creation. Through the General window under Project Management (Library menu) details of the project were created (Figure 27). This included person-in-charge, and planned start and end dates.

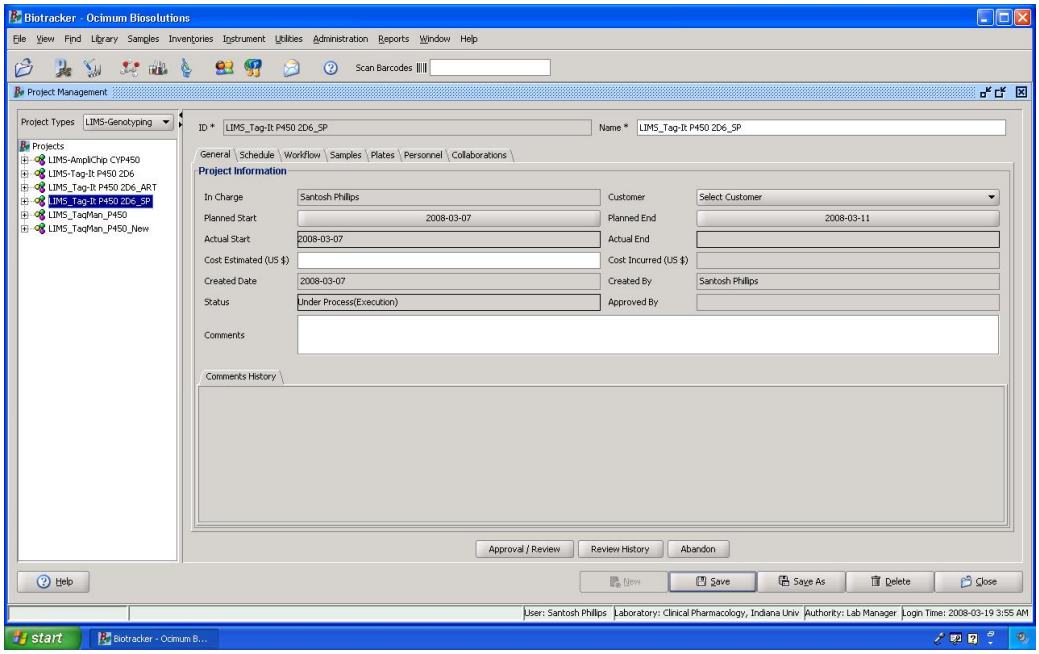


Figure 27: Project setup

Time schedules were set up for the execution of each of the steps of the protocol. This was created as a map (Figure 28) and was linked with a diagrammatic workflow of the project (Figure 29). A hierarchical system of workflow leads to easy resource appraisals and result validations. The researcher gets a composite picture of required resources and expected outputs involved. Once a project has been created, samples, personnel, instruments, and experiments (Figure 30) can be linked to it using the workflow. This can aid the decision-making process.

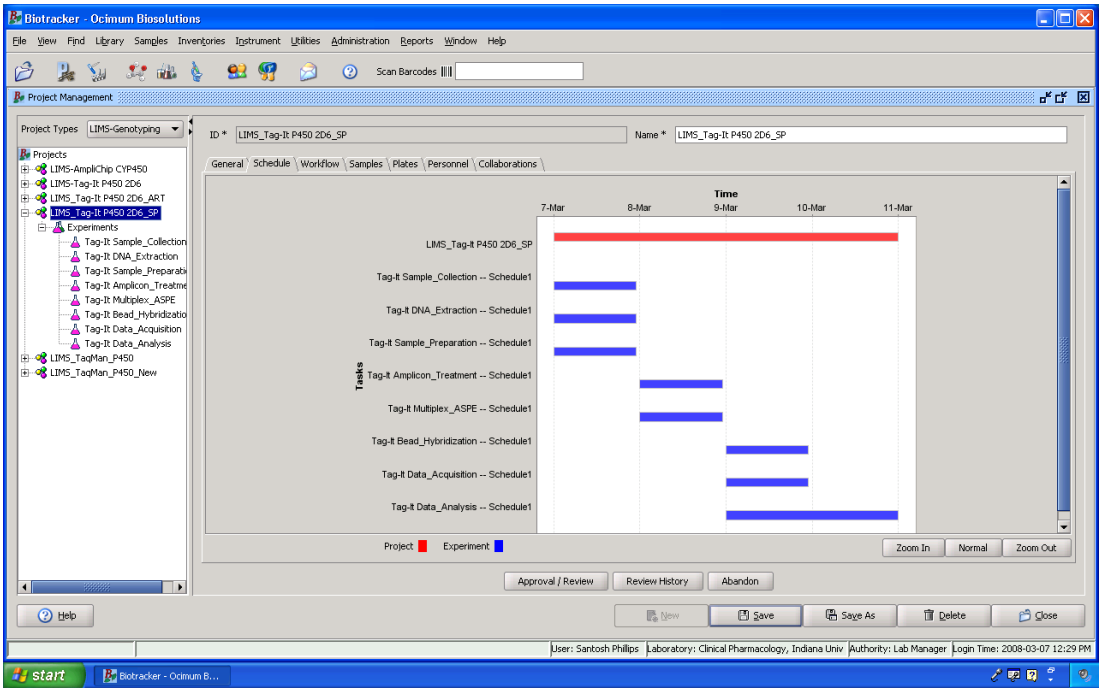


Figure 28: Project schedule management

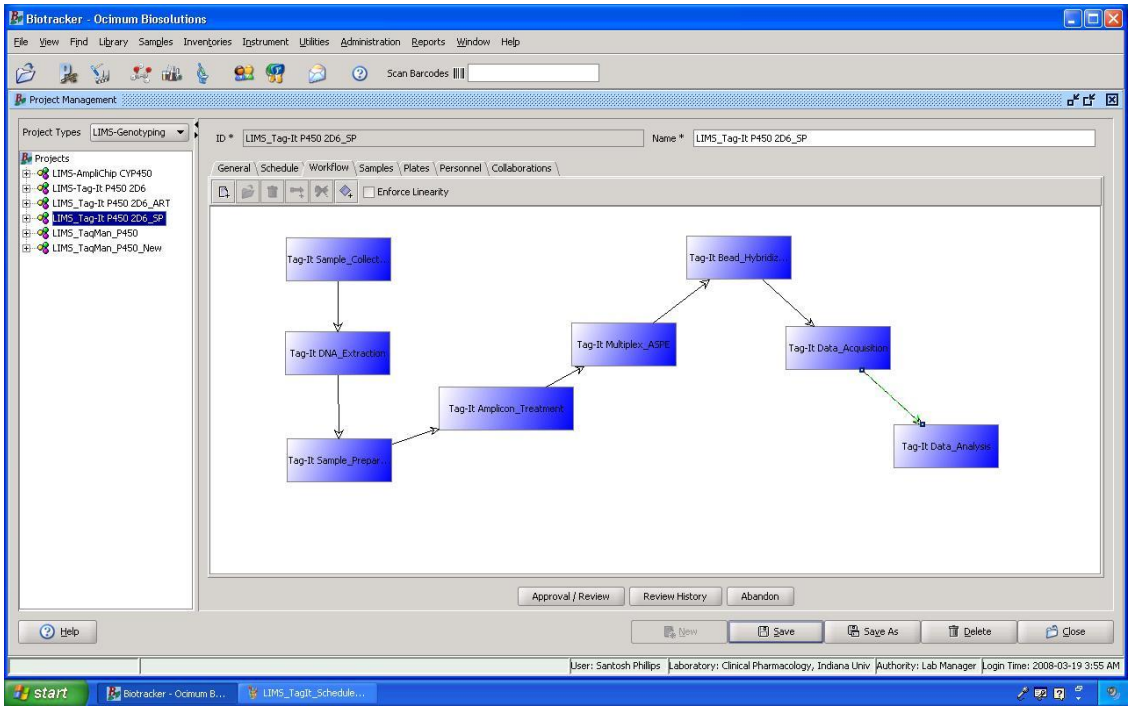


Figure 29: Project workflow

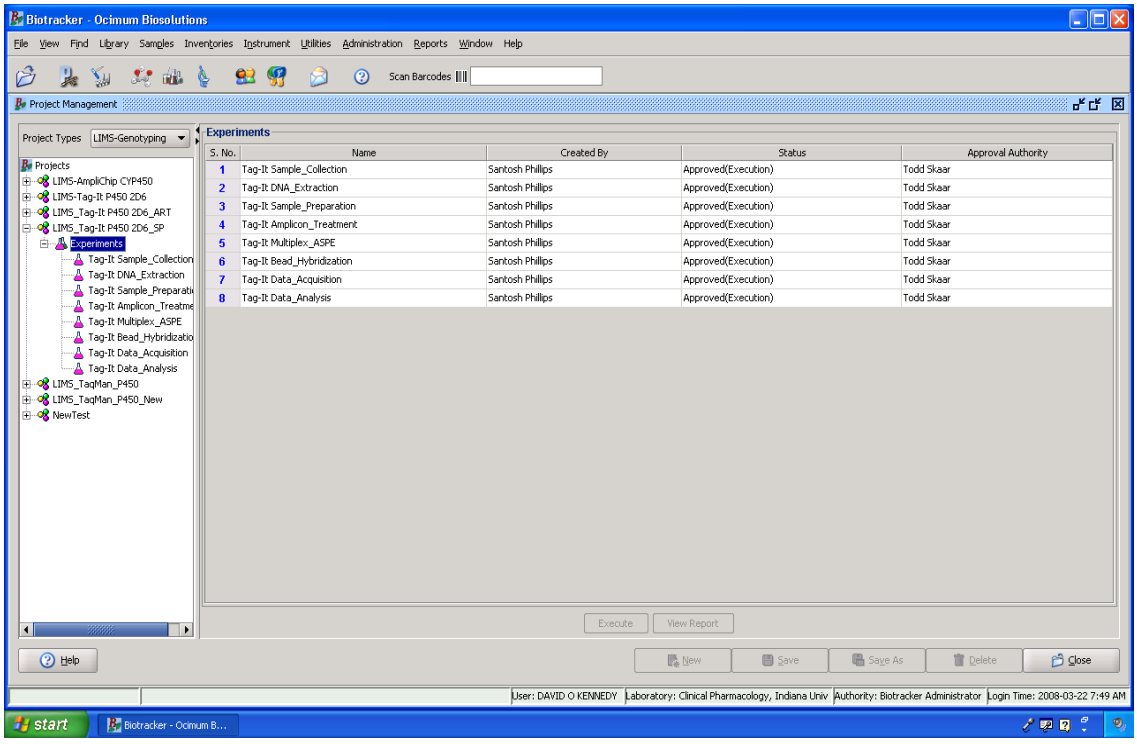


Figure 30: Project experiments

Figure 31 shows the 96-well plate composition from the Tag-It Bead hybridization step just before data acquisition.

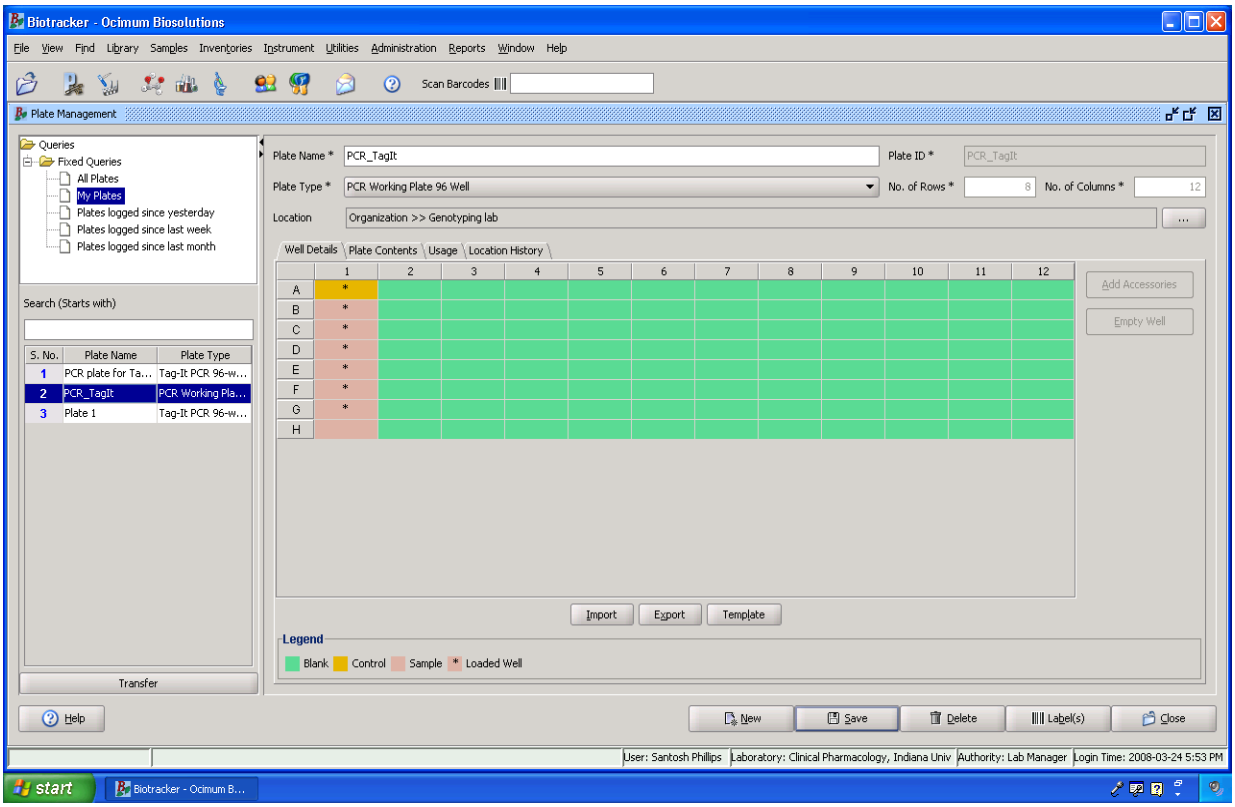


Figure 31: Plate management

Figure 32 shows the details of the plate contents. This enables a researcher to trace back to the origin of the individual samples.

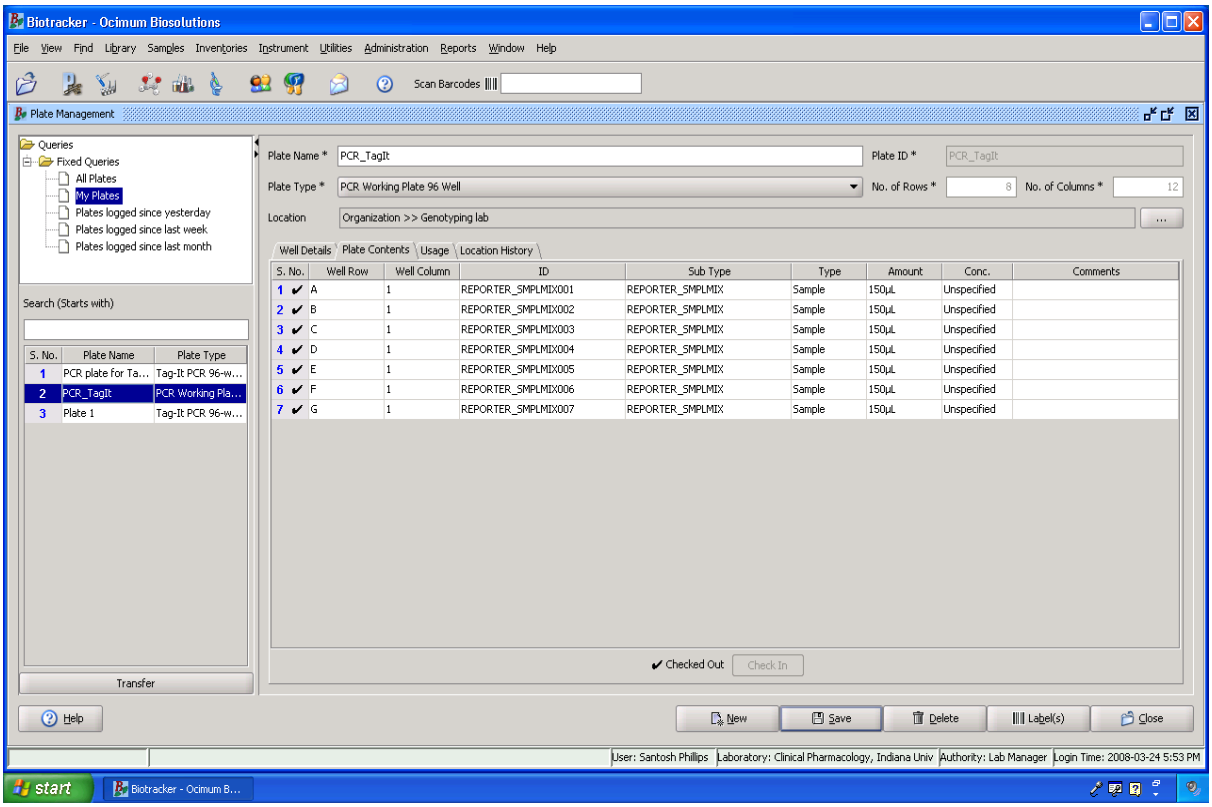


Figure 32: Plate content details

The final results generated with the Tag-It Data analysis software showed the variations for each sample (Figures 33 and 34 for two samples). A determination of whether the wild-type/mutant allele for each of the 12 small nucleotide variants had been detected or whether the samples carry an allele with the deletion or duplication was then made (Figure 35). The Tag-It Data Analysis Software displays, for each sample, the calls for the variations. The possible calls for a given variation of a specific sample are:

Bi-allelic variations (presence of two different gene forms or alleles):

WT: only the wild-type allele has been

HET: both the wild-type and the mutant alleles have been detected

MUT: only the mutant allele has been detected

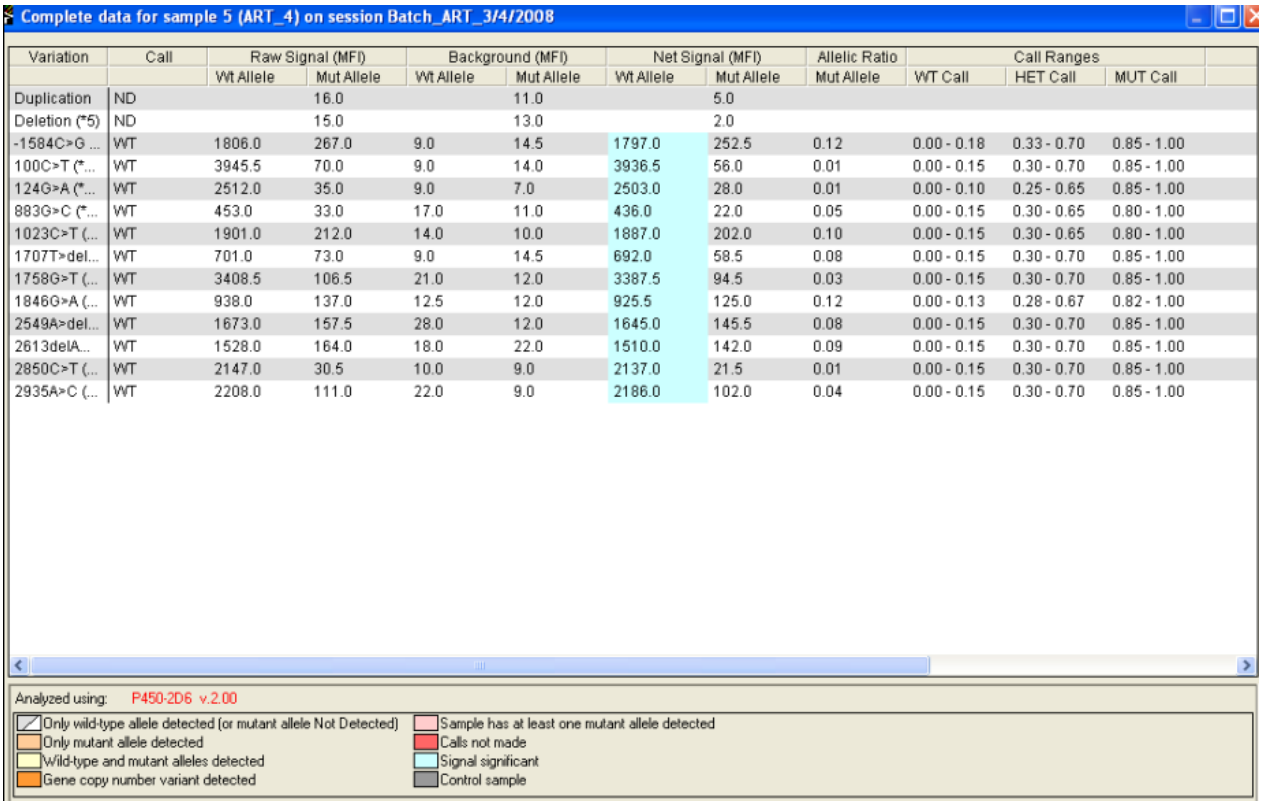
No Call: a call could not be made

Gene copy variation (duplication and deletion)

ND: specific gene copy variation not detected (duplication or deletion)

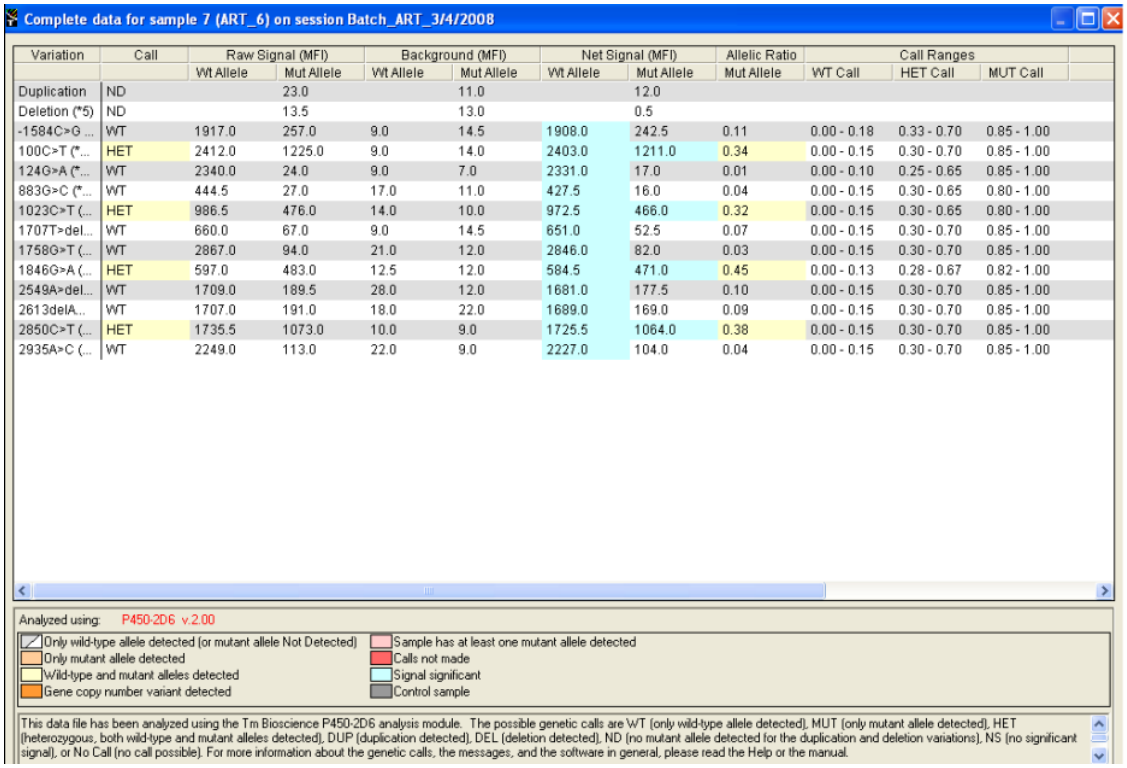
DUP/DEL: duplication or deletion detected

No Call: a call could not be made



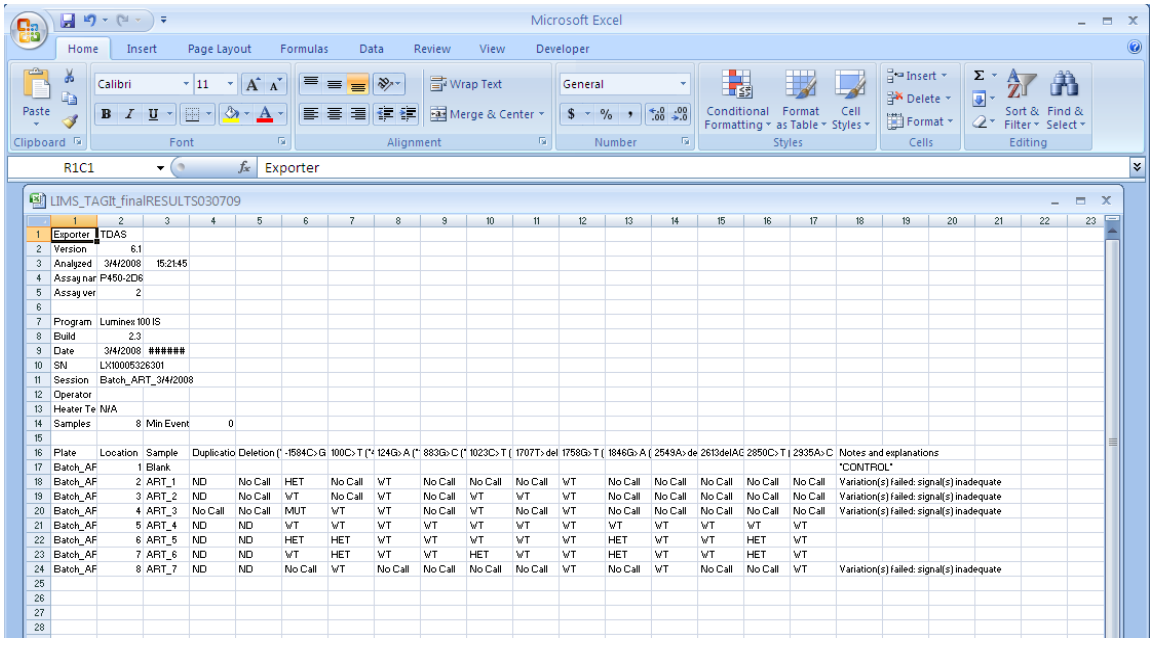
Variation	Call	Raw Signal (MFI)		Background (MFI)		Net Signal (MFI)		Allelic Ratio	Call Ranges		
		Wt Allele	Mut Allele	Wt Allele	Mut Allele	Wt Allele	Mut Allele	Mut Allele	WT Call	HET Call	MUT Call
Duplication	ND		16.0		11.0		5.0				
Deletion (*5)	ND		15.0		13.0		2.0				
-1584C>G ...	WT	1806.0	267.0	9.0	14.5	1797.0	252.5	0.12	0.00 - 0.18	0.33 - 0.70	0.85 - 1.00
100C>T (*...	WT	3945.5	70.0	9.0	14.0	3936.5	56.0	0.01	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00
124G>A (*...	WT	2512.0	35.0	9.0	7.0	2503.0	28.0	0.01	0.00 - 0.10	0.25 - 0.65	0.85 - 1.00
883G>C (*...	WT	453.0	33.0	17.0	11.0	436.0	22.0	0.05	0.00 - 0.15	0.30 - 0.65	0.80 - 1.00
1023C>T (...	WT	1901.0	212.0	14.0	10.0	1887.0	202.0	0.10	0.00 - 0.15	0.30 - 0.65	0.80 - 1.00
1707T>del...	WT	701.0	73.0	9.0	14.5	692.0	58.5	0.08	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00
1758G>T (...	WT	3408.5	106.5	21.0	12.0	3387.5	94.5	0.03	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00
1846G>A (...	WT	938.0	137.0	12.5	12.0	925.5	125.0	0.12	0.00 - 0.13	0.28 - 0.67	0.82 - 1.00
2549A>del...	WT	1673.0	157.5	28.0	12.0	1645.0	145.5	0.08	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00
2613delA...	WT	1528.0	164.0	18.0	22.0	1510.0	142.0	0.09	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00
2850C>T (...	WT	2147.0	30.5	10.0	9.0	2137.0	21.5	0.01	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00
2935A>C (...	WT	2208.0	111.0	22.0	9.0	2186.0	102.0	0.04	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00

Figure 33: Complete variant call data for an individual sample



Variation	Call	Raw Signal (MFI)		Background (MFI)		Net Signal (MFI)		Allelic Ratio	Call Ranges		
		Wt Allele	Mut Allele	Wt Allele	Mut Allele	Wt Allele	Mut Allele	Mut Allele	WT Call	HET Call	MUT Call
Duplication	ND		23.0		11.0		12.0				
Deletion (*5)	ND		13.5		13.0		0.5				
-1584C>G ...	WT	1917.0	257.0	9.0	14.5	1908.0	242.5	0.11	0.00 - 0.18	0.33 - 0.70	0.85 - 1.00
100C>T (*...	HET	2412.0	1225.0	9.0	14.0	2403.0	1211.0	0.34	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00
124G>A (*...	WT	2340.0	24.0	9.0	7.0	2331.0	17.0	0.01	0.00 - 0.10	0.25 - 0.65	0.85 - 1.00
883G>C (*...	WT	444.5	27.0	17.0	11.0	427.5	16.0	0.04	0.00 - 0.15	0.30 - 0.65	0.80 - 1.00
1023C>T (...	HET	986.5	476.0	14.0	10.0	972.5	466.0	0.32	0.00 - 0.15	0.30 - 0.65	0.80 - 1.00
1707T>del...	WT	660.0	67.0	9.0	14.5	651.0	52.5	0.07	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00
1758G>T (...	WT	2867.0	94.0	21.0	12.0	2846.0	82.0	0.03	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00
1846G>A (...	HET	597.0	483.0	12.5	12.0	584.5	471.0	0.45	0.00 - 0.13	0.28 - 0.67	0.82 - 1.00
2549A>del...	WT	1709.0	189.5	28.0	12.0	1681.0	177.5	0.10	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00
2613delA...	WT	1707.0	191.0	18.0	22.0	1689.0	169.0	0.09	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00
2850C>T (...	HET	1735.5	1073.0	10.0	9.0	1725.5	1064.0	0.38	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00
2935A>C (...	WT	2249.0	113.0	22.0	9.0	2227.0	104.0	0.04	0.00 - 0.15	0.30 - 0.70	0.85 - 1.00

Figure 34: Complete variant call data for another individual sample



	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	Exporter	TDAS																
2	Version	6.1																
3	Analyzed	3/4/2008	15:21:45															
4	Assay nar	P450-2D6																
5	Assay ver	2																
6																		
7	Program	Luminex 100 IS																
8	Build	2.3																
9	Date	3/4/2008	######															
10	SN	LX10005326301																
11	Session	Batch_ART_3/4/2008																
12	Operator																	
13	Heater Te	N/A																
14	Samples	8	Min Event	0														
15																		
16	Plate	Location	Sample	Duplicatio	Deletion (*	-1584C>G	100C>T (*	124G>A (*	883G>C (*	1023C>T (	1707T>del	1758G>T (	1846G>A (	2549A>de	2613delAC	2850C>T (	2935A>C	Notes and explanations
17	Batch_AF	1	Blank															"CONTROL"
18	Batch_AF	2	ART_1	ND	No Call	HET	No Call	WT	No Call	No Call	No Call	WT	No Call	No Call	No Call	No Call	No Call	Variation(s) failed: signal(s) inadequate
19	Batch_AF	3	ART_2	ND	No Call	WT	No Call	WT	No Call	WT	WT	WT	No Call	No Call	No Call	No Call	No Call	Variation(s) failed: signal(s) inadequate
20	Batch_AF	4	ART_3	No Call	No Call	MUT	WT	WT	No Call	WT	No Call	WT	No Call	No Call	No Call	No Call	No Call	Variation(s) failed: signal(s) inadequate
21	Batch_AF	5	ART_4	ND	ND	WT	WT	WT	WT	WT	WT	WT	WT	WT	WT	WT	WT	
22	Batch_AF	6	ART_5	ND	ND	HET	HET	WT	WT	WT	WT	WT	HET	WT	WT	HET	WT	
23	Batch_AF	7	ART_6	ND	ND	WT	HET	WT	WT	HET	WT	WT	HET	WT	WT	HET	WT	
24	Batch_AF	8	ART_7	ND	ND	No Call	WT	No Call	No Call	No Call	No Call	WT	No Call	WT	No Call	No Call	WT	Variation(s) failed: signal(s) inadequate

Figure 35: Complete call for all samples

This data was exported into LIMS and managed through the Document management module. Privileges can be assigned to who should see the data. Data checked in or out can also be monitored with LIMS (Figure 36).

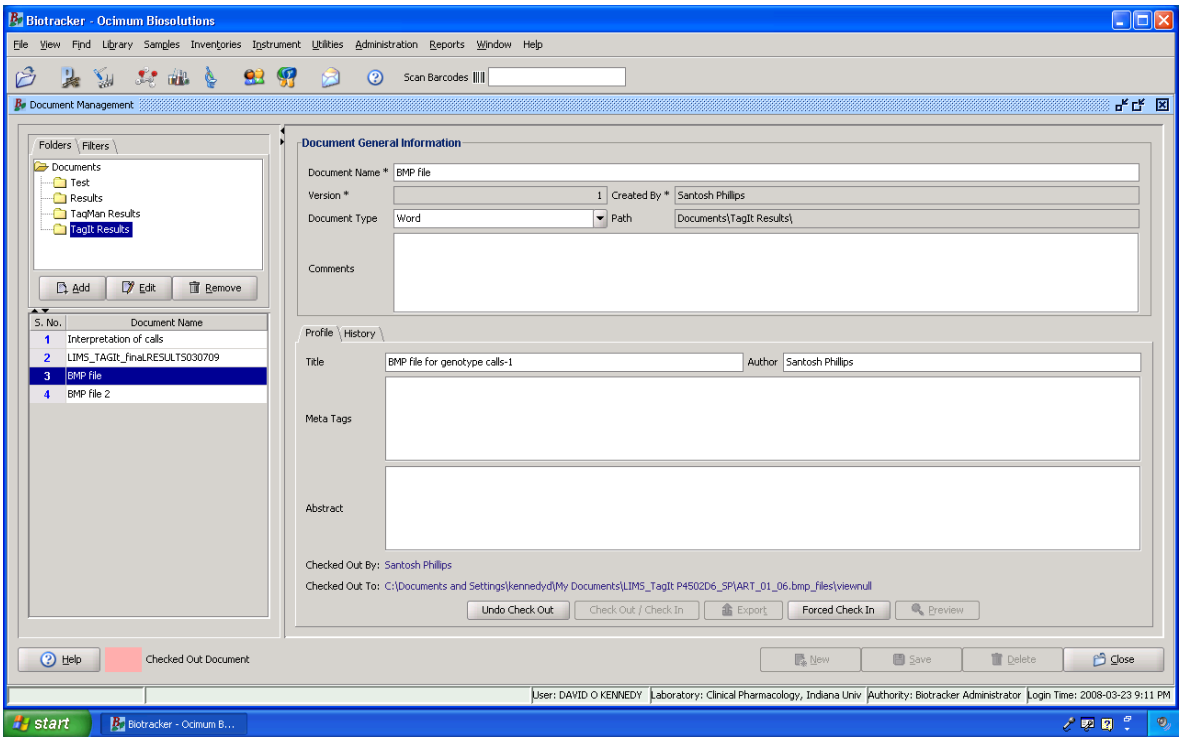


Figure 36: Document management

4.1.2. LIMS administration and project management reports

Different reports can be generated with the Report module on the main menu. Reports of interest generated included:

(1) Stock overview report which shows all the inventories one selected and their quantities (Figure 37).

(2) Inventory threshold report shows how much of each item is left, and therefore should be re-ordered. Items running below threshold stock are shown in red (Figure 38).

(3) Overall project report: This shows the final report of a project and shows the experiments, runs, inventory, personnel, time schedule, who submitted the project, who approved runs, experiments and project, instrument schedules, and names of all files and documents associated with the project (Appendix A).

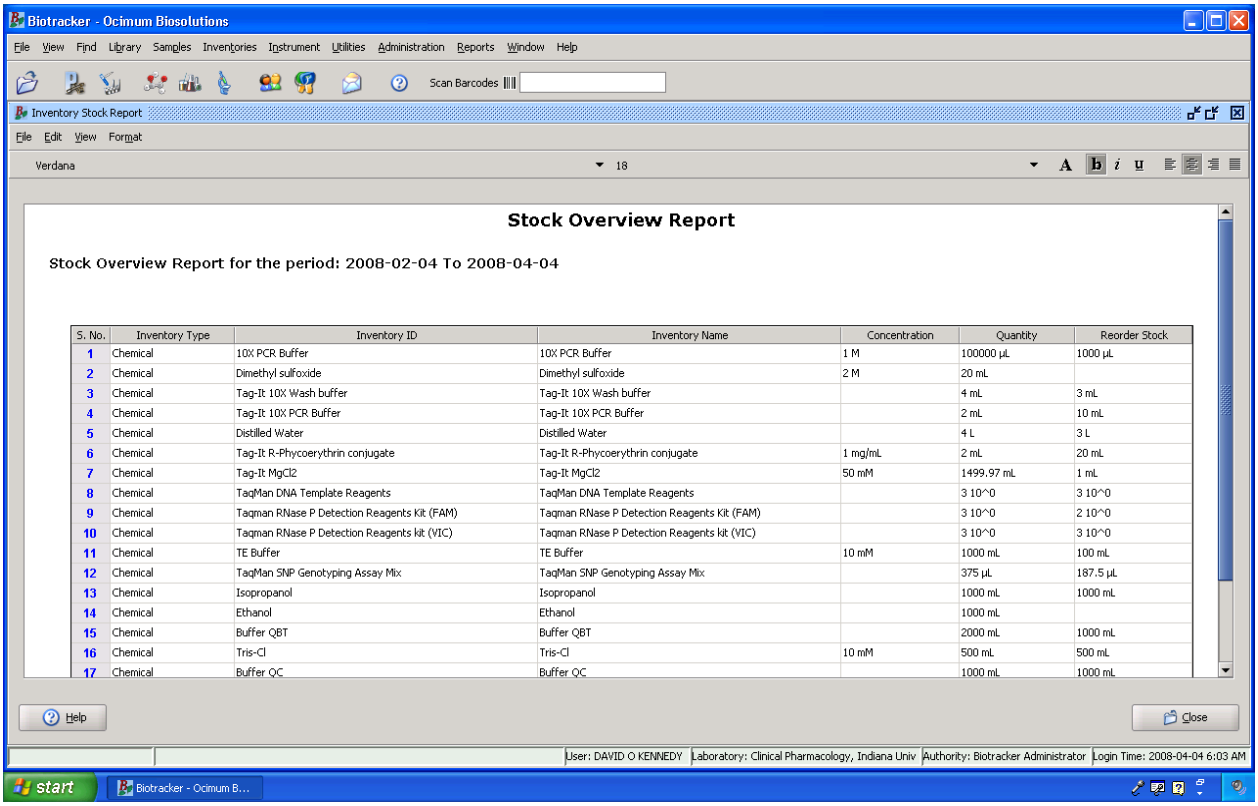


Figure 37: Stock overview report

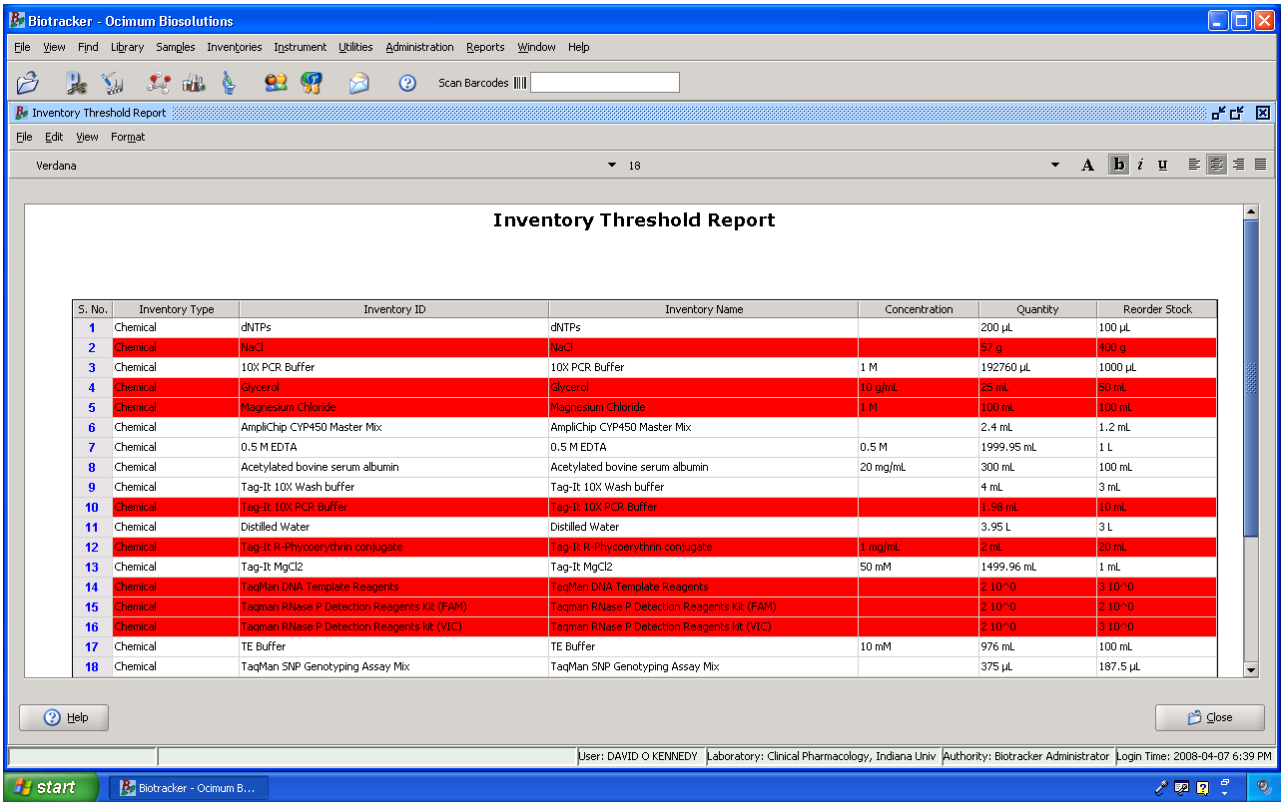


Figure 38: Inventory threshold report

4.2. LIMS in academic research

Respondents to questionnaires and phone interviews were given a definition of LIMS as computer software that is used in the laboratory for the management of samples, laboratory users, instruments, standards, and other laboratory functions such as invoicing, plate management, and workflow automation. They were then asked to fill out the questionnaires or respond via phone.

A total of 100 questionnaires and phone interviews were conducted. The response was 32/100 (32%). Out of this, 23 were male scientist (71.9%) and 9 females (28.1%) (Table 1).

Sex

		Frequency	Percent	Cumulative Percent
Valid	Male	23	71.9	71.9
	Female	9	28.1	100.0
	Total	32	100.0	

Table 1: Sex

Most of the respondents were between the ages of 31 and 50 (71.9%) (Table 2), and majority (71.9%) had 5 or more years of experience in their field of study (Table 3).

		Frequency	Percent	Cumulative Percent
Valid	20-30 yrs	5	15.6	15.6
	31-40 yrs	12	37.5	53.1
	41-50	11	34.4	87.5
	50 yrs plus	4	12.5	100.0
	Total	32	100.0	

Table 2: Age

		Frequency	Percent	Cumulative Percent
Valid	Less than 1 year	1	3.1	3.1
	1-2 yrs	3	9.4	12.5
	3-5 yrs	5	15.6	28.1
	5 yrs or more	23	71.9	100.0
	Total	32	100.0	

Table 3: Experience in field

Field of expertise varied greatly, but there was a broad representation of scientists in research (Figure 39). The rationale behind the question was to find out which field of research would most likely use LIMS.

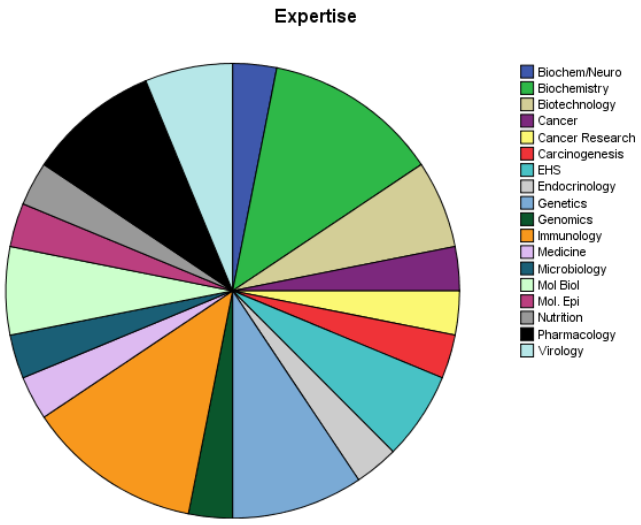


Figure 39: Field of research expertise

Table 4 shows most respondents come from laboratories where there were more than 6 scientists (53.1%). This question was posed to find out whether the number of people in a laboratory may influence the decision to use LIMS.

		Frequency	Percent	Cumulative Percent
Valid	Only one	3	9.4	9.4
	Less than 3	1	3.1	12.5
	3-5	11	34.4	46.9
	6 or more people	17	53.1	100.0
	Total	32	100.0	

Table 4: Number of staff present in laboratory

Table 5 shows that majority of respondents said their laboratories had modern and adequate equipment (68.8%). The question was to help determine whether the use of modern technology had a relation with LIMS use.

		Frequency	Percent	Cumulative Percent
Valid	Present in own lab, modern, adequate	22	68.8	68.8
	Present in own lab, outdated, adequate	7	21.9	90.6
	Present in own lab, modern, inadequate	2	6.3	96.9
	Present in own lab, outdated, inadequate	1	3.1	100.0
	Total	32	100.0	

Table 5: Laboratory technology

Both private and public institutions were almost equally represented (Table 6). This question was to ascertain which type of institution, public or private, will have more people using LIMS.

		Frequency	Percent	Cumulative Percent
Valid	Public	15	46.9	46.9
	Private	17	53.1	100.0
	Total	32	100.0	

Table 6: Institution

Majority of respondents worked more than 5 hours a day during the week (90.7%) (Table 7), and majority did not work on weekends (68.8%) (Table 8). The question was to ascertain whether time in research facility influenced LIMS use.

DayHours

		Frequency	Percent	Cumulative Percent
Valid	Less than 1 hr	2	6.3	6.3
	1-4 hrs	1	3.1	9.4
	5-8 hrs	10	31.3	40.6
	8 hrs or more	19	59.4	100.0
	Total	32	100.0	

Table 7: Working hours - week days

WkendHours

		Frequency	Percent	Cumulative Percent
Valid	Never	12	37.5	37.5
	Less than 1 hr	10	31.3	68.8
	1-4 hrs	5	15.6	84.4
	5-8 hrs	4	12.5	96.9
	8 hrs or more	1	3.1	100.0
	Total	32	100.0	

Table 8: Working hours - weekend

The use of software technology was analyzed with six items namely, using software to automatically record any part of an experiment (SFrecTime), to transfer experimental results automatically from measuring equipment or instrument to storage site (SFtrnresSto), to record every change made to records (SFrecChng), to detect who performed an experiment (SFdetectUser), to detect when experiment was performed

(SFexpTime), or to automatically run an experiment (SFautoRunExp). Responses were grouped under Never-1, Rarely-2, Sometimes-3, Often-4, or Always-5. As shown in Figure 40, the distribution of responses to using software to automatically record any part of an experiment or to transfer experimental results automatically from measuring equipment or instrument to storage site were fairly normal. However, responses to using software to record every change made to records, to detect who performed an experiment, or to detect when experiment was performed, or to automatically run an experiment, all were skewed to the left of the distribution. Reliability testing resulted in a Cronbach's alpha of 0.796. Hence, the reliability for using all six items as an index was high (reliability coefficient of 0.70 or higher is considered "acceptable" in most Social Science research situations). Software technology was then used in further analysis as an index for analyzing LIMS use.

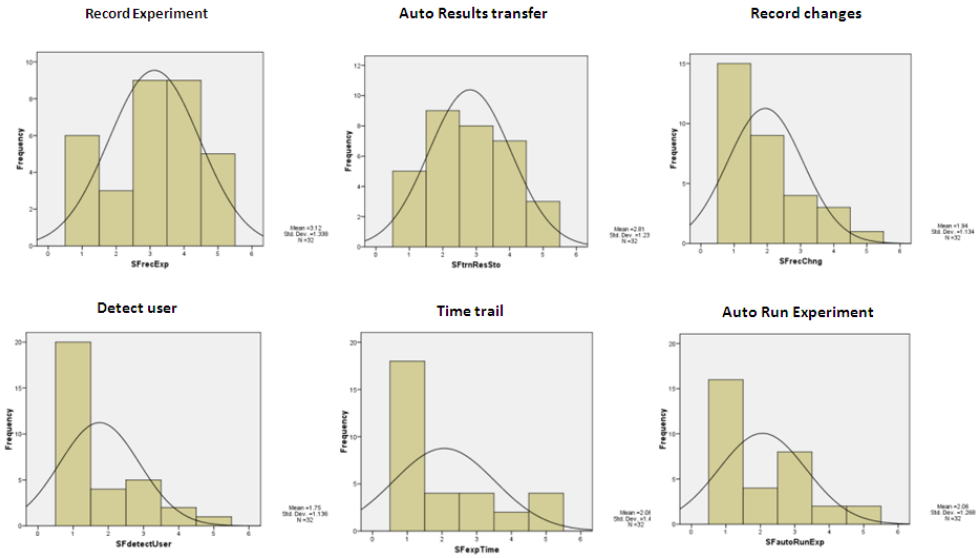


Figure 40: Software technology used

Never-1, rarely-2, sometimes-3, often-4, always-5

Responses to how long LIMS had been used are given in Table 9. Length of LIMS use was to help identify respondents who had or had not used LIMS. Hence, respondents were classified into two groups of whether they had used LIMS before, Yes-25%, Never - 75%. These two groups were then used for analysis in subsequent testing.

		Frequency	Percent	Cumulative Percent
Valid	Never	24	75.0	75.0
	Less than 1 month	1	3.1	78.1
	1-6 months	2	6.3	84.4
	7-23 months	1	3.1	87.5
	2-5 years	3	9.4	96.9
	5 years or more	1	3.1	100.0
	Total	32	100.0	

Table 9: Time of LIMS use

Multiple regression analysis of the correlation between LIMS usage (Yes or Never) and the demographic measures are shown in Table 10. None of the demographic correlated statistically significant with LIMS usage. For Sex, the negative correlation (-.040, p=.414) indicates that more Males (assigned 1) than Females (assigned 2) were more likely to use LIMS.

		Actual LIMS usage	Sig. (1-tailed)
Pearson Correlation	Actual LIMS usage	1.000	
	StaffPresent	.197	.140
	Sex	-.040	.414
	Age	-.040	.414
	Institution	-.181	.161
	FieldExp	.229	.104
	LabExp	.000	.500
	DayHours	.044	.406
	WkendHours	-.190	.149
	LabTechnology	-.145	.214

Table 10: Factors affecting LIMS use

The negative correlation between Age and LIMS use (R=-.040, p=0.414) indicates that more young scientist (lower scale of 2 and 3) than older ones (scale of 4) correlated with LIMS use. For Institution, the negative correlation (R=-.181, p=0.161) indicates that scientists in private (scale 1) than public institutions (scale 2) correlated with LIMS use. The less time (scale 1-2) a scientist spends working at the weekend correlated with LIMS use (R=-0.190, p=0.149) than more time spent (scale 3-5). Scientists with more adequate and modern equipment in their own laboratory (lower scale of 1) correlated with LIMS use (R=-0.145, p=0.214). These correlations were however, not statistically significant.

Linear regression analysis was used to determine the overall fit of the software technology model. Table 11 shows the percentage accounting for the variation in LIMS use by each of the software technology use responses. Overall this model accounts for 7.9%, hence, 92.1% of the variation in LIMS use cannot be accounted for by software technology responses alone.

SFrecExp	2.7
SFtrnResSto	4.4
SFrecChng	2.6
SFdetectUser	0.4
SFexpTime	0.1
SFautoRunExp	2.1
Total	7.9%

Table 11: Software technology and LIMS use

Table 12 shows LIMS is implemented mostly in gene expression and genotyping studies (40%).

		Responses	
		N	Percent
LIMSFuncUsed[a]	FNSequencing	3	9.4%
	FNGeneExpre	6	18.8%
	FNGenotyping	7	21.9%
	FNProteoCore	1	3.1%
	FNBioSpeBnk	2	6.3%
	FNLabAdmn	1	3.1%
	FNWrkFlow	2	6.3%
	FNInventory	3	9.4%
	FNAudit	1	3.1%
	FNReport	2	6.3%
	FNProtocol	1	3.1%
	FNInstInteg	2	6.3%
	FNRevAppr	1	3.1%
Total		32	100.0%

a. Dichotomy group tabulated at value 1.

Table 12: LIMS functionality used

Reasons given for why LIMS has never been used showed that lack of knowledge about LIMS (43.8%) was the main factor, followed by unavailability (21.9%) (Table 13).

NoLIMSreason

		Frequency	Percent	Cumulative Percent
Valid	Unavailability	7	21.9	28.0
	Financial constraints	1	3.1	32.0
	Do not know much about it	14	43.8	88.0
	Will not affect production	1	3.1	92.0
	Other	2	6.3	100.0
	Total	25	78.1	
Missing	System	7	21.9	
Total		32	100.0	

Table 13: Reasons for not having used LIMS

CHAPTER FIVE: DISCUSSION

5.1. Implementation of LIMS in a genotyping study

5.1.1. Explanation of outcome

In this project a commercial LIMS was successfully implemented in a genotype study to track workflow from protocol designing, sample acquisition, genotyping, data acquisition and analysis, to record generation. Besides serving as a workflow manager, the Biotracker LIMS also provided visible quality checks and centralization of data (Figure 40). The ability to track data and communicate quality information helps a laboratory to improve methods and work practices.

A challenging task facing life science researchers in small-sized laboratories is to effectively manage the entire process as well as the data that is generated. In a genotyping laboratory, this task can be most challenging, given the nature of the workflow. Samples may possibly fail at different steps of the workflow, resulting in a need to repeat the process from the start. Records for a particular sample may need to be revised over time, and data storage becomes a key issue. Segregation of steps, ineffective inventorying practices, and no easy way of collating all the data to draw meaningful inferences are among some of the challenges faced. Usually, data is managed using a combination of Microsoft Excel, Word, and sometimes publicly available tools and in-house applications.

Biotracker is an application designed for use in different discovery studies. Its modular design can be used to meet a laboratory's specific needs by combining modules.

In this study, its genotyping functionality was used. After the genotype workflow had been established, the use of the overall system led to a minimization of manual user input and paperwork. Biotracker presents a friendly and intuitive user interface, and users navigate within the application through several navigation options, using menus that follow the laboratory workflows. The interface includes several display screens that are specific for each step in the process and in which the related data are presented in tables and windows. Some of the functions are managed through forms that use pull-down menus users create, and this helped to minimize form-filling errors. Validations checks were made possible during system configuration of the data type, units, dates, as well as integrity with respect to other tables in the database. Users are guided through the workflows by being prompted to fill the required fields of one step before moving on to the next step. Sometimes, an experimental step needs to be approved by an authority before one can move to another step, placing more checks on the integrity of the overall data. Barcodes were used to track samples and inventories, and most activities are monitored or executed with the user's name and password. Data could also be imported in bulk, reducing errors due to manual entry. LIMS can also import and store data from different forms of applications, and therefore provides a central repository for all the information and data for the genotyping process (Figure 41).

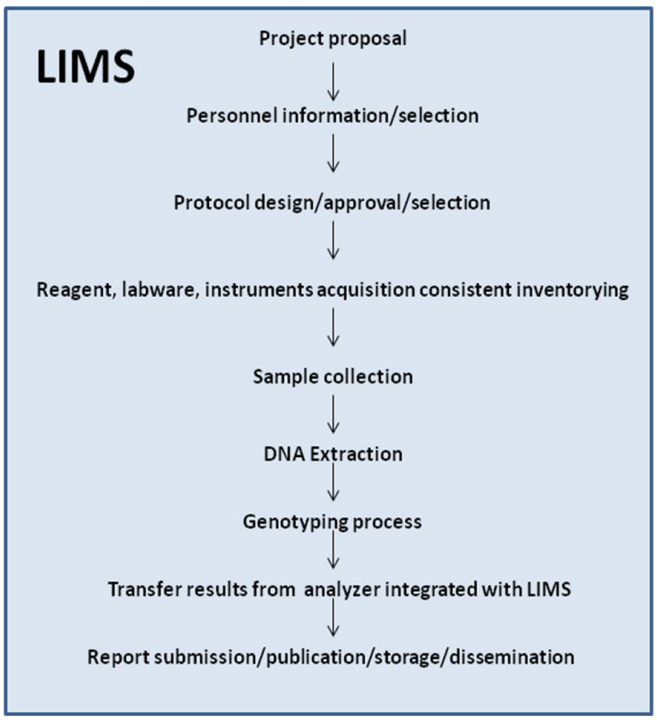


Figure 41: Integration of information with LIMS

Although LIMS are effective in the pharmaceutical and biotech industries, most are too costly and not readily available for small research labs. As mentioned earlier, individual laboratories have designed their own LIMS to fit their particular research, but this took time and effort, and may not be easily adopted by other laboratories. However, with academic pricing now becoming available from the commercial software designers, the money spent may become worth the efficiency in research execution and overall outcome of data from academic laboratories.

5.1.2. Importance of outcome

The use of LIMS in combination with automation of laboratory processes improves the efficiency and quality of the work by reducing potential for human errors,

accelerating the throughput of analysis, and enables sample tracking activities that are very difficult to perform without error by hand. This study shows that academic laboratories can use commercial LIMS to effectively manage workflow, store data, and get data off instruments into storage systems, and doing so in a manner that is lossless and not sacrificing speed for interruptions in data. Another feature of LIMS observed in this study is securing data and proprietary information with the use of access-restricted items such as passwords and electronic signatures.

5.2. Implementation of LIMS in academic research

5.2.1. Outcome of study

This study found that there were low correlations between demographic factors such as age, sex, experience, field of expertise, type of academic institution, number of scientific personnel in laboratory, and the type of technology used, and LIMS usage. None of these correlations were significant. No combination of these factors could constitute an index with a reliability coefficient high enough to be acceptable. It was also observed that there is a disparate use of software technologies in academia. Researchers use different software technologies in segregated steps, such as to record any part of an experiment, to automatically transfer results to final storage site, or to automatically run an experiment. Very few respondents reported using a single software to carry out most of their processes. Owing to this, software technology could not be used as a model to predict actual LIMS use, despite an "acceptable" reliability coefficient obtained for the six items used together as an index to test LIMS usage (0.796). The correlation

coefficient between this index and LIMS usage computed from having or never having used LIMS before, were very low and not statistically significant. LIMS was not found to be widespread in academia (75% never-users), but where they were present they are mostly used for studies involving genotyping and gene sequencing. The major reason for lack of LIMS use is lack of knowledge about them. Perry (2002) found a similar trend together, with financial constraints, but in this study financial constraint was one of the reasons least cited.

5.2.2. Implication of study

The outcome of this study implies that LIMS software companies should advertise their products by encouraging academic researchers to try them out first. When the benefits of such system become evident, scientists are more likely to use them. Also some of the modules and functionalities of commercial LIMS could be deleted to fit academic research needs and budget. Despite having the latest and sophisticated equipments in their laboratories, much attempt is not made to research the need for software systems such as LIMS to aid research. As many as 68.8% of respondents reported having modern and adequate equipments in their laboratory as opposed to just 25% having used LIMS before. Academic research may seem to be fragmented and therefore one LIMS may be difficult to meet all functions. However, LIMS like Biotracker feature different modules that can be adapted for different functionalities. Therefore, both LIMS vendors and academic scientists need to work together to bridge this knowledge divide.

CHAPTER SIX: CONCLUSION

6.1. Limitations of study

Both studies presented with some challenges and these are outlined below.

6.1.1. LIMS implementation in genotype studies

The full functionality of Biotracker was not used in this study as this was a limited version. However, the functionalities used were enough to see the benefits of LIMS implementation in a genotyping workflow. Of particular benefit was the location management functionality which eased the search for inventories for the project. This was a fairly busy laboratory with many tissue, sample, and reagent storage facilities. At the end of the study, the scientists were impressed with the usefulness of LIMS. A key feature of LIMS is instrument integration. This functionality was not available on the student version of the LIMS, but this did not present much difficulty in transferring data into LIMS from the bioanalyzer used.

6.1.2. LIMS implementation in academic research

A greater sample size may present a much more diverse result for analyses. A better outcome might have been seen if the questionnaire had been web-based. Questionnaire research by email is becoming increasingly difficult as mails are screened for solicitation or lack thereof, and most often attachments are rejected. However, in some instances, initial emails to ask for permission came back with responses of scientist being busy or unavailable. This was a two-page 16-item questionnaire, with the rationale

to cut down on time for filling them out. However, more indices examining LIMS use may shed more light on factors that contribute to the 'LIMS-lag' in academia, and help software developers meet the challenges of making their products available to academics. This may also eventually help academics in making good and informed decisions about conducting research, and help to implement some of these sophisticated and useful tools for their research.

6.2. Further research

It is hoped that future research will involve a whole academic laboratory adopting Biotracker LIMS for a similar study to determine the usefulness of LIMS. At the same time, an investigator could perform an ethnographic study to evaluate in details the practices associated with LIMS usage in academia to shed more light on the lack of use. It is possible that unwillingness to change the status quo could be playing a major role.

6.3. Summary

A commercial LIMS was successfully implemented in a genotyping study in an academic laboratory to integrate all steps and data management activities for efficient workflow. LIMs use in academic research is very fragmented and limited, and lack of knowledge of its existence and usefulness was cited as the major reason for this situation. Both software vendors and academic researchers need to work together to close the divide between them, as this has a negative impact on both business and academic research. Academic scientists are missing out on a potentially valuable research technology in LIMS, and LIMS developers and vendors are missing the opportunity to

establish themselves in the larger scientific community. With the completion of the human genome project and the race to find answers to life's medical issues, LIMS may play a big role in discovery laboratories such as those in academia.

REFERENCES

Abravaya, K., Huff, J., Marshall, R., Merchant, B., Mullen, C., Schneider, G., and Robinson, J. Molecular beacons as diagnostic tools: technology and applications. Clin. Chem. Lab. Med., 41:468-474, 2003.

Borges, S., Desta, Z., Li, L., Skaar, T.C., Ward, B.A., Nguyen, A., Jin, Y., Storniolo, A.M., Nikoloff, D.M., Wu, L., Hillman, G., Hayes, D.F., Stearns, V., Flockhart, D.A. Quantitative effect of CYP2D6 genotype and inhibitors on tamoxifen metabolism: implication for optimization of breast cancer treatment. Clin Pharmacol Ther. 80(1):61-74, 2006

Cagnd, O. and Otle, S. Importance of laboratory information management systems (LIMS) software for food processing factories. J. Food Engineering 65 (4), 565-568, 2004.

Collins, F.S., Patrinos, A., Jordan, E., Chakravarti, A., Gesteland, R., and LeRoy, C. New Goals for the U.S. Human Genome Project: 1998-2003. Science 282 (5389): 682-689, 1998.

Donofrio, N.M., Rajagopalan, R., Brown, D.E., Diener, S.E., Windham, D.E., Nolin, S., Floyd, A., Mitchell, T.K., Galadima, N., Tucker, S., Orbach, M. J., Patel, G., Farman, M. L., Pampanwar, V., Soderlund, C., Lee, Y-H., and Deen, R, A. PACLIMS: A component LIM system for high throughput functional genomic analysis. BMC Bioinformatics, 6:94, 2005.

Easton, D. F., Pooley, K. A., Dunning, A. M., et al. Genome-wide association study identifies novel breast cancer susceptibility loci. Nature 447: 1087-1093, 2007.

Food and Drug Administration. Title 21 Code of Federal Regulations (21 CFR Part 11) Electronic Records; Electronic Signatures. http://www.fda.gov/cder/guidance/5667fnl.pdf, 2003.

Fulton, K.F., Ervine, S., Faux, N., Forster, R., Jodun, R.A., Ly, W., Robilliard, L., Sonsini, J., Whelan, D., Whisstocka, J.C., Bucklea, A. M. CLIMS: Crystallography Laboratory Information Management System. Acta Cryst. D60, 1691-1693, 2004.

Giacomini, K. M., Brett, C. M., Altman, R. B., Benowitz, N. L., Dolan, M. E., Flockhart, D. A., Johnson, J. A., Hayes, D. F., Klein, T., Skaar, T., et al. The pharmacogenetics research network: from SNP discovery to clinical drug response. Clin. Pharmacol. Ther., 81 (3):328-45, 2007.

Gibbon, G. A Brief History of LIMS. Laboratory Automation and Information Management 32, 1-5, 1996.

Gingeras, T.R. Origin of phenotypes: Genes and transcripts. Genome Res. 17: 682-690, 2007.

Helgadottir, A., Thorleifsson, G., Manolescu, A., Gretarsdottir, S., Blondal, T., Jonasdottir, A., Jonasdottir, A., Sigurdsson, A., Baker, A., Palsson, A., Masson, G., Gudbjartsson, D. F., Magnusson, K. P., et al. A Common Variant on Chromosome 9p21 Affects the Risk of Myocardial Infarction. Science 316: 1491-1493, 2007.

Hendricks, R.W. & Learn, M.R. (2003). A Laboratory Information Management System (LIMS) for an Academic Microchip Fabrication Facility http://ieeexplore.ieee.org/iel5/8682/27506/01225703.pdf

Howell, W., Jobs M., Gyllensten, U., and Brookes, A. Dynamic allele-specific hybridization. A new method for scoring single nucleotide polymorphisms. Nat. Biotechnol., 17(1):87-8, 1999.

Isler, J.A., Vesterqvist, O. E., and Burczynski. M. E. Analytical validation of genotyping assays in the biomarker laboratory. Pharmacogenomics, 8(4):353, 2007.

Kennedy, D.O., Agrawal, M., Shen, J., Terry, M. B., Zhang, F. F., Senie, R.T., Motykiewicz, G., and Santella R. M. DNA Repair Capacity of Lymphoblastoid Cell Lines from Sisters Discordant for Breast Cancer. J. Natl. Cancer Inst., 97 (2): 127-132, 2005.

Kirchheiner, J., Heesch, C., Bauer, S., et al. Impact of the ultrarapid metabolizer genotype of cytochrome P450 2D6 on metoprolol pharmacokinetics and pharmacodynamics. Clin. Pharmacol. Ther., 76 (4):302-12, 2004.

Klito, N.G., Tan Q, Nyegaard, M., Brusgaard, K., Thomassen, M., Skouboe, C., Dahlgaard, J., and Kruse, T.A. Arrayed primer extension in the "array of arrays" format: a rational approach for microarray-based SNP genotyping. Genet. Test., 11(2):160-6, 2007.

Kwok, P-Y. Methods for genotyping single nucleotide polymorphisms. Ann. Rev. Genomics Human Genet. 2: 235-258, 2001.

LabVantage Solutions Signs Contract with National Cancer Institute Core Genotyping Center. http://www.labvantage.com/newsevents/pressreleases/2002/nci.html

Lim, Y.C., Li, L., Desta, Z., Zhao, Q., Rae, J.M., Flockhart, D.A., Skaar, T.C. Endoxifen, a secondary metabolite of tamoxifen, and 4-OH-tamoxifen induce similar changes

in global gene expression patterns in MCF-7 breast cancer cells. J Pharmacol Exp Ther. 318(2):503-12.2006

Maurer, M., Molidor, R., Sturn, A Hartler, J., Hackl, H., Stocker, G., Prokesch, A., Scheideler, M., and Trajanoski, Z. MARS: Microarray analysis, retrieval, and storage system. BMC Bioinformatics 6:101, 2005.

McGuigan, F.E. and Ralston, S.H. Single nucleotide polymorphism detection: allelic discrimination using TaqMan. Psychiatr. Genet. 12(3):133-6, 2002.

Monnier, S., Cox, D.G., Albion, T. and Canzian, F. T.I.M.S: Taqman Information Management System, tools to organize data flow in a genotyping laboratory. BMC Bioinformatics, 6:246-249, 2005.

Nelson, D. (2008). http://drnelson.utmem.edu/P450.statsfile.html

Nelson, D. R., Koymans, L., Kamataki, T., Stegeman, J. J., Feyreisen, R., Waxman, D. J. et al. P450 superfamily: update on new sequences, gene mapping, accession numbers and nomenclature. Pharmacogenetics, 6: 1–42, 1996.

Olivier, M. The Invader assay for SNP genotyping. Mutat. Res., 573(1-2):103-10, 2005.

Perry, D. LIMS in the academic world. Today's Chemist 11 (1), 15-16, 19, 2002.

Prilusky, J., Oueillet, E., Ulryck, N., Pajon, A., Bernauer, J., Krimm, I., Quevillon-Cheruel, S., Leulliot, N., Graille, M., Liger, D., Tre´saugues, L., Sussman, J. L., Janin, J., van Tilbeurgh, H., and Pouponb, A. HalX: an open-source LIMS (Laboratory Information Management System) for small to large-scale laboratories. Acta Cryst. D61, 671–678, 2005.

Roeder, K., Bacanu, S.A., Sonpar, V., Zhang X., and Devlin B. Analysis of single-locus tests to detect gene/disease associations. Genet. Epidemiol. 28(3): 207-19, 2005

Santella, R. M., Gammon, M., Terry, M. B., Senie, R, Shen, J., Kennedy D.O., Agrawal M., Faraglia, B., and Zhang F. F. DNA adducts, DNA Repair Genotype/Phenotype and Cancer Risk. Mutat. Res., 592: 29-35, 2005.

Saxena, R., Voight, B. F., Lyssenko, V., Burtt, N. P., de Bakker, P. I. W., Chen, H., Roix, J.J., Kathiresan, S., Hirschhorn, J. N., Daly, M. J., Hughes, T. E., Groop,L., Altshuler, D., Almgren, P., Florez, J. C., et al. Genome-Wide Association Analysis Identifies Loci for Type 2 Diabetes and Triglyceride Levels Diabetes. Science 316: 1331-1336, 2007.

Schreier, A.A., Wilson, K. & Resnik, D. (2006). Academic Research Record-Keeping: Best Practices for Individuals, Group Leaders, and Institutions. Academic Medicine, 81(1), 42-47.

Schubbert, S. Genotyping and Drug Response: Use of Single Nucleotide Polymorphisms (SNPs) versus Haplotypes to Predict Albuterol Efficacy. AAPS Pharmacol. Science 3 (3): 1, 2001.

Shankar, K. Recordkeeping in the production of scientific knowledge: An ethnographic study. Archival Science, 4 (3-4), 367-382, 2004.

Shen, J., Desai, M., Agrawal, M., Kennedy, D. O., Senie, R.T., Santella, R. M., and Terry, M.B. Polymorphisms in Nucleotide Excision Repair Genes and DNA Repair Capacity Phenotype in Sisters Discordant for Breast Cancer. Cancer Epidemiol. Biomarkers Prev. 15(9):1614–9, 2006.

Stamer, U.M. and Stüber, F. Genetic factors in pain and its treatment. Curr. Opin. Anesthesiol., 20(5): 478-84, 2007.

Stamer, U.M., Bayerer, B. & Stüber, F. Genetics and variability in opioid response. Euro. J. Pain 9(2): 101-4, 2005.

Steinlechner, M. & Parson W. (2001). Automation and high through-put for a DNA database laboratory: development of a laboratory information management system. Croatian Medical Journal, 42(3):252-5.

Syvanen, A.C. Accessing genetic variation: genotyping single nucleotide polymorphisms. Nat. Rev. Genet., 2(12):930-42, 2001.

Useche, F.J., Gao, G., Harafey, M., and Rafalski, A. High-throughput identification, database storage and analysis of SNPs in EST sequences. Genome Inform. 12:194-203, 2001.

Vanderslice, L.M. Trends in laboratory information systems: 1980-1990. Health Informatics, 7(3), 34, 1990.

Venter, J.C., Adams, M.D., Myers, E.W., Li, P.W., Mural, R.J., Sutton, G.G., Smith, H.O., Yandell, M., Evans, C.A., Holt, R.A., Gocayne, J.D., Amanatides, P. The Sequence of the Human Genome. Science, 291 (5507): 1304-1351 (2001).

Viksna, J, Celms, E, Opmanis, M, Podnieks, K, Rucevskis, P, Zarins, A, Barrett, A, Neogi, SG, Krestyaninova, M, McCarthy, MI, Brazma, A, & Sarkans, U. (2007). PASSIM--an open source software system for managing information in biomedical studies. BMC Bioinformatics 8:52.

APPENDICES

Appendix A: Overall project report

Project(s) Selected for Report:

S. No.	Project ID	Name	Status
1	LIMS_Tag-It P450 2D6_SP	LIMS_Tag-It P450 2D6_SP	Approved(Execution)

Project Name : LIMS_Tag-It P450 2D6_SP

In Charge :Santosh Phillips
Created By :Santosh Phillips
Planned Start :2008-03-07
Planned End :2008-03-11
Actual Start :2008-03-07
Actual End:2008-03-19
Status :Approved(Execution)
Comments
Comments History :

Comments from Santosh Phillips, Mar 19, 2008 10:37:39 AM
The title for this project,in collaboration with Laboratory Informatics, School of Informatics, is "Laboratory Information Management Systems and Genotyping Workflows: Applications in High-throughput Drug Metabolism Genotyping"

Project Samples :
No samples have been added to this project.
Project Plates :
No plates have been added to this project.
Personnel :

S. No.	ID	Name	Role
1	ADMIN-2	DAVID O KENNEDY	Biotracker Adminstrator
2	Skaar	Todd Skaar	Professor/Head
3	Sudha	Sudha Johnson	Student

Project Collaboration :

S. No.	ID	Name
1	Riley Children's hospital	Riley Children's Hospital
2	School of Informatics	Laboratory Informatics

Contacts : No contacts have been added to this project.

Documents/Images : No documents have been added to this project.

Contacts

S. No.	ID	Name
1	David	David Kennedy
2	Merchant	Mahesh Merchant

Experiment(s) Selected for Report:

S. No.	Name	Created By	Status	Approval Authority
1	Tag-It Sample_Collection	Santosh Phillips	Approved(Execution)	Todd Skaar
2	Tag-It DNA_Extraction	Santosh Phillips	Approved(Execution)	Todd Skaar
3	Tag-It Sample_Preparation	Santosh Phillips	Approved(Execution)	Todd Skaar
4	Tag-It Amplicon_Treatment	Santosh Phillips	Approved(Execution)	Todd Skaar
5	Tag-It Multiplex_ASPE	Santosh Phillips	Approved(Execution)	Todd Skaar
6	Tag-It Bead_Hybridization	Santosh Phillips	Approved(Execution)	Todd Skaar
7	Tag-It Data_Acquisition	Santosh Phillips	Approved(Execution)	Todd Skaar
8	Tag-It Data_Analysis	Santosh Phillips	Approved(Execution)	Todd Skaar

EXPERIMENT DETAILS (Tag-It Sample_Collection)

Status :Approved(Execution)
Approved By :Skaar
Created By :Santosh Phillips
Created Date :2008-03-07
Comments History

Comments from Santosh Phillips, Mar 19, 2008 9:58:46 AM
Experiment was delayed

Schedule:

S. No.	Planned Start	Planned End	Actual Start	Actual End
1	2008-03-07	2008-03-07	2008-03-07	2008-03-19

Protocols:

S. No.	ID	Name
1	Tag-It-Sample Collection	Tag-It-Sample Collection (1.2)
2	Tag-It-Sample Collection	Tag-It-Sample Collection (1.3)

RESOURCE SCHEDULING

Personnel:

S. No.	Person Name	Role *	Schedule Start Date	Schedule End Date
1	DAVID O KENNEDY	Biotracker Adminstrator	2008-03-07 0:0	2008-03-07 0:0
2	Todd Skaar	Professor/Head		
3	Sudha Johnson	Student	2008-03-07 0:0	2008-03-07 0:0

Run(s) Selected for Report:

S. No.	Name	Used Protocol	Created By	Status
1	Sample Collection	Tag-It-Sample Collection (1.2)	Santosh Phillips	Approved(Execution)
2	Sample Collection 2	Tag-It-Sample Collection (1.3)	Santosh Phillips	Approved(Execution)

For Run : Sample Collection

Project Name : LIMS_Tag-It P450 2D6_SP
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date :2008-03-07

Experiment Name : Tag-It Sample_Collection
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date : 2008-03-07

Status :Approved(Execution)
Approved By :Todd Skaar
Protocol :Tag-It-Sample Collection (1.2)
Comments :

Comments from Santosh Phillips, Mar 19, 2008 4:15:08 AM
There are no input samples. Only whole blood sample as output samples.

RUN INPUTS

Inventory:

S. No.	Inventory	Inventory Type	Concentration	Protocol Quantity/Sample	Required Quantity	Used Quantity	Container Type	Location
1	10 ml Collection tube	Labware		1 10^0	1 10^0	16 10^0	Tube	Organization >> Genotyping lab

Review/Approval History For Run: Sample Collection

Requested by	:Santosh Phillips
Requested Date	:2008-03-19
Requester Comments	:Please, review and approve.
Approved by	:Todd Skaar
Approved Date	:2008-03-19
Approver Comments	:Approved

For Run : Sample Collection 2

Project Name	: LIMS_Tag-It P450 2D6_SP
Status	: Approved(Execution)
Created By	: Santosh Phillips
Created Date	:2008-03-07
Experiment Name	: Tag-It Sample_Collection
Status	: Approved(Execution)
Created By	: Santosh Phillips
Created Date	: 2008-03-07

Status	:Approved(Execution)
Approved By	:Todd Skaar
Protocol	:Tag-It-Sample Collection (1.3)
Comments	:Additional protocol

Execution Parameters :
No Execution Parameters are available.

RUN INPUTS

Inventory:

S. No.	Inventory	Inventory Type	Concentration	Protocol Quantity/Sample	Required Quantity	Used Quantity	Container Type	Location
1	10 ml Collection tube	Labware		1 10^0	8 10^0			

Samples:

S. No.	ID	Name	Type	Container Type	Location	Quantity	Protocol Quantity
1	LTP450_001	LTP450_001	Whole blood		Organization >> Inbox	10 mL	
2	LTP450_002	LTP450_002	Whole blood		Organization >> Inbox	10 mL	
3	LTP450_003	LTP450_003	Whole blood		Organization >> Inbox	10 mL	
4	LTP450_004	LTP450_004	Whole blood		Organization >> Inbox	10 mL	
5	LTP450_005	LTP450_005	Whole blood		Organization >> Inbox	10 mL	
6	LTP450_006	LTP450_006	Whole blood		Organization >> Inbox	10 mL	
7	LTP450_007	LTP450_007	Whole blood		Organization >> Inbox	10 mL	
8	LTP450_008	LTP450_008	Whole blood		Organization >> Inbox	10 mL	

Review/Approval History For Experiment: Tag-It Sample_Collection

Requested by :Santosh Phillips
Requested Date :2008-03-19
Requested Comments :Please, review and approve.

Approved by :Todd Skaar
Approved Date :2008-03-19
Approver Comments :Approved.

EXPERIMENT DETAILS (Tag-It DNA_Extraction)

Status :Approved(Execution)
Approved By :Skaar
Created By :Santosh Phillips
Created Date :2008-03-07
Comments History

Comments from Santosh Phillips, Mar 19, 2008 9:59:01 AM
Experiment was delayed

Schedule:

S. No.	Planned Start	Planned End	Actual Start	Actual End
1	2008-03-07	2008-03-07	2008-03-07	2008-03-19

Protocols:

S. No.	ID	Name
1	Tag-It-DNA Extraction	Tag-It-DNA Extraction (1.2)

RESOURCE SCHEDULING
Personnel:

S. No.	Person Name	Role *	Schedule Start Date	Schedule End Date
1	DAVID O KENNEDY	Biotracker Adminstrator	2008-03-07 0:0	2008-03-07 0:0
2	Todd Skaar	Professor/Head	2008-03-07 0:0	2008-03-07 0:0
3	Sudha Johnson	Student	2008-03-07 0:0	2008-03-07 0:0

Instrument Types: No instrument schedules have been added to this experiment.

Laboratories: No laboratory schedules have been added to this experiment.

Experiment Samples :
No samples have been added to this experiment.

Run(s) Selected for Report:

S. No.	Name	Used Protocol	Created By	Status
1	DNA extraction	Tag-It-DNA Extraction (1.2)	Santosh Phillips	Approved(Execution)

RUN INPUTS

Inventory:

S. No.	Inventory	Inventory Type	Concentration	Protocol Quantity/Sa...	Required Quan...	Used Quantity	Container Type	Location
1	Tubes 0.5	Labware		1 10^0	8 10^0	8 10^0	Tube	Organization >> Genotyping lab
2	Triton X-100 surfac...	Chemical	100 mg/mL	2 µL	14.4 µL - 17.6 µL	16 µL	Bottle	Organization >> Clin. Pharmacol Lab 1 >> ...
3	TE Buffer	Chemical	10 mM	3 mL	23.2 mL - 24.8...	24 mL	Bottle	Organization >> Clin. Pharmacol Lab 1 >> ...
4	Isopropanol	Chemical		1.4 mL	10.4 mL - 12 mL	11.2 mL	Bottle	Organization >> Clin. Pharmacol Lab 1 >> F...
5	Ethanol	Chemical		2 mL	15.2 mL - 16.8...	16 mL	Bottle	Organization >> Inbox
6	Buffer QBT	Chemical		5 mL	39.2 mL - 40.8...	40 mL	Bottle	Organization >> Inbox
7	Buffer QC	Chemical		3 mL	23.2 mL - 24.8...	24 mL	Bottle	Organization >> Genotyping lab
8	Buffer QF	Chemical		2 mL	15.2 mL - 16.8...	16 mL	Bottle	Organization >> Genotyping lab

Samples:

S. No.	ID	Name	Type	Container Type	Location	Quantity	Protocol Quantity
1	P450_LIMS_WB001	P450_LIMS_WB001	P450_LIMS_WholeBlood		Organization >> Genotyping lab	5 mL	
2	P450_LIMS_WB002	P450_LIMS_WB002	P450_LIMS_WholeBlood		Organization >> Genotyping lab	5 mL	
3	P450_LIMS_WB003	P450_LIMS_WB003	P450_LIMS_WholeBlood		Organization >> Genotyping lab	5 mL	
4	P450_LIMS_WB004	P450_LIMS_WB004	P450_LIMS_WholeBlood		Organization >> Genotyping lab	4 mL	
5	P450_LIMS_WB005	P450_LIMS_WB005	P450_LIMS_WholeBlood		Organization >> Genotyping lab	5 mL	
6	P450_LIMS_WB006	P450_LIMS_WB006	P450_LIMS_WholeBlood		Organization >> Genotyping lab	5 mL	
7	P450_LIMS_WB007	P450_LIMS_WB007	P450_LIMS_WholeBlood		Organization >> Genotyping lab	5 mL	
8	P450_LIMS_WB008	P450_LIMS_WB008	P450_LIMS_WholeBlood		Organization >> Genotyping lab	5 mL	

RUN OUTPUTS

Instrument Files:
No output files/instruments have been added to this run.

Sample Observations:

S. No.	Sample Name
1	P450_LIMS_WB001
2	P450_LIMS_WB002
3	P450_LIMS_WB003
4	P450_LIMS_WB004
5	P450_LIMS_WB005
6	P450_LIMS_WB006
7	P450_LIMS_WB007
8	P450_LIMS_WB008

Output Samples:

S. No.	Input Samples	Output Samples	Container Type	Created By	Location
1	P450_LIMS_WB001	P450_LIMS_DNA_ART01-1		Santosh Phillips	Organization >> Genotyping lab >> Freezer >> Rack[2, 10]
2	P450_LIMS_WB002	P450_LIMS_DNA_ART02-1		Santosh Phillips	Organization >> Genotyping lab >> Freezer >> Rack[3, 10]
3	P450_LIMS_WB003	P450_LIMS_DNA_ART03-1		Santosh Phillips	Organization >> Genotyping lab >> Freezer >> Rack[4, 10]
4	P450_LIMS_WB004	P450_LIMS_DNA_ART04-1		Santosh Phillips	Organization >> Genotyping lab >> Freezer >> Rack[5, 10]
5	P450_LIMS_WB005	P450_LIMS_DNA_ART05-1		Santosh Phillips	Organization >> Genotyping lab >> Freezer >> Rack[6, 10]
6	P450_LIMS_WB006	P450_LIMS_DNA_ART06-1		Santosh Phillips	Organization >> Genotyping lab >> Freezer >> Rack[7, 10]
7	P450_LIMS_WB007	P450_LIMS_DNA_ART07-1		Santosh Phillips	Organization >> Genotyping lab >> Freezer >> Rack[8, 10]
8	P450_LIMS_WB008	P450_LIMS_DNA_ART08-1		Santosh Phillips	Organization >> Genotyping lab >> Freezer >> Rack[9, 10]

Review/Approval History For Run: DNA extraction

Requested by	:Santosh Phillips
Requested Date	:2008-03-07
Requester Comments	:
Reviewed by	:Santosh Phillips
Reviewed Date	:2008-03-07
Reviewer Comments	:

Review/Approval History For Run: DNA extraction

Requested by	:Santosh Phillips
Requested Date	:2008-03-19
Requester Comments	:Please, review and approve.
Reviewed by	:Todd Skaar
Reviewed Date	:2008-03-19
Reviewer Comments	:

Review/Approval History For Run: DNA extraction

Requested by	:Santosh Phillips
Requested Date	:2008-03-19
Requester Comments	:Please, review and approve.
Approved by	:Todd Skaar
Approved Date	:2008-03-19
Approver Comments	:

Review/Approval History For Experiment: Tag-It DNA_Extraction

Requested by :Santosh Phillips
Requested Date :2008-03-19
Requested Comments :Please, review and approve.

Approved by :Todd Skaar
Approved Date :2008-03-19
Approver Comments :Approved.

EXPERIMENT DETAILS (Tag-It Sample_Preparation)

Status :Approved(Execution)
Approved By :Skaar
Created By :Santosh Phillips
Created Date :2008-03-07
Comments History

Comments from Santosh Phillips, Mar 19, 2008 9:59:17 AM
Experiment was delayed

Schedule:

S. No.	Planned Start	Planned End	Actual Start	Actual End
1	2008-03-07	2008-03-07	2008-03-19	2008-03-19

Protocols:

S. No.	ID	Name
1	Tag-It Sample Preparation	Tag-It Sample Preparation-Multiplex PCR (1.2)

RESOURCE SCHEDULING
Personnel:

S. No.	Person Name	Role *	Schedule Start Date	Schedule End Date
1	DAVID O KENNEDY	Biotracker Adminstrator	2008-03-07 0:0	2008-03-07 0:0
2	Todd Skaar	Professor/Head	2008-03-07 0:0	2008-03-07 0:0
3	Sudha Johnson	Student	2008-03-07 0:0	2008-03-07 0:0

Run(s) Selected for Report:

S. No.	Name	Used Protocol	Created By	Status
1	Sample preparation	Tag-It Sample Preparation-Multiplex PCR (1.2)	Santosh Phillips	Approved(Execution)

For Run : Sample preparation

Project Name : LIMS_Tag-It P450 2D6_SP
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date :2008-03-07

Experiment Name : Tag-It Sample_Preparation
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date : 2008-03-07

Status :Approved(Execution)
Approved By :Todd Skaar
Protocol :Tag-It Sample Preparation-Multiplex PCR (1.2)
Comments :Experiment was slightly delayed

RUN INPUTS

Inventory:

S. No.	Inventory	Inventory T...	Concentra...	Protocol Quantity/S...	Required Qua...	Used Quan...	Container T...	Location
1	Tag-It PCR Primer ...	Primer		2 µL	16 µL	16 µL	Vial	Organization >> Clin. Pharmacol Lab 1 >> Fridge 2...
2	Tag-It PCR Primer ...	Primer		2 µL	16 µL	16 µL	Tube	Organization >> Clin. Pharmacol Lab 1 >> Fridge 2...
3	PCR Master Mix	Stock Solution		12 µL	96 µL	96 µL	Tube	Organization >> Clin. Pharmacol Lab 1 >> Fridge 2...
4	0.2 ml Thin wall PCR...	Labware		2 10^0	16 10^0	16 10^0	Labware	Organization >> Clin. Pharmacol Lab 1 >> Cabinet

Samples:

S. No.	ID	Name	Type	Container Type	Location	Quantity	Protocol Quan...
1	P450_LIMS_DNA_ART...	P450_LIMS_DNA_A...	P450_LIMS_DNA_...		Organization >> Genotyping lab >> Freezer >> Rac...	4 µL	4 µL
2	P450_LIMS_DNA_ART...	P450_LIMS_DNA_A...	P450_LIMS_DNA_...		Organization >> Genotyping lab >> Freezer >> Rac...	4 µL	4 µL
3	P450_LIMS_DNA_ART...	P450_LIMS_DNA_A...	P450_LIMS_DNA_...		Organization >> Genotyping lab >> Freezer >> Rac...	4 µL	4 µL
4	P450_LIMS_DNA_ART...	P450_LIMS_DNA_A...	P450_LIMS_DNA_...		Organization >> Genotyping lab >> Freezer >> Rac...	4 µL	4 µL
5	P450_LIMS_DNA_ART...	P450_LIMS_DNA_A...	P450_LIMS_DNA_...		Organization >> Genotyping lab >> Freezer >> Rac...	4 µL	4 µL
6	P450_LIMS_DNA_ART...	P450_LIMS_DNA_A...	P450_LIMS_DNA_...		Organization >> Genotyping lab >> Freezer >> Rac...	4 µL	4 µL
7	P450_LIMS_DNA_ART...	P450_LIMS_DNA_A...	P450_LIMS_DNA_...		Organization >> Genotyping lab >> Freezer >> Rac...	4 µL	4 µL
8	P450_LIMS_DNA_ART...	P450_LIMS_DNA_A...	P450_LIMS_DNA_...		Organization >> Genotyping lab >> Freezer >> Rac...	4 µL	4 µL

Output Samples:

S. No.	Input Samples	Output Samples	Container Type	Created By	Location
1	P450_LIMS_DNA_ART01	PRIMER_SMPLMIX_-1		Santosh Phillips	Organization >> Genotyping lab
2	P450_LIMS_DNA_ART02	PRIMER_SMPLMIX_02-1		Santosh Phillips	Organization >> Genotyping lab
3	P450_LIMS_DNA_ART03	PRIMER_SMPLMIX_03-1		Santosh Phillips	Organization >> Genotyping lab
4	P450_LIMS_DNA_ART04	PRIMER_SMPLMIX_04-1		Santosh Phillips	Organization >> Genotyping lab
5	P450_LIMS_DNA_ART05	PRIMER_SMPLMIX_05-1		Santosh Phillips	Organization >> Genotyping lab
6	P450_LIMS_DNA_ART06	PRIMER_SMPLMIX_06-1		Santosh Phillips	Organization >> Genotyping lab
7	P450_LIMS_DNA_ART07	PRIMER_SMPLMIX_07-1		Santosh Phillips	Organization >> Genotyping lab
8	P450_LIMS_DNA_ART08	PRIMER_SMPLMIX_08-1		Santosh Phillips	Organization >> Genotyping lab

Review/Approval History For Run: Sample preparation

Requested by :Santosh Phillips
Requested Date :2008-03-19
Requester Comments :Please, review and approve.

Approved by :Todd Skaar
Approved Date :2008-03-19
Approver Comments :Approved

Review/Approval History For Experiment: Tag-It Sample_Preparation

Requested by :Santosh Phillips
Requested Date :2008-03-19
Requested Comments :Please, review and approve.

Approved by :Todd Skaar
Approved Date :2008-03-19
Approver Comments :Approved.

EXPERIMENT DETAILS (Tag-It Amplicon_Treatment)

Status :Approved(Execution)
Approved By :Skaar
Created By :Santosh Phillips
Created Date :2008-03-07
Comments History

Comments from Santosh Phillips, Mar 19, 2008 9:59:41 AM
Experiment was delayed.

Schedule:

S. No.	Planned Start	Planned End	Actual Start	Actual End
1	2008-03-08	2008-03-08	2008-03-19	2008-03-19

Protocols:

S. No.	ID	Name
1	Tag-It-Amplicon Treatment	Tag-It-Amplicon Treatment (1.2)

RESOURCE SCHEDULING
Personnel:

S. No.	Person Name	Role *	Schedule Start Date	Schedule End Date
1	DAVID O KENNEDY	Biotracker Adminstrator	2008-03-08 0:0	2008-03-08 0:0
2	Todd Skaar	Professor/Head	2008-03-08 0:0	2008-03-08 0:0
3	Sudha Johnson	Student	2008-03-08 0:0	2008-03-08 0:0

Run(s) Selected for Report:

S. No.	Name	Used Protocol	Created By	Status
1	Amplicon treatment	Tag-It-Amplicon Treatment (1.2)	Santosh Phillips	Approved(Execution)

For Run : Amplicon treatment

Project Name : LIMS_Tag-It P450 2D6_SP
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date :2008-03-07

Experiment Name : Tag-It Amplicon_Treatment
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date : 2008-03-07

Status :Approved(Execution)
Approved By :Todd Skaar
Protocol :Tag-It-Amplicon Treatment (1.2)
Comments :Experiment was delayed

Execution Parameters :
No Execution Parameters are available.

RUN INPUTS

Inventory:

S. No.	Inventory	Inventory ...	Concentra...	Protocol Quantity/...	Required Qu...	Used Qua...	Container ...	Location
1	Tag-It Enzyme mix	Stock Solu...		2.5 µL	20 µL	20 µL	Tube	Organization >> Clin. Pharmacol Lab 1 >> Fridge 1 >> ...
2	0.2 ml Thin wall PC...	Labware		1 10^0	8 10^0	8 10^0	Labware	Organization >> Clin. Pharmacol Lab 1 >> Cabinet

Samples:

S. No.	ID	Name	Type	Container Type	Location	Quantity	Protocol Quantity
1	PRIMER_SMPLMIX_-1	PRIMER_SMPLMIX_	PRIMER_SMPLMIX		Organization >> Genotyping lab	20 µL	20 µL
2	PRIMER_SMPLMIX_02-1	PRIMER_SMPLMIX_02	PRIMER_SMPLMIX		Organization >> Genotyping lab	20 µL	20 µL
3	PRIMER_SMPLMIX_03-1	PRIMER_SMPLMIX_03	PRIMER_SMPLMIX		Organization >> Genotyping lab	20 µL	20 µL
4	PRIMER_SMPLMIX_04-1	PRIMER_SMPLMIX_04	PRIMER_SMPLMIX		Organization >> Genotyping lab	20 µL	20 µL
5	PRIMER_SMPLMIX_05-1	PRIMER_SMPLMIX_05	PRIMER_SMPLMIX		Organization >> Genotyping lab	20 µL	20 µL
6	PRIMER_SMPLMIX_06-1	PRIMER_SMPLMIX_06	PRIMER_SMPLMIX		Organization >> Genotyping lab	20 µL	20 µL
7	PRIMER_SMPLMIX_07-1	PRIMER_SMPLMIX_07	PRIMER_SMPLMIX		Organization >> Genotyping lab	20 µL	20 µL
8	PRIMER_SMPLMIX_08-1	PRIMER_SMPLMIX_08	PRIMER_SMPLMIX		Organization >> Genotyping lab	20 µL	20 µL

Output Samples:

S. No.	Input Samples	Output Samples	Container Type	Created By	Location
1	PRIMER_SMPLMIX_	Amplicon_PCR_product01-1		Santosh Phillips	Organization >> Genotyping lab
2	PRIMER_SMPLMIX_02	Amplicon_PCR_product02-1		Santosh Phillips	Organization >> Genotyping lab
3	PRIMER_SMPLMIX_03	Amplicon_PCR_product03-1		Santosh Phillips	Organization >> Genotyping lab
4	PRIMER_SMPLMIX_04	Amplicon_PCR_product04-1		Santosh Phillips	Organization >> Genotyping lab
5	PRIMER_SMPLMIX_05	Amplicon_PCR_product05-1		Santosh Phillips	Organization >> Genotyping lab
6	PRIMER_SMPLMIX_06	Amplicon_PCR_product06-1		Santosh Phillips	Organization >> Genotyping lab
7	PRIMER_SMPLMIX_07	Amplicon_PCR_product07-1		Santosh Phillips	Organization >> Genotyping lab
8	PRIMER_SMPLMIX_08	Amplicon_PCR_product08-1		Santosh Phillips	Organization >> Genotyping lab

Review/Approval History For Run: Amplicon treatment

Requested by :Santosh Phillips
Requested Date :2008-03-19
Requester Comments :Please, review and approve.

Approved by :Todd Skaar
Approved Date :2008-03-19
Approver Comments :Approved

Review/Approval History For Experiment: Tag-It Amplicon_Treatment

Requested by :Santosh Phillips
Requested Date :2008-03-19
Requested Comments :Please, review and approve.

Approved by :Todd Skaar
Approved Date :2008-03-19
Approver Comments :Approved.

EXPERIMENT DETAILS (Tag-It Multiplex_ASPE)

Status :Approved(Execution)
Approved By :Skaar
Created By :Santosh Phillips
Created Date :2008-03-07
Comments History

Comments from Santosh Phillips, Mar 19, 2008 9:59:57 AM
Experiment was delayed.

Schedule:

S. No.	Planned Start	Planned End	Actual Start	Actual End
1	2008-03-08	2008-03-08	2008-03-19	2008-03-19

Protocols:

S. No.	ID	Name
1	Tag-It-Multiplex ASPE	Tag-It-Multiplex ASPE (1.2)

Run(s) Selected for Report:

S. No.	Name	Used Protocol	Created By	Status
1	Multiplex ASPE	Tag-It-Multiplex ASPE (1.2)	Santosh Phillips	Approved(Execution)

Run(s) Selected for Report:

S. No.	Name	Used Protocol	Created By	Status
1	Multiplex ASPE	Tag-It-Multiplex ASPE (1.2)	Santosh Phillips	Approved(Execution)

For Run : Multiplex ASPE

Project Name : LIMS_Tag-It P450 2D6_SP
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date :2008-03-07

Experiment Name : Tag-It Multiplex_ASPE
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date : 2008-03-07

Status :Approved(Execution)
Approved By :Todd Skaar
Protocol :Tag-It-Multiplex ASPE (1.2)
Comments :Experiment was slightly delayed

Execution Parameters :
No Execution Parameters are available.

RUN INPUTS

Inventory:

S. No.	Inventory	Inventory T...	Concentra...	Protocol Quantity/S...	Required Qua...	Used Quan...	Container T...	Location
1	ASPE Master Mix	Stock Solution		15 µL	120 µL	120 µL	Tube	Organization >> Clin. Pharmacol Lab 1 >> Fridge 2...
2	0.2 ml Thin wall PCR...	Labware		1 10^0	8 10^0			
3	0.2 ml Thin wall PCR...	Labware		1 10^0	8 10^0	8 10^0	Labware	Organization >> Clin. Pharmacol Lab 1 >> Cabinet

Samples:

S. No.	ID	Name	Type	Container Type	Location	Quantity	Protocol Quantity
1	Amplicon_PCR_product01-1	Amplicon_PCR_product01	Amplicon_PCR_product		Organization >> Genotyping lab	5 µL	5 µL
2	Amplicon_PCR_product02-1	Amplicon_PCR_product02	Amplicon_PCR_product		Organization >> Genotyping lab	5 µL	5 µL
3	Amplicon_PCR_product03-1	Amplicon_PCR_product03	Amplicon_PCR_product		Organization >> Genotyping lab	5 µL	5 µL
4	Amplicon_PCR_product04-1	Amplicon_PCR_product04	Amplicon_PCR_product		Organization >> Genotyping lab	5 µL	5 µL
5	Amplicon_PCR_product05-1	Amplicon_PCR_product05	Amplicon_PCR_product		Organization >> Genotyping lab	5 µL	5 µL
6	Amplicon_PCR_product06-1	Amplicon_PCR_product06	Amplicon_PCR_product		Organization >> Genotyping lab	5 µL	5 µL
7	Amplicon_PCR_product07-1	Amplicon_PCR_product07	Amplicon_PCR_product		Organization >> Genotyping lab	5 µL	5 µL
8	Amplicon_PCR_product08-1	Amplicon_PCR_product08	Amplicon_PCR_product		Organization >> Genotyping lab	5 µL	5 µL

Output Samples:

S. No.	Input Samples	Output Samples	Container Type	Created By	Location
1	Amplicon_PCR_product01	ASPE_PCR_PDT01-1		Santosh Phillips	Organization >> Genotyping lab
2	Amplicon_PCR_product02	ASPE_PCR_PDT02-1		Santosh Phillips	Organization >> Genotyping lab
3	Amplicon_PCR_product03	ASPE_PCR_PDT03-1		Santosh Phillips	Organization >> Genotyping lab
4	Amplicon_PCR_product04	ASPE_PCR_PDT04-1		Santosh Phillips	Organization >> Genotyping lab
5	Amplicon_PCR_product05	ASPE_PCR_PDT05-1		Santosh Phillips	Organization >> Genotyping lab
6	Amplicon_PCR_product06	ASPE_PCR_PDT06-1		Santosh Phillips	Organization >> Genotyping lab
7	Amplicon_PCR_product07	ASPE_PCR_PDT07-1		Santosh Phillips	Organization >> Genotyping lab
8	Amplicon_PCR_product08	ASPE_PCR_PDT08-1		Santosh Phillips	Organization >> Genotyping lab

Review/Approval History For Run: Multiplex ASPE

Requested by	:Santosh Phillips
Requested Date	:2008-03-19
Requester Comments	:Please, review and approve.
Approved by	:Todd Skaar
Approved Date	:2008-03-19
Approver Comments	:Approved

Review/Approval History For Experiment: Tag-It Multiplex_ASPE

Requested by	:Santosh Phillips
Requested Date	:2008-03-19
Requested Comments	:Please, review and approve.
Approved by	:Todd Skaar
Approved Date	:2008-03-19
Approver Comments	:Approved.

EXPERIMENT DETAILS (Tag-It Bead_Hybridization)

Status :Approved(Execution)
Approved By :Skaar
Created By :Santosh Phillips
Created Date :2008-03-07
Comments History

Comments from Santosh Phillips, Mar 19, 2008 10:00:11 AM
Experiment was delayed.

Schedule:

S. No.	Planned Start	Planned End	Actual Start	Actual End
1	2008-03-09	2008-03-09	2008-03-19	2008-03-19

Protocols:

S. No.	ID	Name
1	Tag-It Bead Hybridization	Tag-It Bead Hybridization (1.2)

RESOURCE SCHEDULING
Personnel:

S. No.	Person Name	Role *	Schedule Start Date	Schedule End Date
1	DAVID O KENNEDY	Biotracker Adminstrator	2008-03-09 0:0	2008-03-09 0:0
2	Todd Skaar	Professor/Head	2008-03-09 0:0	2008-03-09 0:0
3	Sudha Johnson	Student	2008-03-09 0:0	2008-03-09 0:0

Run(s) Selected for Report:

S. No.	Name	Used Protocol	Created By	Status
1	Bead Hybridzation	Tag-It Bead Hybridization (1.2)	Santosh Phillips	Approved(Execution)

For Run : Bead Hybridzation

Project Name : LIMS_Tag-It P450 2D6_SP
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date :2008-03-07

Experiment Name : Tag-It Bead_Hybridization
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date : 2008-03-07

Status :Approved(Execution)
Approved By :Todd Skaar
Protocol :Tag-It Bead Hybridization (1.2)
Comments :Experiment slightly delayed

Execution Parameters :
No Execution Parameters are available.

RUN INPUTS

Inventory:

S. No.	Inventory	Inventory T...	Concentra...	Protocol Quantity/S...	Required Qua...	Used Quan...	Container T...	Location
1	1X Wash Buffer	Stock Solution		300 µL	2240 µL - 256...	2400 µL	Bottle	Organization >> Clin. Pharmacol Lab 1
2	Tag_It Bead Mix	Chemical		45 µL	356 µL - 364 µL	360 µL	Tube	Organization >> Clin. Pharmacol Lab 1 >> Freezer...
3	SA-PE Reporter so...	Stock Solution		150 µL	1160 µL - 124...	1160 µL	Bottle	Organization >> Clin. Pharmacol Lab 1

Samples (Input and Output)

S. No.	ID	Name	Type	Container Type	Location	Quantity	Protocol Quantity
1	ASPE_PCR_PDT01-1	ASPE_PCR_PDT01	ASPE_PCR_PDT		Organization >> Genotyping lab	5 µL	5 µL
2	ASPE_PCR_PDT02-1	ASPE_PCR_PDT02	ASPE_PCR_PDT		Organization >> Genotyping lab	5 µL	5 µL
3	ASPE_PCR_PDT03-1	ASPE_PCR_PDT03	ASPE_PCR_PDT		Organization >> Genotyping lab	5 µL	5 µL
4	ASPE_PCR_PDT04-1	ASPE_PCR_PDT04	ASPE_PCR_PDT		Organization >> Genotyping lab	5 µL	5 µL
5	ASPE_PCR_PDT05-1	ASPE_PCR_PDT05	ASPE_PCR_PDT		Organization >> Genotyping lab	5 µL	5 µL
6	ASPE_PCR_PDT06-1	ASPE_PCR_PDT06	ASPE_PCR_PDT		Organization >> Genotyping lab	5 µL	5 µL
7	ASPE_PCR_PDT07-1	ASPE_PCR_PDT07	ASPE_PCR_PDT		Organization >> Genotyping lab	5 µL	5 µL
8	ASPE_PCR_PDT08-1	ASPE_PCR_PDT08	ASPE_PCR_PDT		Organization >> Genotyping lab	5 µL	5 µL

S. No.	Input Samples	Output Samples	Container Type	Created By	Location
1	ASPE_PCR_PDT01	REPORTER_SMPLMIX01-1		Santosh Phillips	Organization >> Genotyping lab
2	ASPE_PCR_PDT02	REPORTER_SMPLMIX02-1		Santosh Phillips	Organization >> Genotyping lab
3	ASPE_PCR_PDT03	REPORTER_SMPLMIX03-1		Santosh Phillips	Organization >> Genotyping lab
4	ASPE_PCR_PDT04	REPORTER_SMPLMIX04-1		Santosh Phillips	Organization >> Genotyping lab
5	ASPE_PCR_PDT05	REPORTER_SMPLMIX05-1		Santosh Phillips	Organization >> Genotyping lab
6	ASPE_PCR_PDT06	REPORTER_SMPLMIX06-1		Santosh Phillips	Organization >> Genotyping lab
7	ASPE_PCR_PDT07	REPORTER_SMPLMIX07-1		Santosh Phillips	Organization >> Genotyping lab
8	ASPE_PCR_PDT08	REPORTER_SMPLMIX08-1		Santosh Phillips	Organization >> Genotyping lab

EXPERIMENT DETAILS (Tag-It Data_Acquisition)

Status :Approved(Execution)
Approved By :Skaar
Created By :Santosh Phillips
Created Date :2008-03-07
Comments History

Comments from Santosh Phillips, Mar 19, 2008 10:00:29 AM
Experiment was delayed.

Schedule:

S. No.	Planned Start	Planned End	Actual Start	Actual End
1	2008-03-09	2008-03-09	2008-03-19	2008-03-19

Protocols:

S. No.	ID	Name
1	Tag-It Dectection on xMAP	Tag-It Dectection on xMAP (1.2)

RESOURCE SCHEDULING
Personnel:

S. No.	Person Name	Role *	Schedule Start Date	Schedule End Date
1	DAVID O KENNEDY	Biotracker Adminstrator	2008-03-09 0:0	2008-03-09 0:0
2	Todd Skaar	Professor/Head	2008-03-09 0:0	2008-03-09 0:0
3	Sudha Johnson	Student	2008-03-09 0:0	2008-03-09 0:0

Run(s) Selected for Report:

S. No.	Name	Used Protocol	Created By	Status
1	Data Acquisition	Tag-It Dectection on xMAP (1.2)	Santosh Phillips	Approved(Execution)

For Run : Data Acquisition

Project Name : LIMS_Tag-It P450 2D6_SP
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date :2008-03-07

Experiment Name : Tag-It Data_Acquisition
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date : 2008-03-07

Status :Approved(Execution)
Approved By :Todd Skaar
Protocol :Tag-It Dectection on xMAP (1.2)
Comments :

RUN INPUTS

Inventory:
No inventories have been added to this run.
Samples:

S. No.	ID	Name	Type	Container Type	Location	Quantity	Protocol Quantity
1	REPORTER_SMPLMIX01-1	REPORTER_SMPLMIX01	REPORTER_SMPLMIX		Organization >> Genotyping lab	150 µL	150 µL
2	REPORTER_SMPLMIX02-1	REPORTER_SMPLMIX02	REPORTER_SMPLMIX		Organization >> Genotyping lab	150 µL	150 µL
3	REPORTER_SMPLMIX03-1	REPORTER_SMPLMIX03	REPORTER_SMPLMIX		Organization >> Genotyping lab	150 µL	150 µL
4	REPORTER_SMPLMIX04-1	REPORTER_SMPLMIX04	REPORTER_SMPLMIX		Organization >> Genotyping lab	150 µL	150 µL
5	REPORTER_SMPLMIX05-1	REPORTER_SMPLMIX05	REPORTER_SMPLMIX		Organization >> Genotyping lab	150 µL	150 µL
6	REPORTER_SMPLMIX06-1	REPORTER_SMPLMIX06	REPORTER_SMPLMIX		Organization >> Genotyping lab	150 µL	150 µL
7	REPORTER_SMPLMIX07-1	REPORTER_SMPLMIX07	REPORTER_SMPLMIX		Organization >> Genotyping lab	150 µL	150 µL
8	REPORTER_SMPLMIX08-1	REPORTER_SMPLMIX08	REPORTER_SMPLMIX		Organization >> Genotyping lab	150 µL	150 µL

Output Samples:

S. No.	Input Samples	Output Samples	Container Type	Created By	Location
1	REPORTER_SMPLMIX01	TagIt_BEADHYBRI_PDT01-1		Santosh Phillips	Organization >> Inbox
2	REPORTER_SMPLMIX02	TagIt_BEADHYBRI_PDT02-1		Santosh Phillips	Organization >> Inbox
3	REPORTER_SMPLMIX03	TagIt_BEADHYBRI_PDT03-1		Santosh Phillips	Organization >> Inbox
4	REPORTER_SMPLMIX04	TagIt_BEADHYBRI_PDT04-1		Santosh Phillips	Organization >> Inbox
5	REPORTER_SMPLMIX05	TagIt_BEADHYBRI_PDT05-1		Santosh Phillips	Organization >> Inbox
6	REPORTER_SMPLMIX06	TagIt_BEADHYBRI_PDT06-1		Santosh Phillips	Organization >> Inbox
7	REPORTER_SMPLMIX07	TagIt_BEADHYBRI_PDT07-1		Santosh Phillips	Organization >> Inbox
8	REPORTER_SMPLMIX08	TagIt_BEADHYBRI_PDT08-1		Santosh Phillips	Organization >> Inbox

Review/Approval History For Run: Data Acquisition

Requested by	:Santosh Phillips
Requested Date	:2008-03-19
Requester Comments	:Please, review and approve.
Approved by	:Todd Skaar
Approved Date	:2008-03-19
Approver Comments	:Approved

Review/Approval History For Experiment: Tag-It Data_Acquisition

Requested by	:Santosh Phillips
Requested Date	:2008-03-19
Requested Comments	:Please, review and approve.
Approved by	:Todd Skaar
Approved Date	:2008-03-19
Approver Comments	:Approved.

EXPERIMENT DETAILS (Tag-It Data_Analysis)

Status :Approved(Execution)
Approved By :Skaar
Created By :Santosh Phillips
Created Date :2008-03-07
Comments History

Comments from Santosh Phillips, Mar 19, 2008 10:00:51 AM
Experiment was delayed.

Schedule:

S. No.	Planned Start	Planned End	Actual Start	Actual End
1	2008-03-09	2008-03-11	2008-03-19	2008-03-19

Protocols:

S. No.	ID	Name
1	Tag-It-Data Analysis	Tag-It-Data Analysis (1.2)

RESOURCE SCHEDULING
Personnel:

S. No.	Person Name	Role *	Schedule Start Date	Schedule End Date
1	DAVID O KENNEDY	Biotracker Adminstrator	2008-03-10 0:0	2008-03-11 0:0
2	Todd Skaar	Professor/Head	2008-03-10 0:0	2008-03-11 0:0
3	Sudha Johnson	Student	2008-03-10 0:0	2008-03-11 0:0

Run(s) Selected for Report:

S. No.	Name	Used Protocol	Created By	Status
1	Data Analysis	Tag-It-Data Analysis (1.2)	Santosh Phillips	Approved(Execution)

For Run : Data Analysis

Project Name : LIMS_Tag-It P450 2D6_SP
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date :2008-03-07

Experiment Name : Tag-It Data_Analysis
Status : Approved(Execution)
Created By : Santosh Phillips
Created Date : 2008-03-07

Status :Approved(Execution)
Approved By :Todd Skaar
Protocol :Tag-It-Data Analysis (1.2)
Comments :Experiment slightly delayed

Execution Parameters :
No Execution Parameters are available.

RUN INPUTS

Instrument type

S. No.	Instrument	Instrument Type	Location	Duration
1	Data station	Computer	Organization >> Genotyping lab	

Output Files:

S. No.	File Name	File Type
1	Interpretation of calls	.doc
2	LIMS_TAGIt_finaLRESULTS030708-02	.doc
3	LIMS_TAGIt_finaLRESULTS030709	.txt
4	LIMS_TAGIt_finaLRESULTS030709	.xls

Review/Approval History For Run: Data Analysis

Requested by :Santosh Phillips
Requested Date :2008-03-19
Requester Comments :Please, review and approve.

Approved by :Todd Skaar
Approved Date :2008-03-19
Approver Comments :Approved

Review/Approval History For Experiment: Tag-It Data_Analysis

Requested by :Santosh Phillips
Requested Date :2008-03-19
Requested Comments :Please, review and approve.

Approved by :Todd Skaar
Approved Date :2008-03-19
Approver Comments :Approved.

Review/Approval History For Project: LIMS_Tag-It P450 2D6_SP

Requested by :Santosh Phillips
Requested Date :2008-03-19
Requested Comments :To be reviewed and approved on behalf of Todd Skaar.

Approved by :Todd Skaar
Approved Date :2008-03-19
Approver Comments :Approved

Appendix B: Questionnaire

Dear Scientist,
This questionnaire has been designed to solicit your responses to issues about knowledge, attitude, and implementation of Laboratory Informatics Management System (LIMS) in your current laboratory. A LIMS is computer software that is used in the laboratory for the management of samples, laboratory users, instruments, standards and other laboratory functions such as invoicing, plate management, and work flow automation. Your response is very much appreciated.

Part A: (Select and insert your response in the last column)

	ITEM	**CHOICES**	**Response**
A1	Sex	Male (1) Female (2)	
A2	Age	20-30 yrs (1) 30-40 yrs (2) 40-50 yrs (3) 50 yrs +(4)	
A3	City		
A4	State	(Two-letter abbreviation only)	
A5	Type of academic institution	Private (1) Public (2)	
A6	Field of expertise		
A7	How long have you worked in this field?	< 1 yr (1) 1-2 yrs (2) 3-5 yrs (3) 5+ yrs (4)	
A8	How long have you worked in present laboratory?	< 1 yr (1) 1-2 yrs (2) 3-5 yrs (3) 5+ yrs (4)	
A9	How many hours a day do you spend working in the laboratory?	< 1 hr (1) 1-4 hrs (2) 5-8 yrs (3) 8+ hrs (4)	
A10	How many hours do you spend working in the laboratory at the weekends?	Never (1) < 1 hr (2) 1-4 hrs (3) 5-8 yrs (4) 8+ hrs (5)	
A11	How many scientific or technical people (e.g., professors, postdoctorates, students, and technicians) are present in your laboratory?	Only one (1) < 3 (2) 3-5 (3) 6+ (4)	

A12	How would you rate your laboratory in terms of modern technology?	Equipments present in own laboratory, modern, adequate (1) Equipments present in own laboratory, outdated, adequate (2) Equipments present in own laboratory, modern, inadequate (3) Equipments present in own laboratory, outdated, inadequate (4) Rely entirely on core facilities equipments (5)	
Part B: (Select and insert your response in last column)			
	ITEM	**CHOICES**	**Response**
B1	How often have you used any of these technologies below?	Never (1) Rarely (2) Sometimes (3) Often (4) Always (5)	
	Software to electronically and automatically record any part of your experiment		
	Software to transfer your experimental results automatically from your measuring equipment or instrument to storage site		
	Software program to electronically record every change you make to your records		
	Software program to detect who performed an experiment		
	Software program to detect when a real experiment was performed		
	Software program to automatically run an experiment		
B2	If you use LIMS select from among the list those items that best describe the functionalities you use (Insert X in the Response column)	Sequencing	
		Gene expression	
		Genotyping assays	
		Proteomics core labs	
		Bio-specimen banking facilities	
		Laboratory administration	
		Study design and scheduling	
		Workflow design and execution	
		Inventory management and tracking system	
		Audit trails	
		Report building	
		Protocol building	
		Instrument integration for automated data capture	

		Review and approval of documents	
		Other	
B3	How long have you used LIMS?	Never (1) < 1mo (2) 1-6 mos (3) 7– 23mos (4) 2-5yrs (5) 5+ yrs (6)	
B4	What reasons account for your not having used LIMS before? (Insert X in the Response column)	Unavailability	
		Financial constraints	
		Do not know much about it	
		Will not affect research productivity	
		Other…….	

VITA

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EDUCATION

Master of Science in Chemical Informatics (Laboratory Informatics specialization), May 2008
Indiana University-Purdue University Indianapolis

- Course work: Data acquisition, Data Processing, Laboratory Information Management Systems (LIMS), Laboratory Automation, Scientific Data Management, Electronic Laboratory Notebooks, Project Management, Laboratory Robotics, Regulatory Compliance and Validation.
- Project/Thesis: LIMS implementation in P450 2D6 genotyping workflows

Doctor of Philosophy in Nutrition (Biochemistry option), 2001
Osaka City University, Osaka, Japan

- Coursework: Nutritional biochemistry, Nutritional Physiology, Molecular biology, Cell biology, Food Chemistry
- Thesis: Involvement of Protein tyrosine phosphorylation in the anticarcinogenic effect of green tea polyphenols

Bachelor of Science (Honors) in Nutrition, and Biochemistry (minor), 1988
University of Ghana, Legon, Ghana

EXPERIENCE

Private Consultant September 2003 - August 2006
Research Consultancy Caribou, Maine

- Designed Nutrition and cancer studies for Japanese scientists (collaboration)
- Analyzed data from research studies
- Composed and edited manuscripts for Japanese scientists in English for publication in peer-reviewed journals.

Postdoctoral Research Fellow July 2001 – September 2003
Columbia University, Mailman School of Public Health New York, New York

- Conducted (100% contribution) a two-year research on biomarkers for breast cancer risk in sister pairs discordant for the disease
- Performed Epstein -Barr virus cell transformations
- Performed high-throughput genotyping (GSTM, XRCC, XPD genes) and phenotyping assays (DNA repair ability)

Senior Research Assistant, January 1990 - September 1995
Noguchi Memorial Institute for Medical Research, Ghana

- Conducted biochemical assays on blood and tissue samples.
- Analyzed food composition (protein, fat, trace minerals and amino acids).
- Carried out field anthropometric studies.

TECHNICAL SKILLS

Research Science

- Basic cell biology techniques: Cell viability, proliferation, cytotoxicity and apoptotic death assays
- Molecular biology techniques: RNA, DNA, protein analysis, PCR, SDS-PAGE, High-throughput genotyping assays for SNPs, Immunohistochemistry, ELISA
- Research designing
- Independent data analysis

Laboratory Information Management

- Databases: Access
- Languages: G-programming in Labview, Structured Query Language
- Laboratory Information Management Systems: Labware, LabVantage-Sapphire, Biotracker, Electronic Lab Notebook (LabTrack), Visualization software (Spotfire)
- Scientific Data Management Systems: Cyberlab, Waters NuGenesis
- Chromatography Data Management System : PerkinElmer TotalChrom
- Laboratory Robotics: BioWorks (Biomek)
- Miscellaneous: Microsoft Word, Excel, PowerPoint, Photoshop

AWARDS AND HONORS

- Cancer Research and Prevention Foundation Postdoctoral fellowship (New York, 2001)
- LabWare Fellowship for Innovation in Laboratory Informatics (IUPUI, 2006-2007)
- Japanese Government Ministry of Education (Mombusho) PhD scholarship (Osaka, Japan, 1995-2001)