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Virginia Commonwealth University Life Sciences Virginia Commonwealth University

This is to certify that the thesis prepared by Niti Vanee entitled THE GENOME SCALE METABOLIC MODEL OF *Cryptosporidium hominis: i*NV213 has been approved by her committee as satisfactory completion of the thesis requirement for the degree of Masters of Science.

Dr. Gregory A. Buck, Center for the Study of Biological Complexity

Dr. Stephen S. Fong, Chemical and Life Sciences Engineering

Dr. Yuan Gao, Computer Science and Center for the Study of Biological Complexity

Dr. Gregory A. Buck, Director of Center for the Study of Biological Complexity

Dr. Thomas Huff, Dean of VCU Life Sciences

Dr. F. Douglas Boudinot, Dean of the Graduate School

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THE GEOME SCALE METABOLIC MODEL OF CRYPTOSPORIDIUM HOMINIS:

*I*NV213

A thesis submitted in partial fulfillment of the requirements for the degree of Masters of Sciences at Virginia Commonwealth University.

by

NITI VANEE Bachelors of Technology, College of Engineering and Technology IILM Academy of Higher Learning, India, May 2006

Director: DR. GREGORY A. BUCK DIRECTOR, CENTER FOR THE STUDY OF BIOLOGICAL COMPLEXITY

Virginia Commonwealth University Richmond, Virginia August, 2009



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Abstract

THE GENOME SCALE METABOLIC MODEL OF CRYPTOSPORIDIUM HOMINIS:

*i*NV209

By Niti Vanee, B.Tech.

A thesis submitted in partial fulfillment of the requirements for the degree of Master of Science at Virginia Commonwealth University.

Virginia Commonwealth University, 2009

Major Director: Dr. Gregory A. Buck Director, Center for the Study of Biological Complexity

The apicomplexan *Cryptosporidium* is a protozoan parasite of humans and other mammals. *Cryptosporidium* species cause acute gastro-enteritis and diarrheal disease in healthy humans and animals, and cause life-threatening infection in immuno-compromised individuals such as people with AIDS. It has a one-host life cycle and invades intestinal epithelial cells causing diarrhea, or more rarely the pulmonary epithelium. *Cryptosporidium* carries out all the asexual reproductive stages like several other apicomplexans. Current annotation of this organism predicts it to contain 3884 genes of which only 1581 genes have predicted functions. By using a combination of bioinformatics



analysis, biochemical evidence, and high-throughput data, a genome-scale metabolic model of *Cryptosporidium hominis* is being constructed. The current model is comprised of approximately 213 gene-associated enzymes involved in major metabolic pathways including carbohydrate, nucleotide, amino acid, and energy metabolism. The approach of constructing a genome-scale model provides a link between the genotype and the phenotypic behavior of the organism, making it possible to study and predict behavior based upon genome content. This modeling approach provides an overview for evaluating missing components in a metabolic network and provides an analytical framework for interpreting data as more research becomes available. The goal of constructing this model is to systematically study and analyze various functional behaviors of *C. hominis* with respect to its stages in life cycle and pathogenicity.



CHAPTER 1 INTRODUCTION

1.1 Cryptosporidium

Cryptosporidium is a protozoan parasite that belongs to the apicomplexa phylum. It causes acute gastroenteritis and diarrhea. Many outbreaks in United States occurred in water parks, community swimming pools and day care centers. Interest in the study of this parasite has increased in the last two decades especially after the outbreak of cryptosporidiosis in Milwaukee, Wisconsin in 1993 where approximately 403,000 people were affected. It was the largest waterborne disease outbreak documented in the history of United States (Kenzie et al., 1994). Transmission of *Cryptosporidium* occurs mainly through contact with the contaminated water (e.g., drinking and recreational water). It is resistant to chemical treatment of water, like chlorination, as it exists in the form of oocysts when outside the host cell and these oocysts pass through the filtration systems of the water supplies as well.

The two most studied species, *C. hominis* and *C. parvum*, which differ in host range, genotype, and pathogenicity, are more relevant to humans. *C.hominis* infects only humans, whereas *C. parvum* also spreads in other mammals. (Xu et al., 2004).





Figure 1: Infection cycle and life cycle of *Cryptosporidium* (adapted from Cryptosporidiosis figure from Department of Health and Human Services)



1.1.1 Infection cycle and life cycle

Cryptosporidium is transmitted be the fecal-oral route via the oocyst stage. These infections increase with close human-to-human contact and by contact with infected livestock, zoo animals, or companion animals (Fayer, 1997).

Transmission of *Cryptosporidium parvum* and *C. hominis* occurs mainly through contact with contaminated water (e.g., drinking or recreational water) as shown in Figure 1. Sometimes it may also be transmitted by food sources, such as chicken salad. Many outbreaks in the United States have occurred in water parks, community swimming pools, and day care centers. Zoonotic and anthroponotic transmission of *C. parvum* and anthroponotic transmission of *C. hominis* occur through exposure to infected animals or exposure to water contaminated by feces of infected animals.

The life cycle of *Cryptosporidium*, shown diagrammatically in Figure 1, is complex as it involves both sexual and asexual developmental stages. It begins upon the inhalation or the ingestion of sporulated oocysts, which is the only exogenous stage, containing 4 sporozoites within a tough layered wall. It is excreted from the body of an infected host in the feces. Following ingestion (and possibly inhalation) by a suitable host, excystation occurs. The sporozoites are released and infect the epithelial cells of the gastrointestinal tract or other tissues such as the respiratory tract. Here the parasites undergo asexual multiplication (schizogony or merogony stages) and then sexual multiplication (gametogony) producing microgamonts (male) and macrogamonts (female). Upon fertilization of the macrogamonts by the microgametes, oocysts are developed that



sporulate in the infected host. Two different types of oocysts are produced -

 Δ The thick-walled, which is commonly excreted from the host, and

 Δ The thin-walled oocyst, which is primarily involved in autoinfection.

Oocysts are infective upon excretion, thus permitting direct and immediate fecaloral transmission. (Department of Health and Human Services; Thompson et al., 2005)

Oocysts – Thick- as well as thin-walled oocysts are usually recovered from culture after 5 days of inoculation. Approximately 80% of the oocysts formed after the completion of the life cycle are thick- walled oocysts, which are released from the host in the faeces if present in the gastrointestinal tract, or via aerosols or nasal secretions if present in the respiratory tract. However, about 20% of oocysts fails to form a thick oocyst wall and are thus known as thin-walled oocysts. Thin-walled oocysts are important in autoinfection through continuous recycling of sporozoites excysting from ruptures thin-walled oocysts. (Thompson et al., 2005)

Sporozoites – are 5.2 X 1.2 μ m in size and are characterized by having a comma shape with a rounded posterior end and a pointed tapered anterior end. They actively move inside the oocysts, excysting and exhibits gliding movement. (Thompson et al., 2005)

1.1.2 Maintenance and amplification of Cryptosporidium

Cryptosporidium species are not very well studied because culturing and amplification of the organism of a big challenge. One of the major objectives of many



laboratories is to amplify the parasite and develop reproducible models of infection to facilitate biological, pathological, immunological and molecular and drug evaluation studies. There are two ways by which *Cryptosporidium* can be amplified: *in vivo*, in animal models and *in vitro* using different cell lines.

1.1.2.1 Challenges faced in vivo.

The majority of *in vivo* infections have been carried out using the *C. parvum* cattle genotype. Experimental infections with *C. parvum* have been successfully established in a variety of domestic and laboratory animals, especially neonates, immunosuppressed or immunodeficient animals. But there is a high level of difference in infectivity for laboratory animals even between two closely related species of *Cryptosporidium - C. parvum* and *C. hominis. C. parvum* cattle genotype can readily infect mice and cattle whereas *C.hominis* does not infect them. (Peng et al., 1997)

In summary, *Cryptosporidium* does not support the infection with multiple genotypes. Apart from this, the amplification of *Cryptosporidium* in animal models is labor-intensive, expensive beyond the budget of most of the laboratories, and will not support the growth of the parasite for long period of time. (Thompson et al., 2005)

1.1.2.2 Challenges faced in vitro

There are many factors that affect the development and proliferation of *Cryptosporidium* in culture. These include the excystation protocol, age and strain of parasite, stage and size of the inoculum, host cell types and maturity, and culture



conditions such as pH, medium supplements and atmosphere. (Thompson et al., 2005)

Although, major improvements in culturing *Cryptosporidium* in vitro have occurred since 1984, infections could not be maintained for more than a few days and only asexual phases of the parasite life cycle could be consistently maintained for short periods. Efforts are going on in the direction to optimize the conditions for growth in order to increase the number of parasite stages produced and days to maintain the culture for longer period of time. (Thompson et al., 2005)

1.1.3 Host-pathogen interaction - disease caused

Cryptosporidium lives in the intestine of the infected humans and animals, is transmitted by ingestion of oocycsts, and completes its life cycle in a single host (Figure 1). In healthy humans, the parasite is responsible for symptoms such as watery diarrhea, abdominal cramps or pain, dehydration, nausea, vomiting, fever, and weight loss. Its major impact has been among those with weakened immune systems, including, people with HIV or AIDS or Transplant recipients. They may develop serious, chronic, and sometimes fatal version of the illness (P. Xu et al., 2004). There is no therapy available so far to treat patients suffering from cryptosporidiosis.

The time from ingestion of oocysts to the appearance of clinical signs is between 2 and 14 days. The first clinical signs associated with infection is, diarrhea, which may or may not be associated with abdominal cramping. Severity varies from continuous voluminous watery diarrhea to scant or intermittent diarrhea. Blood is infrequently observed in the stool. Other clinical signs include general malaise, fever, and fatigue, loss



of appetite, nausea and vomiting. Dehydration and weight loss are also direct result from the symptoms (Ramirez, et al., 2004).

In immunocompetent host, clinical signs last for 10-14 days, but in the immunocompromised individuals they can persist for months to years. (Thompson et al., 2005)

It is of particular concern for four reasons:

- The oocyst is extremely resistant to disinfection and cannot be killed with routine water-disinfection procedures;
- 2. The disease is not treatable with antibiotics;
- The mortality from infection in severely immunocompromised patients can be as high as 50-60%; and
- 4. Animal and human fecal wastes are associated with transmission of the disease to humans. (Bates, 2007)

1.1.4 Genome of Cryptosporidium hominis

The parasite genome was sequenced in 2004 by Xu et al. describes that it has eightchromosome, approximately 9.2 mb genome size and contains an estimated 3994 genes. *In silico* reconstitution of *C.hominis* biochemical properties reveal that basic metabolic pathways are extremely streamlined. The parasite depends mainly on glycolysis for energy production. It supports both aerobic and anaerobic metabolism. However, it shows limited



biosynthetic pathways and mainly relies on transporters. Following figure from Xu et al. explains the major metabolic pathways inside the *C.hominis*. (Xu et al., 2004)



Figure 2: Predicted metabolic network inside *C.hominis* on the basis of genome annotation (Xu et al., 2004)

1.2 Systems Biology

Genome Sequencing has enabled us to determine the biological components that make up a cell or an organism. The new discipline of systems biology examines how these components interact and form networks and how the networks generate the whole cell



functions corresponding to observable phenotypes. The study of whole systems, with the inclusion of genomic, proteomic, metabolomic, and fluxomic data together, is termed Systems Biology (Figure 3).



Figure 3: Several elements that describe an organism (Fong, 2008)

This approach focuses on finding the relation between the genotype and phenotype of an organism by using a network model, permitting a better understanding of the cellular processes. Recently, many network models of various organisms have been constructed and validated for use in biological prediction including *Bacillus subtilis, Escherichia coli, Saccharomyces cerevisiae,* Human cardiac mitochondria and Human RBCs. (Joyce &



Palsson, 2007)

1.2.1 Modeling approach - Constraint Based Modeling

Bringing together all the potential biochemical reactions of an organism, builds up a network chart of metabolic pathways however, in the biological world, cells are subjected to various constraints from environmental, physiochemical, evolutionary, and regulatory sources. By incorporating metabolic reactions as well as other above-mentioned properties into the systemic network reconstruction, these models account for the constraints that restrict an organism's phenotypic behavior. Apart from constraints that arise from network topology and stoichiometry, other constraints can be incorporated into these models, e.g. experimentally determined maximum enzyme fluxes, thermodynamic limitation, internal metabolic flux determinations, transcriptional regulation, etc. The constraint-based modeling approach helps distinguish the networks states that a system can achieve from those it cannot achieve rather than exactly predicting the network behavior. (Joyce & Palsson, 2007; Raghunathan et al., 2009)

1.2.2 Mathematical algorithms used for optimization

Once the model is ready in the mathematical form we use mathematical optimization algorithm to investigate the production capabilities and systemic properties of the metabolic network (Joyce & Palsson, 2007; Shlomi et al., 2008).



1.2.2.1 Linear programming algorithm - Flux Balance Analysis

Flux Balance Analysis (FBA) is a type of analysis that imposes mass balance and flux capacity constraints on the network and uses an optimization procedure to find a steady-state flux distribution that maximizes the biomass yield of the cell without the need for measurement of kinetic parameters. FBA relies on Linear programming based optimization. We define an objective function of our network such as biomass production, byproduct secretion, ATP production, etc. and try to optimize that objective. Linear programming works on optimizing the flux distribution for the network model that maximizes the stated objective. (Raman & Chandra, 2009; Roberts et al., 2009)

1.2.2.2 Mixed integer linear programming algorithm – MILP

Another type of optimization algorithm that is used in model analysis is MILP. It is called so because it unlike FBA when we use this algorithm we get the results in terms of integer (-1, 0, 1) that denoting if the reaction is in active state or inactive state and also gives us the flux value of the reaction which may be any decimal value between -1000 to 1000. The flux values are calculated from by linear programming as in FBA.

MILP used in the current work is from Shlomi et al. and the basis for MILP is to optimize the agreement between the two sets of information used (the metabolic model and the proteomic or expression data). (Shlomi et al., 2008)

In the ideal situation, the reactions that are expressed implies that the proteins coding for that specific reaction are active and the reactions that are inactive should mean that the proteins are inactive. In the biological world its not an ideal situation i.e. there is a



possibility that a specific protein is found in the system but reaction is still in affective because of other factors affecting it such as presence of substrate.

To better understand the functioning of MILP consider the following figure where the region of interested is either the active state of reaction and protein or the inactive state of reaction and protein and the aim is to maximize the information related to these 2 regions and minimize the false positive and negative region.



Reaction Expression

Figure 4: Optimization through MILP algorithm aims at maximizing the information related to the shaded region where reactions and proteins are both found either active or inactive and reducing the other regions. Note: false negative is the region where the protein is found in the systems but the reaction is not present or active where as false positive denotes the case where protein is absent in the system but the reaction is still expressed. The region of false positive exists with the gene expression data where genes are highly expressed or lowly expressed and not with the proteomic data.



1.3 Metabolic modeling

1.3.1 Introduction

Detailed, comprehensive-modeling efforts led to the development of three types of networks: metabolic networks, transcriptional regulatory networks and signaling networks (Palsson, 2007). The most commonly reconstructed and used networks are the metabolic networks that integrate the biochemical interactions present in the organism. Genome annotation provides the basis for the initial prediction of metabolic enzymes and the preliminary genome-scale model. Figure 4 shows the major steps involved construction genome scale metabolic models.

Metabolic network interacts with essentially all other cellular processes. The reconstruction of these processes and the integration of multiple networks will lead to the description of a comprehensive range of cellular functions.





Figure 5: Overall process of genome scale metabolic reconstruction (adapted from Palsson, 2007)

The metabolic reconstruction requires mainly 4 steps:

Step 1: Network reconstruction, i.e. obtaining the genome annotation of the target organism. Genome annotations are available at several only databases such as, IMG (Integrated Microbial Genome), EntrezGene, CMR (Comprehensive Microbial Resource), Genome Reviews (through EBI, European Bioinformatics Institute), etc. Also there are several organism specific sources of genome like EcoCyc for *E.coli*, SGD (*Saccharomyces* Genome Database), etc.



Other databases such as KEGG, MetaCyc, Transport DB can be used to provide metabolic and transport reaction that's have been shown to occur in a range of organisms. (Feist, et al., 2009)

Step 2: Refining the draft reconstruction. The draft reconstruction created in previous step needs to manually curated, ideally with the inputs from organism specific experts. This step of manual curation is labor intensive and sometimes tedious. Organism- specific databases, textbooks, primary publication, review articles, and experts familiar with the legacy data for an organism are the main sources of information for the manual curation step. These sources of information provide direct or indirect evidence for the inclusion of specific reactions in the metabolic reconstruction. (Feist et al., 2009)

Step 3: Mathematical modeling and analysis of the network. Applying mathematical algorithm to the curated biochemical to perform simulations and analysis. Once the network was reconstructed, the list of metabolic reactions was transformed into a stoichiometric matrix (S), i.e., the mathematical representation of the reconstructed network. The S matrix dimensions are $m \ge n$, where m is the number of metabolites and n is the number of reactions. Each element S_{ij} represents the stoichiometric coefficient of metabolite i in reaction j. If the metabolite in a particular reaction is a reactant, the coefficient is negative (the metabolite is consumed by the reaction); if it is a product, the coefficient is positive (the



metabolite is produced by the reaction). The S matrix was then used as the basis of further analysis, i.e., Flux Balance Analysis. FBA uses linear programming based optimization to identify a particular flux distribution distribution (a single point in the multidimensional space of possible metabolic behaviors) that optimizes a given metabolic objective (see Biomass Equation, below). The LP optimization problem is formulated as:

> Maximize Z, Subject to $\mathbf{S} \cdot \mathbf{v} = \mathbf{0}$, $\mathbf{a}_i < \mathbf{v}_i < \mathbf{b}_i$ for all reactions *i*.

Z is the objective function; for this study, Z was defined as the biomass equation. The second two statements are the flux constraints. **S** is the stoichiometric matrix defined above. Each reaction flux is subject to lower and upper bounds, as indicated (in cases where these are not known, a_i and b_i are set to some arbitrary numbers that exceed any feasible internal flux). The solution to this problem is an optimal flux distribution, **v**, a vector that contains flux values for each reaction in the network. The solution is optimal in the sense that it maximizes the flux through the objective Z.

Mathematically, S is a transformation of the reaction flux vector, v, to a vector of time derivatives for each metabolite concentration:

$$\mathbf{S} \cdot \mathbf{v} = d\mathbf{x}/dt.$$



Since the time constants for metabolic transients are fast (< tens of seconds), but the time constants for cell growth are long (hours to days), the metabolites can be considered as existing in a quasi-steady state (Joyce & Palsson, 2007). This leads to the second equation of the LP optimization problem above. Because of the emphasis on steady states, assumptions regarding reaction kinetics are not needed.

Biomass Equation: In FBA, optimization is used to find a particular flux distribution that maximizes a given metabolic objective. Typical metabolic objectives chosen for optimization include maximization of ATP production, byproduct secretion, or biomass production. In our work, we chose to optimize for biomass production (Roberts et al., 2009). Biomass production is represented in our model by an additional metabolic reaction. Its reactants include such critical metabolites as ATP, acetyl-CoA, and NADPH; its products include ADP, inorganic phosphate, and other metabolites that represented byproducts of anabolic metabolism.

Step 4: Integration of the high-throughput data. Further, the specific experimental or stage specific or tissue specific expression data or proteomic data is integrated with the existing comprehensive reconstructed metabolic network to



study the organisms' performance with respect to the data and thus make further predictions.

1.3.2 Application

Such model once completed can be applied to study the specific growth condition from which the training data were based and can be used to explore additional environmental condition. Network reconstructions help us to build mechanistic genotypephenotype relationships and thus obtain quantitative (such as, what is the cellular growth rate) and qualitative (such as, will the organism grow in a particular condition) predictions about the organism. (Feist et al., 2009)

In recent year with the growing popularity of the systems biology approach of solving biological problem, researchers from various fields have tried the metabolic reconstructs to analyze the target organism and explain the basis behind some of the previously discovered facts (de Figueiredo et al., 2008). Some of the important applications of metabolic model reconstruction include, optimization of production of certain metabolites (Hjersted & Henson, 2009), study host pathogen interaction (Raghunathan et al., 2009), studying single gene deletions (Xu, Sun, & Yu, 2009) or gene knock out screening (Plaimas et al., 2008) or identifying novel antimicrobial drugs targets (Lee et al., 2009).

1.4 Parasite study and metabolic modeling

In context of pathogenic organisms, a metabolic reconstruction has a potential to



plays important role in drug discovery. With the completion of genome projects of several parasites, there are efforts going on to make sense of that information in terms of genes, their products, interactions in growth and development and survival of parasite. (Wambua, Mcconkey, & Westhead, 2009)

1.4.1 Predicting new drug targets

Genomic information provides an accurate picture of the metabolic reactions that are present in the organism. With the analysis of essential reactions from the whole network we can predict the enzymes or transporters that might be viable targets for few new drug target.

1.4.2 Comparative genomics of host and pathogen metabolism

In the study for potential drug targets against the pathogens, one of the most area of study is the interaction between the host and pathogen. Many parasites are found to have lost pathways that are essential for free-living species. For example, *Mycoplasm genitalium* contains 580 genes (Suthers et al., 2009), *C. parvum* lacks Kreb's cycle enzymes (Fayer, 1997). Often, they depend on the host cell for these incomplete but required missing links. These kinds of interactions between host and pathogen can be compared and studied as potential targets to fight against parasitic disease.

In the current project a metabolic model of parasite *Cryptosporidium hominis* is constructed and integrated with proteomic data, and analyzed to make further predictions.



CHAPTER 2 METHODS

2.1 Reconstruction process – genome to metabolic network

The process of reconstructing the metabolic network of C.hominis is shown in Figure

- 5. The overall process is divided into 4 major steps:
 - Step 1. Network reconstruction
 - Step 2. Network refinement
 - Step 3. Network analysis and simulation
 - Step 4. Proteomic data integration

In brief, the reconstruction process starts with genome annotation that defines the list of functionally identifiable genes present in *C.hominis* (P. Xu et al., 2004). This serves as the basis for a set of possible reactions that are catalyzed by these annotated gene products (enzymes coded by genes). Tables 1 and 2 contain information on the online genome and pathway databases and key references used for the reconstruction process.





Figure 6: Summary for the C.hominis metabolic network reconstruction

Database	Link
Genome Database:	
CSBC Cryptosporidium hominis research	http://www.hominis.mic.vcu.edu
Integrated Microbial Genomes (IMG)	http://img.jgi.doe.gov
Pathways and other databases	
KEGG	http://www.genome.jp/kegg/pathway.html
Transport Classification database (TCDB)	http://www.tcdb.org/
Gene Protein Reaction (GPR)	
Uniprot	ftp://ftp.genome.jp/pub/kegg/genes/organis
	ms/cho/cho_xrefall.list

Table 1. Online resources for the reconstruction of metabolic network of C. hominis



Metabolism	References
Complete metabolism overview	Thompson et al. 2005
Carbohydrates	Thompson et al. 2005
Energy	Thompson et al. 2005
Nucleic acid Amino acid	Thompson et al. 2005
Fatty acids	Fritzler et al. 2007
-	Mazumdar et al. 2007
	Thompson et al. 2005

 Table 2. Key references consulted additional to the online resources for the reconstruction of metabolic network of C. hominis

2.2 Refining the model

EC numbers from the genome annotation were used to look for all possible reactions catalyzed by each enzyme. This created the list of possible reactions in the model. Also the gene IDs were added to the model for each reaction to create **Gene Protein Relation** (GPR) files file for further usage.

A list of metabolites required by the set of reactions was compiled within a **Source** file and also there was a compiled list of byproducts, as **Escapes** file were created with literature reviews of closely related species model available. These files were revised with data available for *C.hominis* experimental information and with simulation runs. Also, draft biomass equation was derived based on the existing equation for *B. subtilis* (Oh et al., 2007), as qualitative results of FBA are relatively insensitive to minor mis-specification of the coefficient values. The goal is to eventually have experimental values for *C.hominis*. All these files contain necessary inputs for steady state operation and simulate the availability of certain metabolites in culture medium.



2.3 Analysis of network using Metmodel and FBA

2.3.1 Gap analysis

The Python-based framework, Metmodel (Roberts & Buck, 2007) was used to build and analyze an initial genome scale model of metabolism of *C.hominis*. The model is stored in a series of text file. Metmodel uses these files as input, performs FBA and outputs the predicted fluxes for each reaction in the model, given a set of objective (biomass production). Some of the reactions were added after the first simulation run as the original network/annotation was found to have gaps.

Gap filling, also known as filling pathway holes, is a procedure for including the reactions that might be important and necessary to complete certain pathway for which only one or two reactions are missing. Most of the time it is possible that these reaction are present in the organism but the enzymes responsible for these reactions are not annotated in the genome, as there are several hypothetical proteins that are yet to be studied for their function. There is a possibility that these hypothetical proteins might code for some of these missing reaction.

2.3.2 Essential reaction

Metmodel also helped in finding the essential reaction, i.e. the subset of lethal reactions in the model. The steps of determining them were as follows:

For each reaction, X:


- 1. Set the upper and lower bounds of reaction X to zero by setting up constrain on the reaction to have zero flux. This simulates the loss of reaction.
- 2. Run FBA,
 - → If objective value from FBA run comes out to be 0 (or ~ 0), the reaction is predicted to be lethal which means that there is no growth when the reaction is inactivated.
 - → If not, then the reaction is predicted to be non-lethal, i.e. the parasite can still grow, even though reaction is inactivated.
- **3.** Reset the upper and lower bounds of reaction X to their original values.
- 4. Continue to next reaction.

2.4 Integrating the proteomic data with the model

As mentioned in the figure 1, parasite has a life cycle and the first two stages – oocysts and sporozoite were analyzed in terms of proteomic composition. Unpublished inhouse proteomic data that's was used in this project describes the list of active proteins in a specific stage. This information was used to active or inactive the reactions in the model and see how the model will perform. This stage specific proteomic data was integrated with an optimization algorithm from Shlomi et. al (Shlomi et al., 2008).

The graphical representation of the performance of metabolites in the 2 stages was shown using python based program designed in the laboratory. Figure 7 shows the graphical representation of the difference between the 2 stages. The following graph includes the metabolites that are used in highly different way in two stages. To draw this



chart, the difference in the conditions of both the stages was determined; all the metabolites involved in these conditions were listed. A score was assigned to these metabolites depending on the level of difference of usage of these metabolites in both the stages (i.e. highly different manner \sim highest score). Then the score was ranked and a threshold was set. To draw the final chart, the top list of metabolites was used.





Figure 7: Graphical representation of comparative analysis of 2 stages oocyst and sporozoite in *Cryptosporidium hominis* depending upon the unpublished in-house proteomic data. Blue arrows shows oocyst stage activity and red arrows denote the sporozoite stage activity. This graphical representation only includes the reactions that show maximum level of difference only



CHAPTER 3 RESULTS

3.1 Metabolic Reconstruction

The *i*NV213 network reconstruction accounts for the function of 213 genes and includes 540 reactions with 514 metabolic reaction (including inter-conversion reactions of some metabolites) and 26 are extra-cellular transport reaction. Due to lack of direct biochemical evidences for many reactions, information from genomic data, literature derived conclusions and information from the related organism is used to evidences used to include these reaction in the model. Despite the fact that *C. hominis* is a Eukaryote, the current model contains only one intracellular compartment – the cytosol - as there is not much of information available in terms of compartments and specific pathways that take place inside of the organism.

Figure 8 provides an overview of reactions of *i*NV213. Among, the pathways included in the model, carbohydrate metabolism seem the most functional metabolism network with glycolysis as one of the complete metabolic pathway. However, other metabolic network includes many reactions that are the inter-conversion reactions.





Figure 8: Reactions distribution in the model under several metabolic pathways. Miscellaneous reaction is the set of reactions that were required for the model but could not be categorized under specific metabolism network. Nucleotide metabolism, which is found to have maximum number of reaction in the network, actually comprises of multiple reactions that are coded by single enzymes but exact evidence could not be found to filter them and get the exact minimal set of reactions. Conclusively, carbohydrate metabolism was found to be the most functional and complete network in the model. After completion of reconstruction network a small set of reactions was added to the network to make it functional and yellow bars in each of the metabolic pathways highlights these reaction.

Above figure shows the reaction distribution of each of the metabolic pathway.

Genomic evidences support the completeness of metabolic networks such as, Energy



metabolism, glycan metabolism, metabolism of secondary products, and metabolism of other amino acids but some minor additions were required in the amino acid metabolism (3 reactions), carbohydrate metabolism (3 reactions), and nucleotide metabolism (7 reactions). Lipid metabolism accounts for 117 reactions with genomic evidence for 87 reactions. Other 30 reactions were added through gap analysis to complete the metabolic network to of the organism. These reactions are explained in next section of gap analysis.



Figure 9: Graphical representation of carbohydrate metabolism network that was found to be the active



3.2 Gap analysis – filling the missing links

The next important step in completion of the model was filling up the missing links - the gaps. There were some of the reactions added to the original *i*NV213 after performing the FBA simulation. This process is termed as gap analysis in network modeling. These reactions are required in order to complete certain pathways e.g., lipid metabolism cannot be functional if these 30 reactions (Supplementary file 2) are absent in the network. Similarly, there is a small set of reaction added to many other pathways including fructose mannose metabolism, glycolysis / gluconeogenesis, aminosugar metabolism, tyrosine metabolism, extra-cellular transport reactions, valine, leucine and isoleucine biosynthesis, pyrimidine metabolism and purine metabolism. There is a set of 29 reactions added to the model through gap analysis but their exact sub systems were not studied. These reactions are listed in the supplement data file 2 but are not included in the following figure of gap analysis reactions chart.

For some of these reaction filled in lipid metabolism by gap analysis, the enzymes responsible for them were further checked in genome of *C. hominis*. This was done by isolating the hypothetical protein sequences from the whole genome of *C.hominis* and performing the translated nucleotide BLAST against non-redundant protein sequences to see if there genome annotation can be updated after the developments since 2004 when this genome was last annotated. This might help us answer some of the questions about the reactions added through the gap analysis. At the current stage of this procedure, no significant matches were found but efforts are going on to optimize the search process.





Figure 9: Distribution of reactions added to the known metabolic networks by gap analysis algorithm. Almost 50% of the reactions are found to fill the gaps in lipid metabolism with most of the reaction in fatty acid biosynthesis, biosynthesis of steroids, glycerophospholipid metabolism and sphingolipid metabolism



3.3 Essential reaction

Simulation runs using Metmodel also helped in predicting the lethal reactions from the model. 52 reactions were found to be essential using the deletion prediction algorithm (described above). Summary of those lethal/essential reactions is shown in figure 10. When performing the iterative flux balance analysis to study for reaction deletions it was observed that eliminating reaction either reduces the optimal flux value or does not affects it at all. However, when any of these 52 reaction were removed or masked in the model the optimal flux value became negative which denotes there is no growth seen in the model if these reactions are absent from the pathway network.

Figure 10 shows the lethal reaction distribution among the respective pathways. Individual analysis of each of these reactions and comparing them with the ones added through gap analysis showed that some of these reactions that were found lethal were added in the process of gap analysis eg. in the fatty acid metabolism, 16 reaction were found lethal out of which 9 reactions were added to the model by gap analysis algorithm. Also, among the 3 important reactions of the glycerophospholipid metabolism all of them were added in the above step to complete the metabolic network chart. Other predicted lethal reaction include 5 reactions (out of 10) were found to be lethal. This prediction is well supported by all the previous literature about importance of glycolysis in *Cryptosporidium*. Glycolysis is the fully functional and active pathway in the organism and the major source of energy production as well (Thompson et al., 2005). The lethal reactions found in glycolysis are listed in table 3.





Figure 10: Predicted number of essential reaction in the respective pathway. Green bars denote the lethal reactions found in each of the metabolic pathway where as the yellow bar shows the subset of those lethal reactions, which were included in the model by gap analysis algorithm

Apart from these, other lethal reactions were from some of the amino acid metabolism (arginine and proline metabolism, glutamate metabolism), lipid metabolism (glycerolipid, and glycerophospholipid metabolism), NAD metabolism, and nucleotide metabolism.



Reaction	Enzyme	Reaction	Function
number in Glycolysis			
Reaction #	Fructose	Split Molecule in half:	The six-carbon fructose diphophate is split into two
4	bisphosphate	$fdp \leq => dhap + g3p$	three-carbon compounds, an aldehyde and a ketone.
Reaction #	Glyceraldehyde-	Oxidation/Phosphate Ester	This reaction is first an oxidation involving the
5	3-phosphate	Synthesis:	coenzyme NAD+. The aldehyde is oxidized to an
	denydrogenase	$g_{3}p + had + p_{1} <> 13dpg + h + had + p_{1} <> 13dpg + h + had + h$	NAD+ to NADH + H+. Then an inorganic
			phosphate is added in a phosphate esteer synthesis.
Reaction #	Phosphoglycero	Isomerization:	In this reaction the phosphate group moves from
7	mutase	2pg <==> 3pg	the 3 rd position to the 2 rd position in an
Reaction #	Enolase	Alcohol Dehydration:	In this reaction, which is the dehydration of an
8	Liloidse	$2pg \leq => h2o + pep$	alcohol, the -OH on C-3 and the -H on C-2 are
			removed to make a water molecule. At the same
			time a double bond forms between C-2 and C-3.
			This change makes the compound somewhat
			unstable, but energy for the final step of glycolysis.
Reaction #	Pyruvate kinase	Phosphate Ester Hydrolysis;	This is the final reaction in glycolysis. Again one
9		Synthesis of ATP:	of the phosphate groups undergoes hydrolysis to
		adp + h + pep> atp + pyr	form the acid and a phosphate ion, giving off
			coupled with the next endothermic reaction making
			ATP. The phosphate is transferred directly to an
			ADP to make ATP.

Table 3: Lethal reactions predicted in glycolysis and their function in the pathway (Ophardt, 2003)



3.4 Integrating the proteomic data

Summary of integration of proteomic data with metabolic network can be found in the attached supplementary data file (Appendix D). Out of all the predicted reactions, it was found that 48 reactions were common between both the stages oocyst and sporozoite but 12 reactions were found to be present only in oocyst stage and 14 reactions were listed under sporozoite stage only. An important point to be noticed in the result was that glucokinase is active in sporozoite stage but not in oocyst stage on the other hand hexokinase is active in oocyst stage. Hexokinase in known to have more affinity for glucose where as glucokinase shows less affinity for glucose. This is justified observation as during the sporozoite stage when parasite if inside host cell it has sufficient supply of glucose and thus can afford to have active glucokinase activity where as when in oocyst stage the supply of glucose is not sufficient and thus hexokinase is active instead to make the carbohydrate metabolism work during minimal glucose concentration. Glucokinase activity can be rapidly amplified or damped in response to changes in the glucose supply. Graphical representation of difference in metabolite performance in 2 stages is shown in figure 7.



CHAPTER 4 DISCUSSION

4.1 Model

Previous research has shown that *C. hominis* relies mainly on glycolysis for its energy metabolism (Thompson et al., 2005; Zhu & Rider Jr, 2009). The current annotation of its genome, (P. Xu et al., 2004; *Integrated microbial genome*.) suggests the absence of several biosynthetic capabilities such as synthesis of major amino acids and nucleotides and appears to rely mainly on the extra cellular transport reactions (approximately 69 proteins are annotated as transporters (P. Xu et al., 2004)). Nucleotide and amino acid includes salvage and inter-conversion pathways, but not the reactions for *de novo* synthesis since the parasite lacks that capability. Also, uptake of sugar, and amino acids in the model are facilitated by set transport reactions but the nucleotide and fatty acid uptake mechanism is not well understood and is therefore not completely discussed in the model. Fully functional glycolysis pathway as seen in *i*NV213 is supported by previous biochemical evidence (Fayer, 1997; Thompson et al., 2005; Zhu & Rider Jr, 2009), however some aspects of lipid in *C. hominis* are still not well understood. There is an ongoing analysis of the model to predict more such biochemical facts about the parasite to understand the



systems better and develop new, testable hypotheses.

4.2 Filling the gaps

Cryptosporidium lacks many important links in the minimal set of metabolic pathway that is required for its successful replication and thus, the first simulation runs showed that the reconstructed model is incomplete and lacks some metabolic reactions. Resolving these metabolic gaps entails expanding the model by identifying and including missing biochemical activities. This process basically consists of two steps: (1) identifying plausible candidate reactions that could complete the model and (2) finding genes that could catalyze the hypothesized activities. The current work completes the filling of gaps however, finding gene for the hypothesized activity is one of the future directions for the project.

Lipid metabolism was the metabolic network where most of the reactions were inserted to complete the reaction flow and get the optimal flux. These 30 reactions were in several categories respectively fatty acid metabolism, biosynthesis of steroids, glycerophospholipids, and shingolipids. Many previous and ongoing research suggest that these reactions, especially the glycerophosphlipids metabolism and biosynthesis of steroids are putative drug targets sites for apicomplexans. (Clastre et al., 2007; Ralph, D'Ombrain, & McFadden, 2001; Wambua et al., 2009) It is predicted that the reactions that are added through gap analysis in lipid metabolism might be the required reaction for completion of lipid metabolism but literature suggests that *Cryptosporidium* lacks the MEP pathway (Clastre et al., 2007) and therefore it can be predicted that they depend on the host cell for



these set of reaction. This opens up a prospect to individually analyze the subset of reaction added to the lipid metabolism to study the host – parasite interaction. As these reactions specially the ones added in glycerophospholipid mechanism are well-studied putative drug targets is other apicomplexans. Also, this information may be useful in determining minimal culture media requirement for the in vitro culturing of organism.

A noticeable addition to the glycerolipid pathways in this step was a phospholipase A2 catalyzed hydrolysis of phosphatidyl choline. However, there is a patent pending regarding use of phosphlipase A2 as biocides that neutralizes *C. parvum* sporozoite. (Homan, Imboden, Riggs, Carryn, & Schaefer, 2006) Thus, accuracy and eligibility of this addition of this reaction could not be established.

In a recent review, Zhu et al. (2009) explain the lipid metabolism to a great extent but still there is no evidence for the biosynthetic capabilities of fatty acids in the *C*. *hominis*. But since these reactions are predicted to be required for the metabolic network to complete it might be possible that the parasite depends on host cell for some of these reactions. This finding again leads to these questions: If the parasite needs these reactions for the metabolic network to complete can any of its hypothetical proteins code for any of these reactions? If not, then is it possible to answer question related to the transport mechanism to support the entry of these lipids into the pathogen?

To answer the first question, some of these functional proteins that coded for the newly added reaction were searched in the *C. hominis* genome. So far, no significant matches were found hence with the current understanding of model, no information could be added to the current genome annotation. This however opens up a prospect to perform



homology search for the specific proteins to reanalyze the subset of hypothetical proteins and also to study the transport mechanism of these lipids to update the list of transporter proteins in the parasite.

Another interesting link added to the model was in amino sugar metabolism pathway. UDP acetylglucosamine epimerase catalyzes the reaction involving UDP-N-acetyl-D-glucosamine. This reaction and enzyme is important in cyst-wall formation and Jarroll et al. suggest that this can be a putative drug target for cyst-walled protozoan. (Jarroll & Sener, 2003)

4.3 Essential reactions

The analysis of the essential reactions in the model is the most important outcome as this expected to determine the major potential drug target sites specific to *C.hominis*. From the subset of 52 reactions, Table 3 lists the 5 essential reactions of the glycolysis pathway, which accounts for almost 50% of the glycolysis reaction. But since glycolysis is an active pathway for all the host cells also, it does not prove to be a right direction to look for drug targets. An important extension of the work is to determine which of these lethal reactions are not affecting the human metabolic network. Attacking those sites might be useful in determining the weak link for the parasite.

This reaction deletion approach can be used to find the performance of the cell in presence of enzyme inhibitors. Thus, if reaction X is predicted to be lethal, and an inhibitor of that enzyme is available, then the model can predict what will be the probability of growth of parasite in the presence of inhibitor. And this can be useful find the infection



neutralization chemicals (the enzyme inhibitors).

4.4 From reaction deletion to gene knock out

The ultimate aim of such model reconstruction is to extend the analysis to study gene knockout experiments *in silico*. The reaction deletion approach is useful to find out important reactions in the metabolic network. The GPR (Gene Protein Relation) file was used to study the relation of genes and proteins (enzymes) to determine which gene were important in the metabolism network of parasite.

The supplement data file 3 provides the list of important genes that code for the lethal reactions in the metabolic network. These genes can be computationally switched on and off to study how the flux distribution would change in the presence or absence of a particular gene. Gene knockout experiments may again be useful to find putative drug targets for *Cyrptosporidium*. Some previous studies have shown how this approach can be made useful in predicting essential genes (Lee et al., 2009; Oh et al., 2007; Pinney et al., Nov 2007; Plaimas et al., 2008; Wambua et al., 2009). These genes will then be studied as potential drug targets that could be used to develop novel antibodies.

4.5 Conclusion

Genome-scale models integrate various types of data (genomic, expression and proteomic) and allow modeling of the integrated functions of an organism. It is a powerful tool that facilitates understanding of the whole system of an organism rather than focusing on a particular component or segment. This model-based study can be used to help



researchers prioritize experimental projects and save considerable time at the bench. Beyond serving as a tool for basic biological research, this computational approach also has potential medical and drug development relevance, e.g.: in pathogenic microbial models, each gene that is predicted to be essential by constraint based modeling and analysis, represents a potential drug target that could be used to develop novel antibiotics in future. Also, the network analysis of human biology may help us in detecting several therapeutic targets and thus provide a platform for assessing potentially adverse effects of novel treatments (Mo & Palsson, 2009). The flexibility of constraint-based models will lead to exploration of countless exciting biological questions in the future.



CHAPTER 5 FUTURE DIRECTIONS

5.1 Refining model

There are lot of questions unanswered in terms of nucleotide metabolism, and lipid metabolism. The metabolic networks needs to be more refined with some more literature, biochemical or experimental evidences that individually focus on each of these reactions. For example, in nucleotide metabolism there are many enzymes that work in multiple ways and catalyze more than one reaction (in some cases around 20 reaction) but there were no evidences how so ever to include or exclude any of those multiple reaction. Similar cases were found in lipid metabolism as well. These reactions can be selected by studying the parasite specifically in terms of nucleotide and lipid composition. This question can be answered by some of the facts such as preference of substrate, behavior of organism under specific condition or stages.

5.2 Finding the hypothesized function related gene

With the gap analysis there are several hypothetical functions added to the metabolic network of the parasite. From the pool of hypothetical proteins these function



related genes could be determined. A specific enzyme codes each of the reaction added by gap analysis. If we can find out all the possible nucleotide sequence that may code for these protein and compare it with the hypothetical proteins of *C.hominis* it is possible that this may help to update the genome annotation for the organism

5.3 Host pathogen interaction

This pathogen depends on its host for various essential nutrients that support life, and experimental determination of its growth requirements has proven difficult. As seen in the gap analysis and essential reaction analysis there are several reactions related to lipid metabolism which suggest the presence of fatty acid, steroid, glycerolipid biosynthetic capabilities however, previous biochemical findings do not support this result. It might be possible that the pathogen uses the host cell's biosynthetic capabilities for its survival in these cases. Analysis of this subset of reaction can be done in host cell to study how parasite might get this support of lipid metabolism to complete its growth requirement. This narrows down the list of reaction or pathways to focus on.

5.4 Culturing condition optimization

It is known that perfect culturing media composition could not be established for *C.hominis* growth (explained in section 1). From the gap analysis we have found some of the proteins that may be required by the organism but are not present in it. Experiments can be performed to see if addition of these enzymes in the culture media affects the growth in



some way. If the minimal media list can be derived by all these analysis it is possible to optimize its growth initially *in silico* then *in vitro*.



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Appendices



REACTION IDs	GENE IDs	EC NUMBER	ENZYME NAME	PATHWAY	REACTION
-					
R_BIOMASS	•		biomass	Biomass Equation	[c] : 0.257980584 ala-L + 0.176597196 arg-L + 0.218152121 asn-
R ALAR	Chro.50329 Chro.80047 or Chro.70182 or	5.1.1.1	alanineracemase	Alanine and Aspartate Metabolism	[c] : ala-L <==> ala-D
R ASNTRS	Chro.80047	6.1.1.22	Asparaginyl-tRNAsynthetase	Alanine and Aspartate Metabolism	[c] : asn-L + atp + trnaasn> amp + asntrna + ppi
R ALATRS	Chro.60075	6.1.1.7	Alanyl-tRNAsynthetase	Alanine and Aspartate Metabolism	[c] : ala-L + atp + trnaala> alatrna + amp + ppi
R PETHCI R CHLP	Chro. 70332 Chro. 80135	2.7.7.14	phosphoethanolaminecytidyltransferase cholinenhosphatenhosphatase	Aminophosphonate Metabolism	c : ctp + ethamp + h> cdpea + ppi [c]: choln + h2o> chol + ni
R CYANST	Chro.40314	2.8.1.1	Cyanidesulfurtransferase	Aminophosphonate Metabolism	[c] : cyan + tsul> h + so3 + tcynt
R GF6PTA	Chro.10420	2.6.1.16	glutamine-fructose-6-phosphatetransaminase	Aminosugar Metabolism	[c] : f6p + gln-L> gam6p + glu-L
R_UDPACGLP	Chro.40100 or Chro.70213	2.7.7.23	UDP-N-acetylglucosaminediphosphorylase	Aminosugar Metabolism	[c] : acgam1p + h + utp <==> ppi + udpacgal
R UAG4E		5.1.3.7	R UDP N acetylqlucosamine 4 epimerase	Aminosugar Metabolism	[c] : 1.0 uacgam> 1.0 uacgala
R ACGAMPM	Chro.40374	5.4.2.3	phosphoacetylglucosaminemutase	Aminosugar Metabolism	<pre>[c] : acgam6p <==> acgam1p</pre>
R PROAKGOX1	Chro.30441	1.14.11.2	L-Proline,2-oxoglutarate:oxygenoxidoreductase(4-hydrox	Arginine and Proline Metabolism	[c] : $akg + o2 + pro-L> 4hpro-LT + co2 + succ$
R NOS1	Chro.40304	1.14.13.39	NitricOxideSynthase(Notorning)	Arginine and Proline Metabolism	[c]: arg-L + h + nadph + o2> h2o + nadp + nwharg
R 3MOXTYROX	Chro.21000	1.4.3.4	3-Methoxytyramine:oxygenoxidoreductase(deaminating	Arginine and Proline Metabolism	[c] : 3moxtyr + h2o + o2> 3mox4hpac + h2o2 + nh4
R APRTO2	Chro.21000	1.4.3.4	N-acetylputrescine:oxygenoxireductase(deaminating)	Arginine and Proline Metabolism	[c] : aprut + h2o + o2> h2o2 + n4abutn + nh4
R MAOLNOR	Chro.21000	1.4.3.4	monoamineoxidase(L-Normetanephrine)	Arginine and Proline Metabolism	[c]: h20 + normete-L + o2> 3m4pga + h2o2 + nh4
R 4HGLSD	Chro.70551	1.5.1.12	L-4-hydroxyglutamatesemialdehydedehydrogenase,mitod	Arginine and Proline Metabolism	[c]: 4hglusa + h2o + nad <==> e4hglu + 2 h + nadh
R_HPROym	Chro.70551	1.5.1.12	L-hydroxyprolinedehydrogenase(NADP),mitochondrial	Arginine and Proline Metabolism	[c]: 4hpro-LT + nadp> 1p3h5c + 2 h + nadph
R 4HGLSDm	Chro.70551 Chro.70551	1.5.1.12	L-4-hydroxyolutamatesemialdehydedehydrogenase.mito	Arginine and Proline Metabolism	[c]: 4holusa + h2o + had <==> e4holu + 2 h + hadh
R PYR5CDm	Chro.70551	1.5.1.12	D1-pyrroline-5-carboxylatedehydrogenase, mitochondrial	Arginine and Proline Metabolism	[c] : glu5sa + h2o + nadp> glu-L + 2 h + nadph
R PUTA3	Chro.70551	1.5.1.12	puta3	Arginine and Proline Metabolism	[c] : glu5sa + h2o + nad> glu-L + 2 h + nadh
R HPROb	Chro.60426	1.5.1.2	pyrroline-5-carboxylatereductase	Arginine and Proline Metabolism	[c]: 1pyrsc + 2 n + nadph> nadp + pro-L[c]: 1n3h5c + 2 h + nadph> 4hpro-IT + nadp
R HPROa	Chro.60426	1.5.1.2	L-hydroxyprolinereductase(NAD)	Arginine and Proline Metabolism	[c] : 1p3h5c + 2 h + nadh> 4hpro-LT + nad
R P5CRm	Chro.60426	1.5.1.2	pyrroline-5-carboxylatereductase(m)	Arginine and Proline Metabolism	[c] : 1pyr5c + 2 h + nadph> nadp + pro-L
R PRO1x	Chro 60426	1.5.1.2	pyrroline-5-carboxylatereductase	Arginine and Proline Metabolism	[c] : 1pyr5c + 2 n + nadn> nad + pro-L [c] : nad + pro-L> 1pyr5c + 2 h + nadh
R PROTRS	Chro.60505 or Chro.80098	6.1.1.15	Prolyl-tRNAsynthetase	Arginine and Proline Metabolism	[c] : atp + pro-L + trnapro> amp + ppi + protrna
R ARGTRS	Chro.50402	6.1.1.19	Arginyl-tRNAsynthetase	Arginine and Proline Metabolism	[c] : arg-L + atp + trnaarg> amp + argtrna + ppi
R CDPMEK	•	2.2.1./	_1-ueoxy-D-XyIuIose5-pnosphatesynthase 4-(cytidine5'-diphospho)-2-C-methyl-D-eoythritell/incode	Biosynthesis of Steroids	[c] : 4c2me + atn> 2n4c2me + adn + h
R MEPCT		2.7.7.60	2-C-methyl-D-erythritol4-phosphatecytidylyltransferase	Biosynthesis of Steroids	[c]: 2me4p + ctp + h> 4c2me + ppi
R BACCL	Chro.20303	6.3.4.15	biotin-[acetyl-CoA-carboxylase]ligase	Biotin Metabolism	[c] : atp + btn + h> btamp + ppi
R HACD1	Chro.30048	1.1.1.35	3-hydroxyacyl-CoAdehydrogenase(acetoacetyl-CoA)	Butanoate Metabolism	[c]: aacoa + h + nadh <==> 3hbcoa + nad
R HACD3	Chro.30048	1.1.1.35	3-hydroxyacyl-CoAdehydrogenase(3-oxoorexanoyl-CoA)	Butanoate Metabolism	[c] : 300c0a + h + nadh <==> 3h0c0a + nad
R HACD4	Chro.30048	1.1.1.35	3-hydroxyacyl-CoAdehydrogenase(3-oxodecanoyl-CoA)	Butanoate Metabolism	<pre>[c]: 3odcoa + h + nadh <==> 3hdcoa + nad</pre>
R HACD5	Chro.30048	1.1.1.35	3-hydroxyacyl-CoAdehydrogenase(3-oxododecanoyl-Co	Butanoate Metabolism	[c]: 3oddcoa + h + nadh <==> 3hddcoa + nad
R HACD7	Chro.30048	1.1.1.35	3-hydroxyacyl-CoAdehydrogenase(3-oxotecradecanoyl-	Butanoate Metabolism	[c] : 30hdcoa + h + nadh <==> 3hhdcoa + nad
R PGK	Chro.70113	2.7.2.3	phosphoglyceratekinase	Carbon Fixation	[c]: 3pg + atp <==> 13dpg + adp
R_RPI	Chro.10337	5.3.1.6	ribose-5-phosphateisomerase	Carbon Fixation	[c] : r5p <==> ru5p-D
R MECOPS		4.6.1.12	R 2 oxolsovalerate denydrogenase acylating 4 methy 2-C-methyl-D-erythritol2 4-cyclodinhosphatesynthase	Cofactor and Prosthetic Group Biosynthes	[c]: 1.0 4mop + 1.0 coa + 1.0 nad <==> 1.0 co2 + 1.0 iVcoa + 1.0 nadr [c]: 2n4c2me> 2mecdn + cmn
R CYSTRS	Chro.60125	6.1.1.16	Cysteinyl-tRNAsynthetase	Cysteine Metabolism	[c] : atp + cys-L + trnacys> amp + cystrna + ppi
R MCOATA	Chro.40326 or Chro.30258	2.3.1.39	Malonyl-CoA-ACPtransacylase	Fatty Acid Biosynthesis	[c] : ACP + malcoa <==> coa + malACP
R KASZ R KASR		2.3.1.41	R b ketoacyl synthetase n C140 R b ketoacyl synthetase nalmitate n C160	Fatty Acid Biosynthesis	$[c] : 1.0 \arccos + 1/.0 h + 6.0 malcoa + 12.0 nadph> 6.0 co2 + 7.0 coa[c] : 1.0 accoa + 20.0 h + 7.0 malcoa + 14.0 nadph> 7.0 co2 + 8.0 coa$
R KAS13		2.3.1.41	R b ketoacyl synthetase n C180	Fatty Acid Biosynthesis	[c] : 1.0 accoa + 23.0 h + 8.0 malcoa + 16.0 nadph -> 8.0 co2 + 9.0 coa
R KAS141		2.3.1.41	R b ketoacyl synthetase n C141	Fatty Acid Biosynthesis	[c]: 1.0 accoa + 16.0 h + 6.0 malcoa + 11.0 nadph> 6.0 co2 + 7.0 coa
R KAS/ R KASI7	•	2.3.1.41	R b ketoacyl synthetase n C161	Fatty Acid Biosynthesis	[c]: 1.0 accoa + 19.0 h + 7.0 malcoa + 13.0 nadph> 7.0 co2 + 8.0 coa [c]: 1.0 accoa + 22.0 h + 8.0 malcoa + 15.0 nadph> 8.0 co2 + 9.0 coa
R KAS100iso		2.3.1.41	R b ketoacyl synthetase branched(iso) C100	Fatty Acid Biosynthesis	[c] : 8.0 h + 1.0 ibcoa + 3.0 malcoa + 6.0 nadph -> 3.0 co2 + 4.0 coa +
R KAS130iso		2.3.1.41	R b ketoacyl synthetase branched(iso) C130	Fatty Acid Biosynthesis	[c]: 11.0 h + 1.0 ivcoa + 4.0 malcoa + 8.0 nadph> 4.0 co2 + 5.0 coa -
R_KAS1	•	2.3.1.41	R_b_ketoacyl_synthetaseIso_C140_	Fatty Acid Biosynthesis	[c]: 14.0 h + 1.0 ibcoa + 5.0 malcoa + 10.0 nadph> 5.0 co2 + 6.0 coa
R KAS6		2.3.1.41	R b ketoacyl synthetase Iso C150	Fatty Acid Biosynthesis	[c]: 17.0 h + 1.0 ibcoa + 6.0 malcoa + 12.0 nadph -> 6.0 co2 + 7.0 coa
R KAS11		2.3.1.41	R b ketoacyl synthetase Iso C170	Fatty Acid Biosynthesis	[c]: 17.0 h + 1.0 ivcoa + 6.0 malcoa + 12.0 nadph> 6.0 co2 + 7.0 coa
R KAS180iso		2.3.1.41	R b ketoacyl synthetase Iso C180	Fatty Acid Biosynthesis	[c]: $20.0 \text{ h} + 1.0 \text{ ibcoa} + 7.0 \text{ malcoa} + 14.0 \text{ nadph}> 7.0 \text{ co2} + 8.0 \text{ coa}$ [c]: $16.0 \text{ h} + 1.0 \text{ ibcoa} + 6.0 \text{ malcoa} + 11.0 \text{ nadph}> 6.0 \text{ co2} + 7.0 \text{ coa}$
R KAS9		2.3.1.41	R b ketoacyl synthetase Iso C101	Fatty Acid Biosynthesis	[c]: 16.0 h + 1.0 ivcoa + 6.0 malcoa + 11.0 nadph> 6.0 co2 + 7.0 coa [c]: 16.0 h + 1.0 ivcoa + 6.0 malcoa + 11.0 nadph> 6.0 co2 + 7.0 coa
R KAS4		2.3.1.41	R b ketoacyl synthetase Anteiso C150	Fatty Acid Biosynthesis	[c] : 1.0 2mbcoa + 14.0 h + 5.0 malcoa + 10.0 nadph> 5.0 co2 + 6.0 c
R KAS12		2.3.1.41	R b ketoacyl synthetase Anteiso C170	Fatty Acid Biosynthesis	$[c]: 1.0 \text{ 2mbcoa} + 17.0 \text{ h} + 6.0 \text{ malcoa} + 12.0 \text{ nadph} \rightarrow 6.0 \text{ co2} + 7.0 \text{ co2}$
R ALCD19	Chro.80199 or Chro.80198	1.1.1.1	alcoholdehydrogenase(glycerol)	Fatty Acid Metabolism	[c] : glvald + h + nadh <==> glvc + nad
R 34DHOXPEGOX	Chro.80199 or Chro.80198	1.1.1.1	3,4-Dihydroxyphenylethyleneqlycol:NAD+oxidoreductas	Fatty Acid Metabolism	[c]: 34dhmald + h + nadh <==> 34dhoxpeg + nad
R_LNS14DM	Chro.21001	1.14.14.1	cytochromeP450lanosterol14-alpha-demethylase(NADP)	Fatty Acid Metabolism	[c] : 2 h + lanost + 3 nadph + 3 o2> 44mctr + for + 4 h2o + 3 nadp
R FACOAL1813	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c] : atp + coa + elaid $\langle == \rangle$ amp + od2coa + ppi
R FACOAL1812	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c] : atp + coa + vacc <==> amp + ppi + vacccoa
R FACOAL150	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c] : atp + coa + ptdca <==> amp + ppi + ptdcacoa
R FACOAL2042	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c]: atp + coa + elcostet <==> amp + elcostetcoa + ppi [c]: atp + coa + lnlncg <==> amp + lnlncgcoa + ppi
R FACOAL1832	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c] : atp + coa + InInca <==> amp + InIncacoa + ppi
R FACOAL241	Chro.50052 or Chro.30084	6.2.1.3	tatty-acidCoAligase	Fatty Acid Metabolism	<pre>[c]: atp + coa + nrvnc <==> amp + nrvnccoa + ppi</pre>
R FACOAL244 1	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c] : atp + coa + tettet6 <==> amp + ppi + tettet6coa
R FACOAL182	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase(octadecynoate)	Fatty Acid Metabolism	[c]: atp + coa + ocdcya <==> amp + ocdycacoa + ppi
R FACOAL181	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase(octadecenoate)	Fatty Acid Metabolism	<pre>[c]: atp + coa + ocdcea <==> amp + odecoa + ppi</pre>
R FACOAL180	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c] : atp + coa + strdnc <==> amp + ppi + strdnccoa
R FACOAL141	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase(tetradecenoate)	Fatty Acid Metabolism	[c] : atp + coa + ttdcea <==> amp + ppi + tdecoa
R FACOAL140	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase(tetradecanoate)	Fatty Acid Metabolism	[c]: atp + coa + ttdca <==> amp + ppi + tdcoa
R FACOAL2261	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c] : $acp + coa + crvic> amp + c226coa + ppi$ [c] : $acp + coa + lneldc <==> amp + lneldccoa + nni$
R FACOAL1821	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c] : atp + coa + lnlc <==> amp + lnlccoa + ppi
R FACOAL161	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase(hexadecenoate)	Fatty Acid Metabolism	[c]: atp + coa + hdcea <==> amp + hdcoa + ppi
R FACOAL160	Chro.50052 or Chro.30084 Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase(nexadecanoate) fatty-acidCoAligase	Fatty Acid Metabolism	<pre>[c]: aup + coa + ndca <==> amp + pmtcoa + ppi [c]: arach + atp + coa <==> amp + arachcoa + ppi</pre>
R FACOAL200	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c] : atp + coa + dinlcg <==> amp + dinlcgcoa + ppi
R FACOAL204	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c] : arachd + atp + coa <==> amp + arachdcoa + ppi
R_FACOAL205	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	<pre>[c] : atp + coa + tmndnc <==> amp + ppi + tmndnccoa [c] : atp + coa + pbyt <==> amp + pbytcoa + ppi</pre>
R FACOAL226	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c]: atp + coa + crvnc <==> amp + c226coa + ppi
R FACOAL224	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c] : adrn + atp + coa <==> adrncoa + amp + ppi
R FACOAL240	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	<pre>[c]: atp + coa + lgnc <==> amp + lgnccoa + ppi</pre>
R FACOAL260	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c]: atp + coa + tetpent3 <==> amp + ppi + tetpent3coa
R FACOAL245 1	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c]: atp + coa + tetpent6 <==> amp + ppi + tetpent6coa
R FACOAL191	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	[c] : atp + coa + prist> amp + ppi + pristcoa
R FACOAL2251	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	<pre>[c]: atp + coa + dcsptn1 <==> amp + dcsptn1coa + ppi</pre>
R FACOAL2252	Chro.50052 or Chro.30084	6.2.1.3	fatty-acidCoAligase	Fatty Acid Metabolism	<pre>[c] : atp + clpnd + coa <==> amp + clpndcoa + ppi</pre>
R DHFR	Chro.40506	1.5.1.3	dihydrofolatereductase folatoroductase	Folate-Vit B9 Metabolism	[c] : dhf + h + nadph <==> nadp + thf
R AKP1	Chro.70170	3.1.3.1	alkalinephosphatase(Dihydroneonterin)	Folate-Vit B9 Metabolism	[c] : or + nauph> orn + naup [c] : ahdt + 3 h2o> dhnpt + 2 h + 3 ni
R HEX7	Chro.60435	2.7.1.1	hexokinase(D-fructose:ATP)	Fructose and Mannose Metabolism	[c] : atp + fru> adp + f6p + h
R HEX10	Chro.60435	2.7.1.1	hexokinase(D-glucosamine:ATP)	Fructose and Mannose Metabolism	[c] : atp + gam> adp + gam6p + h
R MAN1PT	Chro.20115	2.7.7.13	o-priosphotructo-2-kinase mannose-1-phosphateguanylyltransferase	Fructose and Mannose Metabolism	$\frac{1}{1} (c_1) = \frac{1}{2} a_1 p + \frac{1}{2} a_2 p + \frac{1}{2} b_2 p + \frac{1}{2} b_1 $
R MAN1PT2r		2.7.7.22	mannose-1-phosphateguanylyltransferase(GDP)reversibl	Fructose and Mannose Metabolism	[c]: gdp + h + man1p <==> gdpmann + pi
R FBA4	Chro.10335	4.1.2.13	D-Fructose1-phosphateD-glyceraldehyde-3-phosphate-ly	Fructose and Mannose Metabolism	[c] : xu1p-D <==> dhap + gcald
K FBA5	Lnro.10335	4.1.2.13	u-lagatose1-phosphateD-glyceraldehyde-3-phosphate-ly	Fructose and Mannose Metabolism	<pre>ici : taq1p-D <==> dhap + qlyald</pre>



R_FBA2 R_FBA3	Chro.10335 Chro.10335	4.1.2.13	D-Fructose1-phosphateD-glyceraldehyde-3-phosphate-ly Sedobentulose1_7-bisphosphateD-glyceraldehyde-3-pho	Fructose and Mannose Metabolism	[c] : f1p <==> dhap + glyald [c] : s17bp <==> dhap + e4p
R TPI	Chro.10337	5.3.1.1	triose-phosphateisomerase	Fructose and Mannose Metabolism	[c]: dhap <==> g3p
R FCI	Chro.20165	5.3.1.25	L-fucoseisomerase	Fructose and Mannose Metabolism	[c] : fuc-L <==> fcl-L
R PMANM	Chro.40115	5.4.2.8	phosphomannomutase	Fructose and Mannose Metabolism	[c] : man1p <==> nop [c] : man1p <==> man6p
R MALT	Chro.30190	3.2.1.20	alpha-glucosidase	Galactose metabolism	[c] : h2o + malt> 2 glc-D
R P5CD	Chro.60426	1.5.1.12	1-pyrroline-5-carboxylatedehydrogenase	Glutamate metabolism	[c] : udpg <==> udpgai [c] : 1pvr5c + 2 h2o + nad> glu-L + h + nadh
R GLUTRS	Chro.60505 or Chro.80098 or	6.1.1.17	Glutamyl-tRNAsynthetase	Glutamate metabolism	[c] : atp + glu-L + trnaglu> amp + glutrna + ppi
R GLNTRS	Chro.10244	6.1.1.18	Glutaminyl-tRNAsynthetase	Glutamate metabolism	[c] : atp + gln-L + trnagln> amp + glntrna + ppi [c] : atp + gln-L + b2o + xmp> amp + glu-L + gmp + 2 b + ppi
R G6PDH3	Chro.40088 or Chro.60425	1.1.1.49	glucose6-phosphatedehydrogenase(F420-Dependent)	Glutathione Metabolism	[c] : f420-2 + g6p> 6pgl + f420-2h2
R_G6PDH2r	Chro.40088 or Chro.60425	1.1.1.49	glucose6-phosphatedehydrogenase	Glutathione Metabolism	[c]: g6p + nadp <==> 6pgl + h + nadph
R GTHP R AMPTASECG	Chro.30063 Chro.80395	1.11.1.9	glutathioneperidoxase alanylaminopentidase(cys-gly)	Glutathione Metabolism	[c]: 2 gthrd + h2o2 <==> gthox + 2 h2o [c]: calv + h2o> cvs-1 + alv
R G3PD1ir	Chro.20028	1.1.1.8	glycerol-3-phosphatedehydrogenase(NAD)	Glycerolipid Metabolism	[c]: dhap + h + nadh> glyc3p + nad
R G3PD6	Chro.80050	1.1.99.5	glycerol-3-phosphatedehydrogenase(menaquinone-8)	Glycerolipid Metabolism	[c] : glyc3p + mgn8> dhap + mgl8
R G3PD7	Chro.80050 Chro.80050	1.1.99.5	givcerol-3-phosphatedenydrogenase(demethylmenaguin givcerol-3-phosphatedehydrogenase(ubiguinone-8)	Glycerolipid Metabolism Glycerolipid Metabolism	[c] : 20mmq8 + giyc3p> 20mmq18 + dnap [c] : glyc3p + g8> dhap + g8h2
R GPAM hs	Chro.60161	2.3.1.15	glycerol-3-phosphateacyltransferase	Glycerolipid Metabolism	[c] : Rtotalcoa + glyc3p> alpa hs + coa
R AGPAT1 R DAGK SA	Chro.80165 Chro.80280	2.3.1.51	1-acylglycerol-3-phosphateO-acyltransferase1 Diacylglycerolkinase	Glycerolipid Metabolism Glycerolipid Metabolism	[c]: Rtotal2coa + alpa hs> coa + pa hs [c]: 0.02 12dor SA + ato> ado + b + 0.02 pa SA
R DAGK EC	Chro.80280	2.7.1.107	Diacylglycerolkinase	Glycerolipid Metabolism	[c] : 0.02 12dgr EC + atp> adp + h + 0.02 pa EC
R CHOLK	Chro.30240	2.7.1.32	Cholinekinase	Glycerolipid Metabolism	[c] : atp + chol> adp + cholp + h
R_ETHAK	Chro. 70332	2.7.1.02	ethanolamine-phosphatecytidylyltransferase	Glycerolipid Metabolism	[c]: acp + ecna> acp + ecnamp + n [c]: 2amenh + ctn + h> cmp2amen + ppi
R CHLPCTD	Chro.80135	2.7.7.15	cholinephosphatecytididyltransferase	Glycerolipid Metabolism	[c] : cholp + ctp + h> cdpchol + ppi
R CPCTDTX	Chro.80135	2.7.7.15	choline-phosphatecytidylyltransferase	Glycerolipid Metabolism	[c]: $ctp + h + ntm2amep> cmpntm2amep + ppi$
R DASYN HP	Chro.70059 or Chro.20170	2.7.7.41	CDP-DiacylqlycerolsynthetaseHpspecific	Glycerolipid Metabolism	[c] : ctp + h + pa Hp <==> cdpdag HP + ppi
R CDGGGS	Chro.70059 or Chro.20170	2.7.7.41	CDP-2,3-di-O-geranylgeranyl-sn-glycerolsynthase	Glycerolipid Metabolism	[c] : ctp + dgggp + h> cdgggp + ppi
R CDSm	Chro. 70059 or Chro. 20170 Chro. 70059 or Chro. 20170	2.7.7.41	DP-Diacyigiycerolsynthetase, cruzi-specific	Glycerolipid Metabolism	[c]: ctp + n + 0.01 pa C <==> 0.01 cdpdag C + pp [c]: ctp + h + pa hs> cdpdag hs + ppi
R DASYN EC	Chro.70059 or Chro.20170	2.7.7.41	CDP-Diacylglycerolsynthetase(Ecoli)	Glycerolipid Metabolism	[c] : ctp + h + 0.02 pa EC <==> 0.02 cdpdag EC + ppi
R DASYN SC	Chro.70059 or Chro.20170	2.7.7.41	CDP-Diacylqlycerolsynthetase, yeast-specific	Glycerolipid Metabolism	[c]: $ctp + h + 0.01 pa SC <==> 0.01 cdpdag SC + ppi$
R DASYNm TC	Chro.70059 or Chro.20170	2.7.7.41	CDP-Diacylqlycerolsynthetase, cruzi-specific, mitochondria	Glycerolipid Metabolism	[c] : ctp + h + 0.01 pa TC <==> 0.01 cdpdag TC + ppi
R_CDS	Chro.70059 or Chro.20170	2.7.7.41	phosphatidatecytidylyltransferase	Glycerolipid Metabolism	[c] : ctp + h + pa_hs> cdpdag_hs + ppi
R PEPT FC	Chro.40314 Chro.40314	2.7.8.1	ethanolaminephosphotransferase ethanolaminephosphotransferase	Giverolipid Metabolism	[c] : cmp + h + 0.02 pe EC <==> cmp + h + 0.01 pe TC
R ETHAPT SC	Chro.40314	2.7.8.1	Ethanolaminephosphotransferase, yeast-specific	Glycerolipid Metabolism	[c]: 0.01 12dgr SC + cdpea <==> cmp + h + 0.01 pe SC
R PEPT HP	Chro.40314	2.7.8.1	ethanolaminephosphotransferase	Glycerolipid Metabolism	[c]: cmp + h + pe HP <==> 12dgr HP + cdpea
R PGPPT	Chro.80072	2.7.8.11	phosphatidyl-CMP: glycerophosphatephosphatidyltransfer	Glycerolipid Metabolism	[c] : cdpdag hs + glyc3p> cmp + h + pqp hs
R PINOS SC	Chro.80072	2.7.8.11	phosphatidylinositolsynthase, yeast-specific	Glycerolipid Metabolism	[c]: 0.01 cdpdag SC + inost> cmp + h + 0.01 ptd1ino SC
R CDGGIPT	Chro.80072 Chro.80072	2.7.8.11	pnospnatidylinositolsynthase(Homosapiens) CDP-digeranyl-sn-glycero-myo-inositol3-nhosphatidyltra	Glycerolipid Metabolism Glycerolipid Metabolism	[c] : capaag hs + inost <==> cmp + h + pail hs [c] : cdagap + inost> cmp + dagni + h
R PSSA1 hs	Chro.10133	2.7.8.8	Phosphatidylserinesynthasehomosapiens	Glycerolipid Metabolism	[c] : pchol hs + ser-L <==> chol + ps hs
R PSSA HP	Chro.10133	2.7.8.8	PhosphatidylserinesynthaseHpspecific	Glycerolipid Metabolism	[c] : cdpdag HP + ser-L <==> cmp + h + ps HP
R PSSA SA	Chro.10133	2.7.8.8	Phosphatidylserinesyntase(Saureus)	Glycerolipid Metabolism	[c]: $0.02 \text{ cdpdag SA} + \text{ser-L} <==> \text{cmp} + h + 0.02 \text{ ps SA}$
R PSSA2 hs	Chro.10133	2.7.8.8	Phosphatidylserinesynthasehomosapiens	Glycerolipid Metabolism	[c] : pe hs + ser-L <==> etha + ps hs
R PSERS SC R PSSA EC	Chro.10133 Chro.10133	2.7.8.8	phosphatidylserinesynthase, yeast-specific Phosphatidylserinesyntase (Ecoli)	Glycerolipid Metabolism Glycerolipid Metabolism	[c]: 0.01 cdpdag SC + ser-L <==> cmp + h + 0.01 ps SC [c]: 0.02 cdpdag FC + ser-L <==> cmp + h + 0.02 ps FC
R LPS2	Chro.11000	3.1.1.3	lipase	Glycerolipid Metabolism	[c] : dag hs + h2o> Rtotal + h + mag hs
R LPS	Chro.11000	3.1.1.3	lipase	Glycerolipid Metabolism	[c] : h2o + tag hs> Rtotal3 + dag hs + h
R ALKP	Chro.70170	3.1.3.1	alkalinephosphatase	Glycerolipid Metabolism	[c]: hap + h2o> ha + pi
R PIPLCn	Chro.80452 or Chro.20310 or	3.1.4.3	phosphatidylinositolphospholipaseC, nucleus	Glycerolipid Metabolism	[c]: h2o + pail hs> dag hs + h + mi1p-D
R GPDDA5	Chro.50344 or Chro.40291 Chro.50344 or Chro.40291	3.1.4.46	Glycerophosphodiesterphosphodiesterase(Glycerophosphodiesterphosphodiesterphosphodiesterase)	Glycerolipid Metabolism	[c] : q3pi + h2o> qlyc3p + h + inost [c] : q3pq + h2o> qlyc + qlyc3p + h
R GPDDA3	Chro.50344 or Chro.40291	3.1.4.46	Glycerophosphodiesterphosphodiesterase(Glycerophosph	Glycerolipid Metabolism	[c]: g3ps + h2o> glyc3p + h + ser-L
R_GPDDA1	Chro.50344 or Chro.40291	3.1.4.46	Glycerophosphodiesterphosphodiesterase(Glycerophosph	Glycerolipid Metabolism	[c] : g3pc + h2o> chol + glyc3p + h
R PSD EC	Chro.30247	4.1.1.65	Phosphatidylserinedecarboxylase(Ecoli)	Glycerolipid Metabolism	[c]: h + 0.02 ps EC> co2 + 0.02 pe EC
R PSD HP	Chro.30247	4.1.1.65	PhosphatidylserinedecarboxylaseHpspecific	Glycerolipid Metabolism	[c] : h + ps HP> co2 + pe HP
R PSD SA	Chro.30247	4.1.1.65	Phosphatidylserinedecarboxylase(Saureus) B. glycerol. 3. phosphate. cytidylyltransferase	Glycerolipid Metabolism Glycerophospholipid Metabolism	[c]: h + 0.02 ps SA> co2 + 0.02 pe SA [c]: 10 ctp + 10 glyc 3p + 10 h> 10 cdpglyc + 10 pp
R CDGPT CT		2.7.8.5	R CDPdiacylglycerolsn glycerol 3 phosphate 3 phosph	Glycerophospholipid Metabolism	[c] : 1.0 cdpdag CT + 1.0 glyc3p> 1.0 cmp + 1.0 h + 1.0 pglyp CT
R PGPPH CT		3.1.3.27	R Phosphatidylglycerophosphate phosphohydrolase	Glycerophospholipid Metabolism	[c]: 1.0 h2o + 1.0 pglyp CT> 1.0 pgly CT + 1.0 pi
R 41R2A1H12BOOX	Chro.21000	1.4.3.4	4-[(1R)-2-Amino-1-hydroxyethyl]-1,2-benzenediol:oxy	Glycine, Serine, and Threonine Metabolish	[c]: h20 + nrpphr + o2> 34dhmald + h2o2 + nh4
R 5HOXINOXDA	Chro.21000	1.4.3.4	5-Hydroxytryptamine:oxygenoxidoreductase(deaminati	Glycine, Serine, and Threonine Metabolisi	[c] : h2o + o2 + srtn> 5hoxindact + h2o2 + nh4
R 5HXKYNOXDA	Chro.21000 Chro.21000	1.4.3.4	3-Hydroxykynurenamine:oxygenoxidoreductase(deamine:oxygenoxidoreductase(deamine:oxygenoxidoreductase(deamine:oxygenoxidoreductase)	Glycine, Serine, and Threonine Metabolisi Glycine, Serine, and Threonine Metabolisi	[c] : 3nxkynam + o2> 48dnoxquin + n2o2 + nn4 [c] : 5hxkynam + o2> 46dhoxquin + h2o2 + nh4
R 41R1H2MAE12BO	Chro.21000	1.4.3.4	4-[(1R)-1-Hydroxy-2-(methylamino)ethyl]-1,2-benzene	Glycine, Serine, and Threonine Metabolisi	[c] : adrnl + h2o + o2> 34dhmald + h2o2 + mma
R 13DAMPPOY	Chro.21000 Chro.80360 or Chro.30399	1.4.3.4	Iryptamine:oxygenoxidoreductase(deaminating)(flavin-o	Glycine, Serine, and Threonine Metabolisi	c : h20 + 02 + trypta> h202 + id3acald + hh4
R HISTASE	Chro.80360 or Chro.30388	1.4.3.6	Histaminase	Glycine, Serine, and Threonine Metabolisi	[c] : h2o + hista + o2> h2o2 + im4act + nh4
R 42A12BOOX	Chro.80360 or Chro.30388	1.4.3.6	4-(2-Aminoethyl)-1,2-benzenediol:oxygenoxidoreducta	Glycine, Serine, and Threonine Metabolisi	[c]: dopa + h2o + o2> 34dhpac + h2o2 + nh4
R TYROXDAc	Chro.80360 or Chro.30388	1.4.3.6	Tyramine:oxygenoxidoreductase(deaminating) (flavin-cor	Glycine, Serine, and Threonine Metabolist Glycine, Serine, and Threonine Metabolist	[c]: h20 + o2 + tym> 4hoxpacd + h202 + hh4
R PEAMNO	Chro.80360 or Chro.30388	1.4.3.6	Phenethylamineoxidase	Glycine, Serine, and Threonine Metabolisi	[c] : h2o + o2 + peamn> h2o2 + nh4 + pacald
R NMPTRCOX	Chro.80360 or Chro.30388 Chro.80360 or Chro.30388	1.4.3.6	N-Methylputrescine:oxygenoxidoreductase(deaminating)	Glycine, Serine, and Threonine Metabolisi Glycine, Serine, and Threonine Metabolisi	[c] : nptrc + o2> 1mpyr + h2o2 + nh4
R HSK	Chro.60426	2.7.1.39	homoserinekinase	Glycine, Serine, and Threonine Metabolis	[c] : atp + hom-L> adp + h + phom
R PSP D	Chro. 70469	3.1.3.3	pnospnoserinephosphatase(L-serine) phosphoserinephosphatase(D-serine)	Glycine, Serine, and Threonine Metabolisi Glycine, Serine, and Threonine Metabolisi	<u> c : nzo + pser-L> pi + ser-L</u> [c] : h2o + pser-D> pi + ser-D
R SERTRS	Chro.80542	6.1.1.11	Seryl-tRNAsynthetase	Glycine, Serine, and Threonine Metabolisi	[c] : atp + ser-L + trnaser> amp + ppi + sertrna
R GLYTRS	Chro.80123	6.1.1.14	Glycyl-tRNAsynthetase	Glycine, Serine, and Threonine Metabolise	[c] : atp + gly + trnagly> amp + glytrna + ppi
R ALCD2x	Chro.80199 or Chro.80198	1.1.1.1	alcoholdehydrogenase(ethanol)	Glycolysis/Gluconeogenesis	[c]: etoh + nad <==> acald + h + nadh
R GAPD	Chro.60434 or Chro.10337	1.2.1.12	glyceraldehyde-3-phosphatedehydrogenase	Glycolysis/Gluconeogenesis	[c]: g3p + nad + pi <==> 13dpg + h + nadh
R PFKg	Chro. 20231 or Chro. 30177	2.7.1.1	phosphofructokinase.glycosome	Glycolysis/Gluconeogenesis	[c] : aup + gic-υ> aop + h + g6p [c] : ato + f6p> ado + fdp + h
R GLUK		2.7.1.2	Glucokinase	Glycolysis/Gluconeogenesis	[c] : atp + glc-D> adp + g6p-B + h
R PYK	Chro.10234 Chro.70113	2.7.1.40	pyruvatekinase phosphoglyceratekinase	Glycolysis/Gluconeogenesis	[c]: $adp + h + pep> atp + pyr$ [c]: $3ng + atp <==> 13dpg + adp$
R ACYP	Chro.70488	3.6.1.7	acylphosphatase	Glycolysis/Gluconeogenesis	[c] : 13dpg + h2o> 3pg + h + pi
R_PYRDC	Chro.70351	4.1.1.1	pyruvatedecarboxylase	Glycolysis/Gluconeogenesis	[c] : h + pyr> acald + co2
K FBA R FNO	Chro. 50184	4.1.2.13	rructose-bisphosphatealdolase enolase	Glycolysis/Gluconeogenesis	[c] : 700 <==> dhap + g3p [c] : 700 <==> h20 + nen
R PGI	Chro.20336	5.3.1.9	glucose-6-phosphateisomerase	Glycolysis/Gluconeogenesis	[c]: g6p <==> f6p
R PGM	Chro.10196 or Chro.70471	5.4.2.1	phosphoglyceratemutase	Glycolysis/Gluconeogenesis	[c]: 2pg <==> 3pg
IN FORT	Chro 20342	5422	and the second sec	Gry Corysis/ Gruconeogenesis	
R ACSm	Chro.20343 Chro.10418	5.4.2.2 6.2.1.1	acetyl-CoAsynthetase	Glycolysis/Gluconeogenesis	[c]: ac + atp + coa> accoa + amp + ppi
R ACSm R RBPC	Chro.20343 Chro.10418 Chro.20166	5.4.2.2 6.2.1.1 4.1.1.39	acetyl-CoAsynthetase ribulose-bisphosphatecarboxylase	Glycolysis/Gluconeogenesis Glyoxylate and dicarboxylate Metabolism	[c] : ac + atp + coa> accoa + amp + ppi [c] : co2 + h2o + rb15bp> 2 3pg + 2 h
R ACSm R RBPC R HISTRS R PIN3K SC	Chro.20343 Chro.10418 Chro.20166 Chro.80461 Chro.80217 or Chro.60213	5.4.2.2 6.2.1.1 4.1.1.39 6.1.1.21 2.7.1.137	nospinolitouruse acety-CoAsynthetase ribulose-bisphosphatecarboxylase Histidyl-tRNAsynthetase 1-phosphatidylinositol3-kinase-yeast-specific	Glycolysis/Gluconeogenesis Glycoxylate and dicarboxylate Metabolism Histidine Metabolism Inositol Phosphate Metabolism	$\begin{array}{l} \hline c : ac + atp + coa> accoa + amp + ppi \\ \hline c : co2 + h2o + rol15bp> 2 3pq + 2 h \\ \hline c : atp + his-L + trnahis> amp + histma + ppi \\ \hline c : atp - 0.01 totd into SC> adn + h + 0.01 ntd Sino SC \\ \hline \end{array}$
R ACSm R RBPC R HISTRS R PIN3K SC R PIK3	Chro.20343 Chro.10418 Chro.20166 Chro.80461 Chro.80217 or Chro.60213 Chro.80217 or Chro.60213	5.4.2.2 6.2.1.1 4.1.1.39 6.1.1.21 2.7.1.137 2.7.1.137	prospinostructimuse acetyl-CoAsynthetase ribulose-bisphosphatecarboxylase Histidyl-tRNAsynthetase 1_phosphatidylinositol3-kinase,yeast-specific phosphatidylinositol3-kinase	Glycotysis/Gluconeogenesis Glyoxylate and dicarboxylate Metabolism Histidine Metabolism Inositol Phosphate Metabolism Inositol Phosphate Metabolism	[c]: ac + atb + coa → accoa + amp + ppi [c]: co2 + h2o + rb15bp → 2 3pg + 2 h [c]: atb + his_1 + trnahis → amp + histrna + ppi [c]: atb + 0.01 ptdlino SC → adp + h + 0.01 ptd3ino SC [c]: atb + pail hs → adp + h + pail3p hs
R ACSm R RBPC R HISTRS R PIN3K SC R PIN4K SC R PIN4K SC R PIAP5K SC	Chro.20343 Chro.10418 Chro.20166 Chro.80461 Chro.80217 or Chro.60213 Chro.80217 or Chro.60213 Chro.60392 or Chro.80518 Chro.2007	5.4.2.2 6.2.1.1 4.1.1.39 6.1.1.21 2.7.1.137 2.7.1.137 2.7.1.67 2.7.1.68	prospirotationmuse acetyl-CoAsynthetase ribulose-bisphosphatecarboxylase Histidyl-RRMsynthetase 1-phosphatidylinositol3-kinase,veast-specific phosphatidylinositol3-kinase phosphatidylinositol4-kinase,veast-specific phosphatidylinositol4-kinase.	Glycolysis/Gluconeogenesis Glycoxylate and dicarboxylate Metabolism Histidine Metabolism Inositol Phosphate Metabolism Inositol Phosphate Metabolism Inositol Phosphate Metabolism Inositol Phosphate Metabolism	[c]: ac + atp + coa> accoa + amp + ppi [c]: co2 + h2o + rol5bp> 2 3pq + 2 h [c]: acb +h5c + trahsin-> amp + histma + ppi [c]: atb +h5c + trahsin-> amp + histma + ppi [c]: atb +0.01 ptdlino SC> adp + h + 0.01 ptdlino SC [c]: atb +0.01 ptdlino SC> adp + h + 0.01 ptdlino SC [c]: atb +0.01 ptdlino SC> adp + h = 0.01 ptdlino SC [c]: atb +0.01 ptdlino SC> adp + h = 0.01 ptdlino SC
R ACSm R RBPC R HISTRS R PIN3K SC R PIN3K SC R PIN4K SC R PI4P5K SC R PI4P5K	Chro.20343 Chro.10418 Chro.20166 Chro.80461 Chro.80217 or Chro.60213 Chro.80217 or Chro.60213 Chro.60392 or Chro.80518 Chro.20207 Chro.20207	5.4.2.2 6.2.1.1 4.1.1.39 6.1.1.21 2.7.1.137 2.7.1.137 2.7.1.67 2.7.1.68 2.7.1.68	prospirotation music acetyl - CoAsynthetase ribulose-bisphosphatecarboxylase Histidyl-RNAsynthetase 1-phosphatidylinositol3-kinase, veast-specific phosphatidylinositol4-kinase phosphatidylinositol4-kinase, veast-specific phosphatidylinositol4-kinase, veast-specific phosphatidylinositol4-aphosphate5-kinase	Glycolysis/Gluconeogenesis Glycoxylate and dicarboxylate Metabolism Histidine Metabolism Inositol Phosphate Metabolism Inositol Phosphate Metabolism Inositol Phosphate Metabolism Inositol Phosphate Metabolism	<pre>1cl : ac + atp + coa> accoa + amp + ppi 1cl : co2 + h2o + rol55p> 2.3pq + 2 h [cl : acb +h5cl + trahsic -> amp + histrna + ppi [cl : atp +h5cl + trahsic -> amp + histrna + ppi [cl : atp + 0.01 ptdlino SC> adp + h + 0.01 ptd3ino SC [cl : atp + and ih s> adp + h + pai30 hs [cl : atp + 0.01 ptdlino SC> adp + h + 0.01 ptdl4ino SC [cl : atp + 0.01 ptdlino SC> adp + h + 0.01 ptdl45p SC [cl : atp + all_6p, hs-> adp + h + pai35p_hs</pre>
R ACSm R RBPC R HISTRS R PIN3K SC R PIN3K SC R PIA4K SC R PIA4P5K SC R PIA4P5K SC R PIA4P5K R MI1345PP P MI44575	Chro.20343 Chro.20166 Chro.80461 Chro.80461 Chro.80217 or Chro.60213 Chro.80217 or Chro.60213 Chro.60322 or Chro.80518 Chro.20207 Chro.20207 Chro.50026	5.4.2.2 6.2.1.1 4.1.1.39 6.1.1.21 2.7.1.137 2.7.1.137 2.7.1.68 2.7.1.68 3.1.3.56	acetv: CoAxynthetase iribulose-bisphosphatecarboxylase Histidvi-RNAsynthetase 1-phosphatidvi/inositol3-kinase,veast-specific phosphatidvi/inositol3-kinase phosphatidvi/inositol3-kinase phosphatidvi/inositol3-kinase phosphatidvi/inositol3-kinase inositol1-13,5-trisphosphate5-kinase inositol-13,5-trisphosphate5-phosphatese	Glycolysis/Gluconeogenesis Glycolyate and dicarboxylate Metabolism Histidine Metabolism Inositol Phosphate Metabolism Inositol Phosphate Metabolism Inositol Phosphate Metabolism Inositol Phosphate Metabolism Inositol Phosphate Metabolism	$ \begin{array}{ll} [c]: ac + ato + coa> accoa + amo + poi \\ [c]: (ac + ho 2 + rb 3bp> 2 3ga + 2 h \\ [c]: (ac + ho 2 + rb 3bp> 2 3ga + 2 h \\ [c]: ato + ho 2 + for a bp + histra + poi \\ [c]: ato + ability + ability + ability + ability + b \\ [c]: ato + ability + ability + ability + b \\ [c]: ato + ability + ability + ability + b \\ [c]: ato + ability + ability + ability + b \\ [c]: ato + ability + ability + ability + b \\ [c]: ato + ability + ability + ability + b \\ [c]: ato + ability + ability + ability + b \\ [c]: ato + ability + ability + ability + b \\ [c]: h \\$
R ACSm R RBPC R HISTRS R PIN3K SC R PIN3K SC R PIN4K SC R PI4P5K SC R PI4P5K R MI1345PP R MI1345PP R PI45PP C	Chro. 20343 Chro. 20148 Chro. 20166 Chro. 80461 Chro. 80217 or Chro. 60213 Chro. 80217 or Chro. 60213 Chro. 60322 or Chro. 80518 Chro. 20207 Chro. 20207 Chro. 20207 Chro. 50026 Chro. 50026 Chro. 50026	5.4.2.2 6.2.1.1 4.1.1.39 6.1.1.21 2.7.1.137 2.7.1.137 2.7.1.68 2.7.1.68 3.1.3.56 3.1.3.56 3.1.4.11	prospirotation metase ribulose-bisphosphatese ribulose-bisphosphatese 1-phosphatidylinositol3-kinase,veast-specific phosphatidylinositol3-kinase phosphatidylinositol4-kinase,veast-specific phosphatidylinositol4-kinase,veast-specific phosphatidylinositol4-phosphate5-kinase inositol-1.4,5-trisphosphate5-phosphatase inositol-1.4,5-trisphosphate5-phosphatase inositol-1.4,5-trisphosphate5-phosphatase inositol-1.4,5-trisphosphate5-phosphatase inositol-1.4,5-trisphosphate5-phosphatase inositol-1.4,5-trisphosphate5-phosphatase inositol-1.4,5-trisphosphate5-phosphatase inositol-1.4,5-trisphosphate5-phosphatase inositol-1.4,5-trisphosphatase inositol-1.4,	Glycolysis/Gluconeogenesis Glycolysta end dicarboxylate Metabolism Histidine Metabolism Inositol Phosphate Metabolism	$ \begin{array}{llllllllllllllllllllllllllllllllllll$
R ACSm R RBPC R HISTRS R PIN3K SC R PIN3K SC R PIN4K SC R PI4P5K SC R PI4P5K R MI1345PP R MI1345PP R MI45PP R PI45PPLC R PI45BPP SC	Chro.20343 Chro.20148 Chro.20166 Chro.80241 Chro.80217 or Chro.60213 Chro.80217 or Chro.60213 Chro.60392 or Chro.80518 Chro.20207 Chro.50026 Chro.40288 Chro.40288	$\begin{array}{c} 5.4.2.2 \\ 6.2.1.1 \\ 4.1.1.39 \\ 6.1.1.21 \\ 2.7.1.137 \\ 2.7.1.67 \\ 2.7.1.68 \\ 3.1.3.56 \\ 3.1.3.56 \\ 3.1.4.11 \\ 3.1.4.11 \end{array}$	prospirotationnesse acctiv - CoAsynthetase irbuidse-bisphosphatecarboxylase Histidvi-RNAsynthetase 1-phosphatidylinositol3-kinase,veast-specific phosphatidylinositol3-kinase,veast-specific phosphatidylinositol4-kinase,veast-specific phosphatidylinositol4-phosphate5-kinase inositol-1,3,4,5-trisphosphate5-phosphatase inositol-1,4,5-trisphosphate5-phosphatase phosphatidylinositol4-5-bisphosphatesphospholipaseC 1-phosphatidylinositol4-5-bisphosphatesphospholipaseC	Glycolysis/Gluconeogenesis Glycolysta and dicarboxylate Metabolism Histidine Metabolism Inositol Phosphate Metabolism	$ \begin{array}{llllllllllllllllllllllllllllllllllll$
R ACSm R RBPC R HISTRS R PIN3K SC R PIN3K SC R PIN4K SC R PIM4K SC R PI44P5K R MI1345PP R MI1345PP R PI45PLC R PI45PC R PI45PP SC R PI45PC R P	Chro.201343 Chro.201348 Chro.201366 Chro.80451 Chro.80217 or Chro.60213 Chro.80217 or Chro.60213 Chro.80212 or Chro.80518 Chro.20207 Chro.50026 Chro.20207 Chro.50026 Chro.40288 Chro.2026 Chro.40288 Chro.20310 or Chro.20310 or Chro.80452 or Chro.20310 or Chro.80452 or Chro.20310 or	5.4.2.2 6.2.1.1 4.1.1.39 6.1.1.21 2.7.1.137 2.7.1.67 2.7.1.68 3.1.3.56 3.1.3.56 3.1.4.11 3.1.4.11 3.1.4.3 1.2.12	prospirotation music acetyl - CoAsynthetase ribuidse-bisphosphatecarboxylase Histidyl-RNAsynthetase 1-phosphatidylinositol3-kinase, yeast-specific phosphatidylinositol4-kinase, yeast-specific phosphatidylinositol4-phosphate5-kinase, yeast-specific phosphatidylinositol4-phosphate5-kinase inositol-1,3,4,5-trisphosphate5-phosphatase inositol-1,3,4,5-trisphosphate5-phosphatase phosphatidylinositol4,5-bisphosphatephospholipaseC 1-phosphatidylinositol4,5-bisphosphatephospholipaseC 1-phosphatidylinositol4,5-bisphosphatephospholipaseC 1-phosphatidylinositol4,5-bisphosphatephospholipaseC 1-phosphatidylinositol4,5-bisphosphatephospholipaseC	Glycokysis/Gluconeogenesis Glycoxylate and dicarboxylate Metabolism Histdine Metabolism Inositol Phosphate Metabolism	[c]: ac + sto + coa \rightarrow accoa + amo + poi [c]: ac + sto 2 + cb5bp \rightarrow 2 3pd + 2 h [c]: at 0 + hist-+ tranhis \rightarrow 2 3pd + 2 h [c]: at 0 + hist-+ tranhis \rightarrow 2 mp + histma + poi [c]: at 0 + 0.01 pddino SC [c]: bt 0 + 0.01 pddis p + ph + 0.01 pddino SC [c]: h20 + null 35p \rightarrow ml 34p + ph [c]: h20 + null 35p \rightarrow ml 34p + ph [c]: h20 + null 35p \rightarrow Sc \rightarrow 0.01 12dar SC + h + mi145p [c]: h20 + poil pdd 145p SC [c]: h20 + poil pdd 145p SC [c]: h20 + poil pdd 145p SC \rightarrow 0.01 12dar SC + h + mi145p [c]: h20 + poil pdd 145p \rightarrow Sc \rightarrow 0.01 12dar SC + h + mi145p [c]: h20 + poil pdd 145p \rightarrow Sc \rightarrow 0.01 12dar SC + h + mi145p [c]: h20 + poil pdd 145p \rightarrow Sc \rightarrow 0.01 12dar SC + h + mi145p [c]: h20 + poil pdd 145p \rightarrow Sc \rightarrow 0.01 12dar SC + h + mi145p [c]: h20 + poil pdd 145p \rightarrow Sc \rightarrow 0.01 12dar SC + h + mi145p [c]: h20 + poil pdd 145p \rightarrow Sc \rightarrow 0.01 12dar SC + h + mi145p [c]: h20 + poil pdd 145p \rightarrow Sc \rightarrow 0.01 12dar SC + h + mi145p [c]: h20 + poil pdd 145p \rightarrow Sc \rightarrow 0.01 12dar SC + h + mi145p [c]: h20 + poil pdd 145p \rightarrow Sc \rightarrow 0.01 12dar SC + h + mi145p [c]: h20 + poil pdd 145p \rightarrow Sc \rightarrow 0.01 12dar SC + h + mi145p [c]: h20 + poil pdd 145p \rightarrow Sc \rightarrow 0.01 12dar SC + h + mi145p [c]: h20 + poil pdd 145p \rightarrow 10 + point (h20 + poil h20 + point (h20 + point (h2
R ACSm R RBPC R HISTRS R PIN4S SC R PIN4S R PIN4S R PIA95K SC R PIA95K R MI1345PP R MI1345PP R MI345PP R MI345PP SC R PIA5BPP SC R PIPLC R AASAD2	Chro.20343 Chro.20148 Chro.80461 Chro.80461 Chro.80217 or Chro.60213 Chro.80217 or Chro.60213 Chro.80217 or Chro.80518 Chro.20207 Chro.50026 Chro.40288 Chro.40288 Chro.40288 Chro.40288 Chro.80452 or Chro.20310 or Chro.80452 or Chro.20310 or Chro.40330	5.4.2.2 6.2.1.1 4.1.1.39 6.1.1.21 2.7.1.137 2.7.1.137 2.7.1.67 2.7.1.68 3.1.3.56 3.1.3.56 3.1.4.11 3.1.4.3 1.2.1.31 1.2.1.31	Jacobi Contextures activi - CoAwnthetase irbuicse-bisphosphateste 1-phosphatidvilnositol3-kinase, veast-specific phosphatidvilnositol3-kinase, veast-specific phosphatidvilnositol3-kinase, veast-specific phosphatidvilnositol4-kinase, veast-specific phosphatidvilnositol4-kinase, veast-specific phosphatidvilnositol4-phosphate5-kinase inositol-1.4,5-trisphosphate5-phosphatase inositol-1.4,5-trisphosphate5-phosphatase inositol-1.4,5-trisphosphate5-phosphatase inositol-1.4,5-trisphosphate5-phosphatase inosphatidvilnositol4,5-bisphosphatehospholipaseC 1-phosphatidvilnositol4,5-bisphosphatehospholiciase (L-aminoadipate-semialdehydedehydrogenase(NADH)	Glycolysis/Gluconeogenesis Glycolysis/Gluconeogenesis Glycolyate and dicarboxylate Metabolism Inositol Phosphate Metabolism Ivsine Biosynthesis Uysine Biosynthesis	$ \begin{array}{llllllllllllllllllllllllllllllllllll$



K_LISIKS	Chro.40267	6.1.1.6	Lysyl-tRNAsynthetase	Lysine Biosynthesis	[c] : atp + lys-L + trnalys> amp + lystrna + ppi
R LYSMTF2	Chro.40051	2.1.1.43	histone-lysineN-methyltransferase, nuclear	Lysine Degradation	[c]: Ndmalys + amet> Ndmalys + ahoys
R LYSMIFS	Chro.40051	2.1.1.43	histone-lysineN-methyltransferase.nuclear	Lysine Degradation	[c] : amet + peplys> Nmelys + alcys
R PRDX	Chro.40093 or Chro.80075 or	1.11.1.7	Peroxidase(multiplesubstrates)	Methane Metabolism	[c] : h2o2 + meoh> fald + 2 h2o
R GHMT3	Chro.80302 or Chro.80306	2.1.2.1	glycinehydroxymethyltransferase	Methane Metabolism	[c] : 3htmelys + h> 4tmeabut + gly
R GHMT2r	Chro.80302 or Chro.80306	2.1.2.1	glycinehydroxymethyltransferase, reversible	Methane Metabolism	[c] : ser-L + thf <==> gly + h2o + mithf
R DNAMISE	Chro 50169	2.1.1.37	DNA(cytosine-5-)-methyltransferase,nucleus	Methionine Metabolism	[c]: amet + dna> ancys + dna5mtc + n [c]: dna + seasmet> dna5mtc + h + seabcys
R METAT	Chro.70301	2.5.1.6	methionineadenosyltransferase	Methionine Metabolism	[c]: atp + h2o + met-L> amet + pi + ppi
R AHC	Chro.30017	3.3.1.1	adenosylhomocysteinase	Methionine Metabolism	[c] : ahcys + h2o <==> adn + hcys-L
R METTRS	Chro.80398	6.1.1.10	Methionyl-tRNAsynthetase	Methionine Metabolism	[c] : atp + met-L + trnamet> amp + mettrna + ppi
R G3POA CI		·	R glycerol 3 phosphate O acyltransferase	Miscellaneous	[c] : 1.0 glyc3p + 0.051 dcacoa + 0.022 trdacoa + 0.023 ta1coa + 0.0092
	•		R_IVSVIPHOSPHALIDVIGIVCEFOL_SVILHESIS	Miscellaneous	$[c] : 1.0 atp + 1.0 tys-L + 1.0 pgty_Ct> 1.0 attp + 1.0 tt + 1.0 tysytpgt[c] : 1.0 12dar CT + 2.0 udpg> 1.0 d12da CT + 2.0 b + 2.0 udp$
R UGT1 CT			R UDP glucosyltransferase monoglucosyl	Miscellaneous	[c]: 1.0 12dqr CT + 1.0 udpq> 1.0 h + 1.0 m12dq CT + 1.0 udp
R UGT2 CT			R UDP glucosyltransferase triglucosyl	Miscellaneous	[c] : 1.0 12dgr CT + 3.0 udpg> 3.0 h + 1.0 t12dg CT + 3.0 udp
R LIPO1S24 CT			R lipoteichoic acid synthesis n24 linked glucose	Miscellaneous	[c] : 24.0 cdpglyc + 1.0 d12dg CT + 24.0 udpg> 24.0 cmp + 48.0 h + .
R LIPO2S24 CT		·	R lipoteichoic acid synthesis n24 linked N acety	Miscellaneous	[c] : 24.0 cdpglyc + 1.0 d12dg CT + 24.0 uacgam> 24.0 cmp + 48.0 h
R LIPO3524 CT			R lipoteichoic acid synthesis n24 linked unsubsti	Miscellaneous	$[c]: 24.0 \text{ alg} + 24.0 \text{ alg} + 24.0 \text{ cupgive} + 1.0 \text{ d120g} + 24.0 \text{ lno4} - 24.0 \text{ lno4} + 1.0 \text{ lno4} - 24.0 \text{ lno4} + 1.0 \text{ lno4} - 24.0 \text{ lno4} + 1.0 \text$
R TECA1S45			R glycerol teichoic acid n45 unlinked unsubstitut	Miscellaneous	[c]: 45.0 cdpqlyc + 1.0 uacgam + 1.0 uacmam> 45.0 cmp + 1.0 qtca1
R TECA2S45			R glycerol teichoic acid n45 unlinked D ala subs	Miscellaneous	[c]: 45.0 ala-D + 45.0 atp + 45.0 cdpglyc + 45.0 h2o + 1.0 uacgam + 1.0
R TECA3S45			R glycerol teichoic acid n45 unlinked glucose su	Miscellaneous	[c] : 45.0 cdpglyc + 1.0 h2o + 1.0 uacgam + 1.0 uacmam + 45.0 udpg
R TEICHAS		· · · ·	R minor teicnoic acid synthesis hau R teichuropic acid p45 uplinked GalNAc GlcA reg	Miscellaneous	[c]: 30.0 n20 + 30.0 uacqala + 30.0 udpg> 60.0 n + 1.0 tcam CI + 30.0 udpgl: 45.0 uacqala + 45.0 udpglcur <> 45.0 h + 1.0 teich 45. CT + 45.
R UAGPT3		1	R UDP N acetylglucosamine N acetylmuramyl pentar	Miscellaneous	$[c]: 1.0 \ \mu acgam + 1.0 \ \mu a g m da> 1.0 \ h + 1.0 \ \mu a g m da + 1.0 \ \mu d n$
R PPTGS CT			R Peptidoglycan subunit synthesis	Miscellaneous	[c] : 1.0 uaagmda> 1.0 h + 1.0 peptido CT + 1.0 udcpdp
R FRTT		· · · · · · · · · · · · · · · · · · ·	R farnesyltranstransferase	Miscellaneous	[c] : 1.0 frdp + 1.0 ipdp> 1.0 ggdp + 1.0 ppi
R GGTT		·	R geranylgeranyltranstransferase	Miscellaneous	[c] : 1.0 ggdp + 1.0 ipdp> 1.0 pendp + 1.0 ppi
R HEXTT			R trans becaprenvitranstransferase	Miscellaneous	[c]: 1.0 (pdp + 1.0 (pdp> 1.0 (nexup + 1.0 pp)]
R ICHORS			R isochorismate synthase	Miscellaneous	[c] : 1.0 chor <==> 1.0 ichor
R 2S6HCCi			R 2 succinyl 6 hydroxy 2 4 cyclohexadiene 1 carbox	Miscellaneous	[c] : 1.0 akg + 1.0 h + 1.0 ichor> 1.0 2shchc + 1.0 co2 + 1.0 pyr
R SUCBZS			R O succinylbenzoate CoA synthase	Miscellaneous	[c] : 1.0 2shchc> 1.0 h2o + 1.0 sucbz
R SUCBZL		+·	K o succinylbenzoate CoA ligase	Miscellaneous	<pre>[c]: 1.0 atp + 1.0 coa + 1.0 sucbz> 1.0 amp + 1.0 ppi + 1.0 sbzcoa</pre>
R DHNAOT7		t:	R 1 4 dihydroxy 2 nanhthoate octanrenyltransferase	Miscellaneous	[c] : 1.0 dhna + 1.0 hepdp + 1.0 nad> 1.0 2dmmo7 + 1 0 co2 ± 1 0 ps
R_AMMQT7		1	R_S_adenosylmethione2_demthylmenaquinone methylt	Miscellaneous	[c] : 1.0 2dmmq7 + 1.0 amet + 1.0 nadph> 1.0 ahcys + 1.0 md7 + 1.0
R H2CO3D2			carboxylicaciddissociation	Miscellaneous	[c] : h + hco3 <==> h2co3
R IPDPS		1.17.1.2	1-hydroxy-2-methyl-2-(E)-butenyl4-diphosphatereduct	Miscellaneous	[c] : h + h2mb4p + nadh> h2o + ipdp + nad
R AGRATE CT	Chro 80165	1.1/.4.3	20-methyl-D-erythritol2,4cyclodiphosphatedehydratase	Miscellaneous	Ici : 2mecdp + h> h2mb4p + h2o
R DAGK CT	Chro.40493	2.7.1.107	R diacylolycerol kinase	Miscellaneous	101.1.0 1agpp C1 + 0.051 0cac0a + 0.022 0r0ac0a + 0.023 ra1c0a + 0.0 [c]: 1.0 12dgr CT + 1.0 atp> 1.0 12dac3n CT + 1.0 adn + 1.0 h
R PHCYT CT	Chro.70332	2.7.7.41	R phosphatidate cytidylyltransferase	Miscellaneous	[c] : 1.0 12dag3p CT + 1.0 ctp + 1.0 h> 1.0 cdpdag CT + 1.0 ppi
R CLPNS2 CT		2.7.8	R cardiolipin synthase	Miscellaneous	[c] : 2.0 pgly CT> 1.0 cdlp CT + 1.0 glyc
R CDPDSP CT	Chro.10133	2.7.8.8	R CDPdiacylglycerol serine O phosphatidyltransferase	Miscellaneous	[c]: 1.0 cdpdag CT + 1.0 ser-L> 1.0 cmp + 1.0 h + 1.0 ps CT
R PSDC CT	Chro.30247	4.1.1.65	R phosphatidylserine decarboxylase	Miscellaneous	[c] : 1.0 ps CT> 1.0 co2 + 1.0 psetha CT
R FACOALIUU	Chro 50052 or Chro 30084	6.2.1.3	R fatty acid CoA ligase Iso C100	Miscellaneous	10 : 1.0 atp + 1.0 coa + 1.0 uca <==> 1.0 amp + 1.0 ucacoa + 1.0 pp
R FACOAL140 ISO	Chro.50052 or Chro.30084	6.2.1.3	R fatty acid CoA ligase Iso C140	Miscellaneous	[c] : 1.0 atp + 1.0 coa + 1.0 fa1 <==> 1.0 amp + 1.0 fa1coa + 1.0 pp
R FACOAL150 anteis	Chro.50052 or Chro.30084	6.2.1.3	R fatty acid CoA ligase anteiso C150	Miscellaneous	[c]: 1.0 atp + 1.0 coa + 1.0 fa4 <==> 1.0 amp + 1.0 fa4coa + 1.0 ppi
R FACOAL150 ISO	Chro.50052 or Chro.30084	6.2.1.3	R fatty acid CoA ligase Iso C150	Miscellaneous	[c]: 1.0 atp + 1.0 coa + 1.0 fa3 <==> 1.0 amp + 1.0 fa3coa + 1.0 ppi
R FACOAL160 ISO	Chro.50052 or Chro.30084	6.2.1.3	R fatty acid CoA ligase Iso C160	Miscellaneous	[c]: 1.0 atp + 1.0 coa + 1.0 fa6 <==> 1.0 amp + 1.0 fa6coa + 1.0 ppi
R FACOALIBI ISO	Chro 50052 or Chro 30084	6.2.1.3	R fatty acid CoA ligase anteiso C170	Miscellaneous	[c]: 1.0 atp + 1.0 coa + 1.0 fa12 <==> 1.0 amp + 1.0 fa12 coa + 1.0 ppi
R FACOAL170 ISO	Chro.50052 or Chro.30084	6.2.1.3	R fatty acid CoA ligase Iso C170	Miscellaneous	[c]: 1.0 atp + 1.0 coa + 1.0 fall <==> 1.0 amp + 1.0 fall coa + 1.0 pp
R FACOAL171 anteis	Chro.50052 or Chro.30084	6.2.1.3	R fatty acid CoA ligase anteiso C171	Miscellaneous	<pre>[c]: 1.0 atp + 1.0 coa + 1.0 fa10 <==> 1.0 amp + 1.0 fa10coa + 1.0 ppi</pre>
R FACOAL171 ISO	Chro.50052 or Chro.30084	6.2.1.3	R fatty acid CoA ligase Iso C171	Miscellaneous	[c]: 1.0 atp + 1.0 coa + 1.0 fa9 <==> 1.0 amp + 1.0 fa9coa + 1.0 ppi
R FACOAL180 ISO	Chro.50052 or Chro.30084	6.2.1.3	R fatty acid CoA ligase Iso C180	Miscellaneous	[c]: 1.0 atp + 1.0 coa + 1.0 ocdcaiso <==> 1.0 amp + 1.0 ppi + 1.0 stro 2 b[c] + codb[c] + codb[c] + 2 b[c] + codb[c] + codb[c]
	Chro 10120	1.6.1.2	NAD(r)(ranshydrogenase	NAD Metabolism	2 n/e + naun(c) + naup(c)> 2 n/c) + nau(c) + naupn(c)
R NADK	Chro.80231	2.7.1.23	NADkinase	NAD Metabolism	[c]: atp + nad> adp + h + nadp
R_UDPDOLPT_U	Chro.50118	2.4.1.117	UDPglucose:dolichyl-phosphatebeta-D-glucosyltransferas	N-Glycan Biosynthesis	[c] : 0.1 dolp_U + udpg> 0.1 dolglcp_U + udp
R UDPDOLPT L	Chro.50118	2.4.1.117	UDPqlucose:dolichyl-phosphatebeta-D-glucosyltransferas	N-Glycan Biosynthesis	[c] : 0.1 dolp L + udpg> 0.1 dolglcp L + udp
R DOLASNT Uer	Chro.20179 or Chro.60585	2.4.1.119	Dolichyl-diphosphooligosaccharide:protein-L-asparagined	N-Glycan Biosynthesis	[c] : Asn-X DASH Ser FSLASH Thr + 0.1 g3m8mpdol U> 0.1 doldp U
R DOLASNI LEP	Chro 50175	2.4.1.119	Dolichyl-diphosphooligosaccharide:protein-L-asparagineg	N-Glycan Biosynthesis	[c]: ASN-X DASH Ser FSLASH INF + U.I g3m8mpdol L> U.I doldp L -
R DOLPMT U	Chro.50175	2.4.1.83	Dolichyl-phosphateD-mannosyltransferase(uterus)	N-Glycan Biosynthesis	[c]: 0.1 dolp U + gdpmann> 0.1 dolmanp U + gdp
R DOLPMTcer	Chro.50175	2.4.1.83	Dolichyl-phosphateD-mannosyltransferase	N-Glycan Biosynthesis	dolp[c] + qdpmann[c]> dolmanp[r] + qdp[c]
R DOLK	Chro.20170	2.7.1.108	Dolicholkinase	N-Glycan Biosynthesis	[c] : ctp + dolichol> cdp + dolp + h
R DOLK U	Chro.20170	2.7.1.108	Dolicholkinase,human(uterus)	N-Glycan Biosynthesis	[c] : $ctp + 0.1$ dolichol U> $cdp + 0.1$ dolp U + h
R GLCNACPT I	Chro.50156	2.7.8.15	UDP-GlcNAc: dolichol-phosphateGlcNAcphosphotransfera;	N-Glycan Biosynthesis	[c]: 0.1 dolp I + uacoam> 0.1 nagle2n I + ump
R GLCNACPT U	Chro.50156	2.7.8.15	UDP-GlcNAc:dolichol-phosphateGlcNAcphosphotransfera	N-Glycan Biosynthesis	[c]: 0.1 dolp U + uacgam -> 0.1 naglc2p U + ump
R_HCO3E	Chro.40064	4.2.1.1	HCO3equilibrationreaction	Nitrogen Metabolism	felters2 (b2e c) b b bes2
R H2CO3D	Chro.40064	4.2.1.1	carboxylicaciddissociation		[C] : co2 + fi2o <==> fi + fico3
R ASNS2	Chro.50501		carboxylicacidaissociación	Nitrogen Metabolism	[c]: co2 + h20 <==> h + hco3 [c]: co2 + h20 <==> h2co3
R ASNS1	Chro 60524	6.3.1.1	asparaginesynthetase	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism	[C]: to 2 + h20 <==> ln + hC03 [C]: co2 + h20 <==> h2co3 [C]: asp-L + atp + hh4 -> amp + asn-L + h + ppi [C]: asp - qlust + pbd +> adm + asp + dm + + m;
	Chro.60524 Chro.30020	6.3.1.1 6.3.1.2 6.3.5.4	asparaginesynthetase alutaminesynthetase asparaginesynthase(glutamine-hydrolysing)	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism	$ \begin{array}{l} [c] : (22 + h20 < ==> h + h003 \\ [c] : (20 + h20 < ==> h2c03 \\ [c] : asp-L + atp + nh4> amp + asn-L + h + ppi \\ [c] : asp-L + atp + nh4> adp + aln-L + h + pi \\ [c] : asp-L + atp + dn-L + h20> amp + asn-L + alu-L + h + nni \\ [c] : asp-L + atp + dn-L + h20> amp + asn-L + alu-L + h + nni \\ \end{array} $
R G1PTT	Chro.60524 Chro.30020 Chro.80452	6.3.1.1 6.3.1.2 6.3.5.4 2.7.7.24	Glicov Hacktadsouton asparatinesynthetase glutaminesynthetase asparaginesynthase(glutamine-hydrolysing) glucose-1-phosphatethymidylyltransferase	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism	[L]: 02 + 120 <==> 1 + 1003 [C]: 02 + 120 <==> 1 + 1003 [C]: 02 + 120 <=>> 1203 [C]: 02 + 1203 [C]: 0
R G1PTT R TDPGDH	Chro.60524 Chro.30020 Chro.80452 Chro.20206	6.3.1.1 6.3.1.2 6.3.5.4 2.7.7.24 4.2.1.46	Jahoory Indeclarity of the second sec	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism Nucleotide Sugar Metabolism	$ \begin{array}{l} [1: 02 + 120 < ==> 1 \text{ In + IROS} \\ [2: 02 + 120 < ==> 1 \text{ In + IROS} \\ [2: 02 + 120 < ==> 1 \text{ Aros} \\ [2: ab = 140 < l + 14 - >> amp + asn-L + h + ppi \\ [2: ab = 140 < l + 140 + ad + aln-L + h + pi \\ [2: abs-L + ab + aln-L + h20 - >> amp + asn-L + glu-L + h + ppi \\ [3: dtyle + alp + h ->> dtdpddg + h20 \\ [3: dtyle - >> dtdpddgd + h20 \\ \end{array} $
R G1PTT R TDPGDH R GALNT	Chro.60524 Chro.30020 Chro.80452 Chro.20206 Chro.60231 or Chro.50322 or	6.3.1.1 6.3.1.2 6.3.5.4 2.7.7.24 4.2.1.46 2.4.1.41	Curvox indecolosised unit aparacines vinthetase (lutamines vinthetase aparacines vinthase (dutamine - hydrolysing) (lucose - 1 ohosphatethymidyl/ltransferase dTDPdlucose/ - dehvdratase GalNActransferase, Golgiapparatus	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism Oucleotide Sugar Metabolism O-Glycan Biosynthesis	[1]: 02 + 120 <==> 1n + 1003 [2]: 022 + 120 <==> h(203 [2]: ozp + 120 <=> h(203 [2]: atp + du-L + nh4> atm + asn-L + h + ppi [2]: atp + du-L + nh4> atm + asn-L + h + ppi [2]: attp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + dn-L + h20> atm p + asn-L + du-L + h + ppi [2]: dttp + atp + atm + atm p + atm
R G1PTT R TDPGDH R GALNT R NADH10 R ECHH 1 PERIOD	Chro.60524 Chro.30020 Chro.80452 Chro.60231 or Chro.50322 or Chro.70218	6.3.1.1 6.3.1.2 6.3.5.4 2.7.7.24 4.2.1.46 2.4.1.41 1.6.5.3 1.6.5.3	appracinesynthetase appracinesynthetase appracinesynthetase alutaminesynthase(alutamine-hydrolysing) alucose-1-phosphatethymidylyltransferase dTDPqlucose4.6-dehydratase GalNActransferase,Golqiapparatus NADHdehydrogenase(menaquinone-8&0protons) Fchtbydroneanse	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism Nucleotide Sugar Metabolism O-Giycan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation	[1]: 02 + 120 <==> 1n + ntos [2]: 02 + 120 <==> 1n + ntos [2]: 02 + 120 <==> 1n + ntos [2]: 02 + 120 <=>> 1n + ntos [2]: 02 + 120 <=>> 1n + ntos [2]: 02 + 120 <=>> 1n + ntos [2]: 02 + 120 + 1n + -> 02 dp + gn-L + h + pi [2]: 02 + 120 + 1n -> 02 dp + gn-L + h + pi [2]: 02 + 120 + 1n -> 02 dp + gn-L + h + pi [2]: 02 + 120 + 1n -> 02 dp + gn-L + h + pi [2]: 02 + 120 +
R G1PTT R TDPGDH R GALNT R NADH10 R ECHH 1 PERIOD R NADH5	Chro.30020 Chro.30020 Chro.80452 Chro.20206 Chro.60231 or Chro.50322 or Chro.70218 Chro.70218 Chro.70218	6.3.1.1 6.3.1.2 6.3.5.4 2.7.7.24 4.2.1.46 2.4.1.41 1.6.5.3 1.6.5.3 1.6.5.3	Construction and a second	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism Nucleotide Sugar Metabolism O-Giycan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation	[1]: 102 + 1120 <==> 1 H + 1103 [2]: 202 + 120 <==> h + h + -> amp + asn-L + h + ppi [2]: atp + qu-L + hh4 -> amp + asn-L + h + ppi [2]: atp + qu-L + hh4 -> adp + qln-L + h + ppi [2]: atg + qu + qln + h + h20 ->> amp + asn-L + qlu-L + h + ppi [2]: dtp + ql = h + -> dtdp4ddq + h20 [2]: dtp + ql = h + -> dtdp4ddq + h20 [2]: h + mach + nadh -> mall + nad 2.fdred[c] + 3.h[c] <==> 2.fdox[c] + h[c] + h2[c] [2]: h + mach + q80 -> nad + q8h2
R GIPTT R TDPGDH R GALNT R NADH10 R ECHH 1 PERIOD R NADH5 R NADH7	Chro.30020 Chro.30020 Chro.80452 Chro.20206 Chro.60231 or Chro.50322 or Chro.70218 Chro.70218 Chro.70218 Chro.70218	$\begin{array}{c} 6.3.1.1 \\ 6.3.5.4 \\ 2.7.7.24 \\ 4.2.1.46 \\ 2.4.1.41 \\ 1.6.5.3 \\ 1.6.5.3 \\ 1.6.5.3 \\ 1.6.5.3 \\ \end{array}$	aparadinesynthetase (alutaminesynthetase (alutaminesynthetase (alutaminesynthetase) (alucose-1-phosphatethymidylyltransferase (all'OPalucose-6-6-dehydratase GallAdtransferase,Golojapparatus NADHdehydrogenase(menaquinone-880protons) Echtydrogenase NADHdehydrogenase(ubiquinone-8) NADHdehydrogenase(menaquinone-8&2protons)	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Givcan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation	$ \begin{array}{l} [1] : 0.24 + 10.26 <==> 1 h + htos \\ [2] : co2 + 10.26 <==> 1 h + htos \\ [2] : co2 + 10.26 <==> h2 co2 \\ [2] : abp - lu-lu-l + h4 -> adp + alm-l_+ h + pi \\ [2] : abp - lu-lu-l_+ hA2 ->> adp + alm-l_+ h + pi \\ [2] : abp - lu-lu-l_+ hA2 ->> amp + asm-l_+ alu-l_+ h + ppi \\ [2] : dtp + alu + alm-l_+ hA2 ->> amp + asm-l_+ alu-l_+ h + ppi \\ [2] : dtp + false hard + h20 \\ [2] : Sar = f3SASH Thr + udpaccal ->> Tn antiqen + h + udp \\ [2] : hr = f3SASH Thr + udpaccal ->> Tn antiqen + h + udp \\ [2] : hr = f3SASH Thr + udpaccal ->> Tn antiqen + h + udp \\ [2] : hr = f3SASH Thr + udpaccal ->> Tn antiqen + h + udp \\ [2] : hr = f3SASH Thr + udpaccal ->> Tn antiqen + h + udp \\ [2] : hr = f3SASH Thr + udpaccal ->> Th antiqen + h + udp \\ [2] : hr = hard + udpaccal ->> The [1 + mul8] (-1 + mul8] (-1$
R GIPTT R TDPGDH R GALNT R NADH10 R ECHH 1 PERIOD R NADH5 R NADH7 R NADH6 B NADH6	Chro. 50524 Chro. 30020 Chro. 80452 Chro. 20206 Chro. 70218 Chro. 70218 Chro. 70218 Chro. 70218 Chro. 70218 Chro. 70218 Chro. 70218	$\begin{array}{c} 6.3.1.1 \\ 6.3.5.4 \\ 2.7.7.24 \\ 4.2.1.46 \\ 2.4.1.41 \\ 1.6.5.3 \\ 1.6.5.$	appracinesynthetase glutaminesynthetase glutaminesynthetase glutaminesynthetase glutaminesynthetase glutaminesynthese glutaminesynthese GallActransferase, Goliapparatus NADHdeinytorgenase Echivytorgenase MADHdeinytorgenase(menaguinone-88.0protons) NADHdeinytorgenase(menaguinone-83.5protons) NADHdeinytorgenase(menaguinone-83.5protons) NADHdeinytorgenase(menaguinone-83.5protons) NADHdeinytorgenase(menaguinone-83.5protons) NADHdeinytorgenase(menaguinone-83.5protons) NADHdeinytorgenase(menaguinone-83.5protons) NADHdeinytorgenase(menaguinone-83.5protons) NADHdeinytorgenase(menaguinone-83.5protons) NADHdeinytorgenase(menaguinone-83.5protons) NADHdeinytorgenase(menaguinone-83.5protons)	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism Oxidetide Sugar Metabolism Oxidetive Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation	$ \begin{array}{l} [1] : 02 + 120 < ==> 1 h + ntos \\ [2] : 02 + 120 < ==> h + ntos \\ [2] : 02 + 120 < ==> h 20 < \\ [2] : 02 + 120 < ==> h 20 < \\ [3] : 02 + 120 < => h + 120 < \\ [3] : 02 + 120 < 120 < \\ [3] : 02 + 120 < 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : 02 + 120 < \\ [3] : $
R G1PTT R TDPGDH R GALNT R NADH10 R NADH10 R NADH5 R NADH7 R NADH6 R NADH9 R NADH9	Chro.60524 Chro.3020 Chro.80452 Chro.20206 Chro.60231 or Chro.50322 or Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218	6.3.1.1 6.3.5.4 2.7.7.24 4.2.1.46 2.4.1.41 1.6.5.3 1.6.5.3 1.6.5.3 1.6.5.3 1.6.5.3 1.6.5.3 1.6.5.3 1.6.5.3	Labor Mindeaduszational Saparadinesynthetase (jutaminesynthetase (jutaminesynthetase (jutaminesynthese(jutamine-hydrolysing) alucose-1-phosphatethymidylvtransferase GallyActransferase, Golgiapparatus MADHdehydrogenase(maquinone-883,2protons) NADHdehydrogenase(menaquinone-882,protons) NADHdehydrogenase(menaquinone-882,protons) NADHdehydrogenase(demethydmenaquinone-882,protons) NADHdehydrogenase(demethydmenaquinone-882,protons) NADHdehydrogenase(demethydmenaquinone-882,protons) NADHdehydrogenase(demethydmenaquinone-882,protons) NADHdehydrogenase(demethydmenaquinone-882,protons) NADHdehydrogenase(demethydmenaquinone-882,protons) NADHdehydrogenase(demethydmenaquinone-882,protons) NADHdehydrogenase(demethydmenaquinone-882,protons)	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Giycan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation	$ \begin{array}{l} [1] : 0.2 + 1.20 < ==> 1 \text{ H} + 1.003 \\ [c] : 0.20 + 1.00 < ==> h + 1.003 \\ [c] : 0.20 + 1.00 < ==> h + 1.003 \\ [c] : 0.20 + 1.00 < ==> h + 1.003 \\ [c] : 0.20 + 1.00 < == h + 1.003 \\ [c] : 0.20 + 1.00 + 1.00 & == h + 1.003 \\ [c] : 0.20 + 1.00 + 1.00 & == h + 1.003 \\ [c] : 0.20 + 1.00 + 1.003 \\ [c] : 0.20 + 1.003 \\$
R G1PTT R TDP5DH R GALNT R GALNT R ADDH10 R ECHH 1 PERIOD R NADH5 R NADH5 R NADH6 R NADH8 R NADH8 R NADH2 DASH US	Chro. 60524 Chro. 30020 Chro. 80452 Chro. 20206 Chro. 70218 Chro. 70218	$\begin{array}{c} 6.3.1.1\\ 6.3.5.4\\ 2.7.7.24\\ 4.2.1.46\\ 2.4.1.41\\ 1.6.5.3\\ 1.6.5.3\\ 1.6.5.3\\ 1.6.5.3\\ 1.6.5.3\\ 1.6.5.3\\ 1.6.5.3\\ 1.6.5.3\\ 1.6.5.3\\ 1.6.5.3\\ 1.6.5.3\\ 1.6.5.3\\ 1.6.9\\ 3\end{array}$	Labore and the second sec	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Givcan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation Oxidative Phosphorylation	$ \begin{array}{l} [1] : 02 + 120 < ==> 1 h + ntos \\ [1] : 02 + 120 < ==> 1 h + ntos \\ [2] : 02 + 120 < ==> 1 h + ntos \\ [2] : 02 + 120 < ==> 1 h + ntos \\ [2] : 02 + 120 < ==> 1 h + ntos \\ [2] : 02 + 120$
R G1PTT R TDP5DH R GALNT R NADH10 R ECHH 1 PERIOD R NADH5 R NADH7 R NADH9 R NADH9 R NADH9 R NADH9 R CYOO HP	Chro.60524 Chro.3020 Chro.80452 Chro.20206 Chro.60231 or Chro.50322 or Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218	$\begin{array}{c} 6.3.1.1\\ 6.3.5.4\\ 2.7.7.24\\ 4.2.1.46\\ 2.4.1.41\\ 1.6.5.3\\ 1.6.5\\ $	La los interestination la logaritation la logaritationa	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Giycan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation	$ \begin{array}{l} [1] : 02 + 120 < ==> 1 h + ntos \\ [c] : 02 + 120 < ==> h(zo + ntos) \\ [c] : abg - 140 < ==> h(zo + nto) \\ [c] : abg - 140 < + hh + -> amg + asn-L + h + pi \\ [c] : abg - 140 < + hh> adg + gln-L + h + pi \\ [c] : abg - 140 + 1 h> dtog + gln-L + h + pi \\ [c] : dtb + 10 + h> dtog + gln-L + h + 20 \\ [c] : dtb + 10 + h> dtog + gln-L + h + dg \\ [c] : dtb + 10 + h> dtog + gln-L + h + dg \\ [c] : h + nand + nad + -> mol8 + nad \\ [c] : h + nadh + q8> nad (+ q8h2 \\ [c] : h + nadh (c] + agh(c] - > 2 h(e] + nad[c] + q8h2(c] \\ [c] : h + nadh (c] + agh(c]> 2 h(e] + nad[c] + q8h2(c] \\ [c] : hc + nadh(c] + agh(c] - > 2 h(e] + nad[c] + q8h2(c] \\ [c] : admmag[c] + nadh(c] - > 2 dmmag[[c] + 2.8 h(e] + nad(c] \\ [c] : 2dmmag[[c] + 2.8 h(c] + nadh(c] - > 2 dmmag[[c] + 2.8 h(e] + nad(c] \\ [c] : -> nad(c] + q6h2(c] \\ [c] : -> nad(c] + q6h2(c] \\ [c] : -> 2 h(e] + 1.98h(c] + 2 h(e) + 1.99h(c) \\ [c] : -> 2 h(e] + 1.98h(c] + 2 h(e) + 1.99h(c) \\ [c] : -> 2 h(e] + 1.98h(c) \\ [c] : -> 2 h(e) + 2 h(e) + 1.99h(c) \\ [c] : -> 2 h(e) + 2 h(e) + 1.99h(c) \\ [c] : -> 2 h(e) + 2 h(e) + 1.99h(c) \\ [c] : -> $
R GIPTT R TDPGDH R GALNT R NADH10 R ECHH 1 PERIOD R NADH5 R NADH5 R NADH6 R NADH6 R NADH6 R NADH8 R NADH2 DA5H U60 R CYOO HP R PPA 1	Chro. 60524 Chro. 30020 Chro. 30020 Chro. 30452 Chro. 70218 Chro. 70185 Chro. 70159	$\begin{array}{c} 6.3.1.1\\ 6.3.5.4\\ 2.7.7.24\\ 4.2.1.46\\ 2.4.1.41\\ 1.6.5.3\\ 1.6.5\\ 1$	Labor Mindeaduszational Laborational and a secondary of the secondary of the secondary Laboration of the secondary of the secondary of the secondary Laboration of the secondary of the second	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Givcan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation	$ \begin{array}{l} [1] : 0.24 + 10.26 < => 1 h + nto.3 \\ [1] : 0.24 + 10.26 < => 1 h + nto.3 \\ [2] : 0.26 + 10.26 < => h + nto.3 \\ [2] : 0.26 + 10.26 < => h + nto.3 \\ [2] : 0.26 + 10.26 < => h + nto.3 \\ [2] : 0.26 + 10.26 < => h + nto.3 \\ [2] : 0.26 + 10.26 < => h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> h + nto.3 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 < d>=> 0.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 10.26 \\ [2] : 0.26 + 1$
R GJPTT R TDPCDH R GALNT R NADH10 R NADH10 R NADH5 R NADH5 R NADH5 R NADH6 R NADH6 R NADH8 R NADH2 R NADH2 R NADH12 R NADH12 R PPA 1 R PPA 2 R PPA 2	Chro. 60524 Chro. 30020 Chro. 30020 Chro. 30452 Chro. 70216 Chro. 70218 Chro.	$\begin{array}{c} 6.3.1.1 \\ 6.3.5.4 \\ 6.3.5.4 \\ 2.7.7.24 \\ 4.2.1.46 \\ 1.6.5.3 \\ 1.6.5.5$	Asparaginesynthetase glutaminesynthetase glutaminesynthetase glutaminesynthetase glutamises gluta	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Givcan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation	$ \begin{array}{l} [1] : 02 + 120 < ==> 1 h + ntos \\ [2] : 02 + 120 < ==> 1 h + ntos \\ [2] : 02 + 120 < ==> 1 h + ntos \\ [2] : 02 + 120 < ==> 1 h + ntos \\ [2] : 02 + 120 < ==> 1 h + ntos \\ [2] : 02 + 120 < ==> 1 h + ntos \\ [2] : 02 + 120 + 1 h -> 2 dtp + gln - L + h + pi \\ [2] : 02 + 120 + 1 h -> 2 dtp + gln - L + h + pi \\ [2] : 02 + 120 + 1 h -> 2 dtp + gln - L + h + pi \\ [2] : 02 + 120 + 1 h -> 2 dtp + gln - 1 h + ntop \\ [2] : 02 + 120 + 1 h -> 2 dtp + gln - 1 h + ntop \\ [2] : 02 + 120 + 12$
R GJPTT R TDPCGH R GGLNT R NADH10 R NADH5 R NADH5 R NADH5 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH7 R NADH6 R NADH7 R	Chro.60524 Chro.3020 Chro.80452 Chro.20206 Chro.60231 or Chro.50322 or Chro.70218 Chro.70159 Ch	$\begin{array}{c} 6.3.1.1 \\ 6.3.1.2 \\ 6.3.5.4 \\ 2.7.7.24 \\ 4.2.1.46 \\ 2.4.1.41 \\ 1.6.5.3 \\ 1.6.5.5 \\ 1.6.5.$	Laboratine conservation Laboration Lab	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Giycan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation	$ \begin{array}{l} [1] : 02 + 120 < ==> 1 h + h(03) \\ [c] : 02 + 120 < ==> h(23) \\ [c] : 02 + 120 < ==> h(23) \\ [c] : atp - 14u - 1 + h4 -> amp + asn-L + h + pi \\ [c] : atp - 14u - 1 + h4 -> amp + asn-L + h + pi \\ [c] : atp - 14u - 1 + h4 -> amp + asn-L + h4u - 1 + pi \\ [c] : atp - 14u - 1 + h-> add p + gin-L + h40 -> amp + asn-L + glu-L + h + ppi \\ [c] : atp - 14u - 1 + h-> add p + gin-L + h20 -> amp + asn-L + glu-L + h + ppi \\ [c] : atp - 14u - 1 + h-> add g + gin-L + h20 -> amp + asn-L + glu-L + h + ppi \\ [c] : ht + nandh + n - mall + nad -> amp + asn-L + glu-L + h + udp \\ [c] : h + nadh + adh -> mall + nad (-1 + glu-L + h40) \\ [c] : h + nadh + adh -> mall + nad (-1 + glu-L + h40) \\ [c] : hadh + gl -> add + glh2 \\ [c] : admagl(-1 + adh(-1 -> 2 hf + malls(c] + nad(c] + glh2(c) \\ [c] : 2dmmagl(-1 + 38 h(c] + nadh(-1 -> 2 hf + nadls(c] + 2.8 h(e] + nad(c) \\ [c] : 2dmmagl(-1 + 5.98 h(c] -> and(c] + ghh2(c) \\ [c] : 2dmmagl(-1 + 5.98 h(c] -> 2 hf (c) + 2.5 h(e] + nadls(c] + 2.8 h(e] + nad(c) \\ [c] : h20 + ppi -> h + 1 + pi \\ [c] : h20 + ppi -> h + 2 ai \\ = add(-1 + h2) + ad(- = -> atd(-1 + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-) = -> add(-1 + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-) = -> add(-1 + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-) = -> add(-1 + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-) = -> add(-1 + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-) = -> add(-1 + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-1 + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-1 + ad(-1 + 2h(c) + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-1 + ad(-1 + 2h(c) + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-1 + ad(-1 + 2h(c) + 2h(c) + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-1 + ad(-1 + 2h(c) + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-1 + ad(-1 + 2h(c) + 2h(c) + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-1 + ad(-1 + 2h(c) + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-1 + ad(-1 + 2h(c) + 2h(c) + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-1 + ad(-1 + 2h(c) + 2h(c) + 2h(c) + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-1 + 2h(c) + 2h(c) + 2h(c) + 2h(c) \\ = add(-1 + h2) + ad(-1 + 2h(c) + 2h(c) + 2h(c) + 2h(c) \\ = add(-1 + h2) + $
R GJPTT R TDPCDH R GALNT R NADH10 R CCHH 1 PERIOD R NADH5 R NADH6 R NADH6 R NADH6 R NADH6 R NADH2 DASH u60 R CYOO HP R PPA 1 R PPA 1 R PPA R ATPS4r R ATPS4r	Chro.60524 Chro.3020 Chro.3020 Chro.30452 Chro.70218 Chro.70159 Chro.60082 and Chro.20424 i Chro.20429 and Chro.20424	$\begin{array}{c} 6.3.1.1\\ 6.3.5.4\\ 2.7.7.24\\ 4.2.1.46\\ 1.6.5.3\\ 1.6$	Labore interesting and a second	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Givcan Biosvnthesis Oxidative Phosphorylation	$ \begin{array}{l} [1] : 02 + 120 < ==> 1 h + h(0.5) \\ [c] : co2 + 120 < ==> 1 h + h(0.5) \\ [c] : co2 + 120 < ==> h(2-0) \\ [c] : abp - [d] + cap + abp - 1 abp - 2 abp - 1 abp - 1 abp - 1 abp - 1 abp - 2 abp - $
R GJPTT R TDPGOH R GGLNT R NADH10 R NADH5 R NADH5 R NADH5 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH8 R NADH2 R PA01 R CYOO HP R PPA 1 R PPA 1 R PPA 2 R PPA 2 R PPA 2 R ATPS4r R ATPS4r R ATPS4-	Chro.60524 Chro.3020 Chro.80452 Chro.20206 Chro.60231 or Chro.50322 or Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70244 and Chro.20424 z Chro.20424 and Chro.2055 e	$\begin{array}{c} 6.3.1.1\\ 6.3.1.2\\ 6.3.5.4\\ 2.7.7.24\\ 4.2.1.46\\ 1.6.5.3\\ 1.6.5.5\\ 1.6.5\\ 1.6.5\\ 1.6.5\\ 1.6.5\\ 1.$	Landow Indexemption L	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Givcan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation	$ \begin{array}{l} [1] : 02 + 120 < => 1 h + ft(03) \\ [2] : 202 + 120 < => 1 h + ft(03) \\ [2] : 202 + 120 < => h / 203 \\ [2] : 202 < => h / 203 \\ [2] : 202 < => h / 203 \\ [2] : 202 < d>=> h / 203 \\ [2] : 202 < d>=> h / 203 \\ [2] : 202 < d>=> h / 203 \\ [2] : 202 < d>=> h / 203 \\ [2] : 202 < d>=> h / 203 \\ [2] : 202 < d>=> h / 203 \\ [2] : 202 < d>=> h / 203 \\ [2] : 202 < d>=> h / 203 \\ [2] : 202 < d>=> h / 203 \\ [2] : 202 < d>=> h / 203 \\ [2] : 202 < d>=> h / 203 \\ [2] :$
R GJPTT R TDPCOH R GALNT R NADH10 R NADH5 R NADH5 R NADH5 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH7 R NADH6 R NADH7 R R R R R R R R R R R R R R R R R R R	Chro.60524 Chro.3020 Chro.80452 Chro.20206 Chro.50231 or Chro.50322 or Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.60082 and Chro.20424 a Chro.20424 and Chro.70559 a	$\begin{array}{c} 6.3.1.1\\ 6.3.5.4\\ 2.7.7.24\\ 4.2.1.46\\ 2.4.1.41\\ 1.6.5.3\\ 1.$	Laboratina and a second a s	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Giycan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation	$ \begin{array}{llllllllllllllllllllllllllllllllllll$
R GJPTT R TDPCDH R GALNT R NADH10 R CCHH 1 PERIOD R NADH5 R NADH7 R NADH6 R NADH6 R NADH6 R NADH7 R NADH8 R NADH12 DASH u60 R CYOO HP R PPA 1 R PPA 1 R PPA 1 R PPA 1 R ATPS4r R ATPS4r R ATPS5 R CATPS R CATPS R CATPS	Chro.60524 Chro.3020 Chro.30452 Chro.20206 Chro.60231 or Chro.50322 or Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70168 Chro.70169 Chro.40159 Chro.40159 Chro.40159 Chro.20424 and Chro.70559 a Chro.20424 and Chro.70559 a Chro.20554 a Chro.70559 a Chro.2055 a Chro.70559 a Chro.2055 a Chro.70559 a Chro.2055 a Chro.70559 a Chro.2055 a Chro.70559 a Chro.2055 a	$\begin{array}{c} 6.3.1.1 \\ 6.3.1.2 \\ 6.3.5.4 \\ 2.7.7.24 \\ 4.2.1.46 \\ 1.6.5.3 \\ 1.6.5.5$	Approximate Construction of the second secon	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Oversteide Sugar Metabolism Oversteide Sug	$ \begin{array}{l} [1] : 02 + 120 < => 1 + n(0.5) \\ [c] : co2 + 120 < => 1 + n(0.5) \\ [c] : co2 + 120 < => h(2 - 0.5) \\ [c] : abp - 14u + + nh4 -> amp + asn-L + h + ppi \\ [c] : abp - 14u + + nh4 -> amp + asn-L + h + ppi \\ [c] : abp - 14u + + nh4 -> amp + asn-L + h + ppi \\ [c] : abp - 14u + 1 + n20 ->> amp + asn-L + ngu-L + h + ppi \\ [c] : dtu + q - 10 + h -> adp + qln-L + h + 20 -> amp + asn-L + glu-L + h + ppi \\ [c] : dtu + q - 10 + h -> adp + qln-L + h + 20 -> amp + asn-L + glu-L + h + ppi \\ [c] : dtu + q - 10 + h -> adp + qln-L + h + 20 -> amp + asn-L + glu-L + h + ppi \\ [c] : dtu + q - 10 + h -> adp + qln-L + h + qln + 10 + 10 + 10 + 10 + 10 + 10 + 10 + 1$
R GJPTT R TDPCGH R GGAINT R NADH10 R NADH5 R NADH5 R NADH5 R NADH5 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH7 R NADH7 R PPA 1 R FPA 2 R FPA 2 R FPA 2 R ATPS4 R ATPS5 R A	Chro.60524 Chro.3020 Chro.80452 Chro.20206 Chro.60231 or Chro.50322 or Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70168 Chro.40159 Chro.40159 Chro.40159 Chro.20424 and Chro.70559 Chro.20424 and Chro.70559 Chro.20424 and Chro.70559 Chro.20424 and Chro.70559 Chro.20445 and Chro.70559 Chro.20455 ac Chro.8055 ac Chro.8	$\begin{array}{c} 6.3.1.1 \\ 6.3.1.2 \\ 6.3.5.4 \\ 2.7.7.24 \\ 4.2.1.46 \\ 1.6.5.3 \\ 1.6.5.5$	Landon Indeconcention Laportal Intervention Laportal Intervention Laportal Intervention Laportal Intervention Laportal Intervention Laportal Laportalaportal Laportalparte Laportal Laportal L	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Glycan Biosynthesis Oxidative Phosphorylation Oxidative Phosphoryl	$ \begin{array}{l} [1] \ (102 + 120 < ==> 1 \text{ H} + \text{Intos} \\ [2] \ (202 + 120 < ==> 1 \text{ H} + \text{Intos} \\ [2] \ (202 + 120 < ==> 1 \text{ H} + \text{Intos} \\ [2] \ (202 + 120 < ==> 1 \text{ H} + \text{Intos} \\ [2] \ (202 + 120 < ==> 1 \text{ H} + \text{Intos} \\ [2] \ (202 + 120 + 11 + 120 - >> \text{ amp} + \text{ asn}_{-} + \text{ hpi} \\ [2] \ (212 + 120 + 11 + 120 - >> \text{ amp} + \text{ asn}_{-} + \text{ hpi} \\ [2] \ (212 + 120 + 11 + 120 - >> \text{ amp} + \text{ asn}_{-} + \text{ hpi} \\ [2] \ (212 + 120 + 11 + 120 - >> \text{ amp} + \text{ asn}_{-} + \text{ spi} \\ [2] \ (212 + 120 + 11 + >> \text{ othere} + 120 - >> \text{ and} \\ [2] \ (212 + 120 + 11 + >> \text{ othere} + 120 - >> \text{ and} \\ [2] \ (212 + 120 + 11 + >> \text{ othere} + 120 - >> \text{ and} \\ [2] \ (212 + 120 + 120 + 120 - >> \text{ and} + 120 + 120 - >> \text{ and} \\ [2] \ (212 + 120 + 120 + 120 + >> \text{ and} + 120 + $
R GJPTT R TDPCDH R GALNT R NADH10 R NADH5 R NADH5 R NADH5 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH7 R NADH7 R NADH8 R NADH8 R NADH2 R NADH8 R NADH2 R NADH8 R NADH2 R NADH9 R R NADH9 R R NADH9 R R PPA 1 R ATPSel R COO H9 R R ATPS R CAAPS R CAAPS R R R R R R R R R R R R R R R R R R R	Chro.60524 Chro.3020 Chro.80452 Chro.20206 Chro.60231 or Chro.50322 or Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.7018 Chro.7018 Chro.7018 Chro.7018 Chro.40159 Chro.60082 and Chro.20424 a Chro.20424 and Chro.70559 a Chro.20425	$\begin{array}{c} 6.3.1.1\\ 6.3.1.2\\ 6.3.5.4\\ 2.7.7.24\\ 4.2.1.46\\ 1.6.5.3\\ 1.6$	Lancon Indeconsequence Lancon Indeconsequence Lancon Indeconsequence Lanconsequence Lan	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Givcan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation	$ \begin{array}{l} [1] : 02 + 120 < ==> 1 + h(0.5) \\ [c] : co2 + 120 < ==> h(-h(0.5)) \\ [c] : co2 + 120 < ==> h(-h(0.5)) \\ [c] : abp - (hu-L + hh(> adp + abn-L + h + pi) \\ [c] : abp - (hu-L + hh(> adp + abn-L + h + pi) \\ [c] : abp - (hu-L + hh(> adp + abn-L + h) \\ [c] : abp - (hu-L + hh(> adp + abn-L + h) \\ [c] : abp - (hu-L + hh(> adp + abn-L + h) \\ [c] : abp - (hu-L + hh(> adp + abn-L + h) \\ [c] : abp - (hu-L + hh(> adp + abn-L + h) \\ [c] : abp - (hu-L + hh(> adp + abn-L + h) \\ [c] : abp - (hu-L + hh(> adp + abn-L + h) \\ [c] : abm - (hu-L + hh(> adp + h) \\ [c] : abm - (hu-L + hh(> adp + abn-L + hh() \\ [c] : abm - (hu-L + hh() + adp + abn-L + hh() \\ [c] : abm - (hu-L + hh() + adp + abn-L + hh() \\ [c] : abm - (hu-L + hh() + adp + abn-L + hh() \\ [c] : abm - (hu-L + hh() + adp + abn-L + hh() \\ [c] : abm - (hu-L + hh() + adp + abn-L + hh() \\ [c] : abm - (hu-L + hh() + abn-L + hh() \\ [c] : abp - (hu-L + hh() + abn-L + hh() \\ [c] : abp - (hu-L + hh() + hh() \\ [c] : abp - (hu-L + hh() + hh() \\ [c] : abp - (hu-L + hh() + hh() \\ [c] : abp - (hu-L + hh() \\$
R GJPTT R TDPCGH R GALNT R NADH10 R NADH5 R NADH5 R NADH5 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH8 R NADH2 R NADH2 R PPA 1 R FPA 1 R JPPA 1 R	Chro.60524 Chro.3020 Chro.80452 Chro.20206 Chro.60231 or Chro.50322 or Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70168 Chro.40159 Chro.40159 Chro.40159 Chro.20424 and Chro.70559 a Chro.20424 and Chro.70559 Chro.20424 and Chro.70559 Chro.20424 and Chro.70559 Chro.202424 and Chro.70559 Chro.20251 Chro.20231	$\begin{array}{c} 6.3.1.1\\ 6.3.1.2\\ 6.3.5.4\\ 2.7.7.24\\ 4.2.1.46\\ 1.6.5.3\\ 1.6$	Landow indexension Landow	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Givcan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation Pantothenate-Vit B5 and CoA biosynthesis Pentose Phosphate Pathway	$ \begin{array}{l} [1] : 02 + 120 < => 1 h + h(03) \\ [2] : 02 + 120 < => h + h(03) \\ [2] : 02 + 120 < => h(2) < a < b < b < b < b < b < b < b < b < b$
R GJPTT R TDPCOH R GGAINT R NADH10 R NADH5 R NADH5 R NADH5 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH7 R NADH7 R PPA 1 R CYCO HP R PPA 1 R CYCO HP R PPA 2 R ATP54r R ATP54r R CATP55 R PFK 2 R PFK 3 R P	Chro.60524 Chro.3020 Chro.80452 Chro.20206 Chro.50231 or Chro.50322 or Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70168 Chro.40159 Chro.40159 Chro.40159 Chro.40159 Chro.40159 Chro.20424 and Chro.70559 c Chro.20424 and Chro.20424 c Chro.20424 and Chro.20424 c Chro.20424 and Chro.70559 c Chro.20424 and Chro.70559 c Chro.20424 and Chro.70559 c Chro.20424 and Chro.20424 c Chro.20424 and Chro.70559 c Chro.20424 and Chro.70559 c Chro.20424 and Chro.70559 c Chro.20424 and Chro.20424 and Chro.20424 c Chro.20424 and Chro.70559 c Chro.20424 and Chro.20424 and Chro.20424 c Chro.20424 and Chro.20424 and Chro.2044 and Chro	$\begin{array}{c} 6.3.1.1\\ 6.3.5.4\\ 2.7.7.24\\ 4.2.1.46\\ 1.6.5.3\\ 1.6$	Laboratine and a second s	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Givcan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation	$ \begin{array}{llllllllllllllllllllllllllllllllllll$
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R GJPTT R TDPCOH R GALNT R NADH10 R NADH5 R NADH5 R NADH5 R NADH5 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH7 R NADH8 R NADH9 R PPA 1 R OFFA 1	Chro. 60524 Chro. 30020 Chro. 30020 Chro. 80452 Chro. 20206 Chro. 60231 or Chro. 50322 or Chro. 70218 Chro. 70168 Chro. 40159 Chro. 40159 Chro. 40159 Chro. 40159 Chro. 40159 Chro. 20424 and Chro. 70559 s Chro. 20424 and Chro. 70559 Chro. 20424 and Chro. 70559 Chro. 202424 and Chro. 70559 Chro. 202421 Chro. 20231 Chro. 20231 Chro. 20231 Chro. 20231 Chro. 20336 Chro. 20336	$\begin{array}{c} 6.3.1.1 \\ 6.3.1.2 \\ 6.3.5.4 \\ 2.7.7.24 \\ 4.2.1.46 \\ 1.6.5.3 \\ 1.6.5.5$	Landon Indeconcentron Landon Indeconcentron Laparadinery intrelease Jularianity and the second indeconcentrate Jularianity and the second indeconcentrate Jularianity and the second indeconcentrate Second Indeconcentrate Second Indeconcentrate Application Application Second Indeconcentrate Second	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Giycan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation Dxidative Phosphorylation Dxidative Phosphorylation Pantothenate-Vit B5 and CoA biosynthesis Pentose Phosphate Pathway Pentose Phosphate Pathway Pentose Phosphate Pathway Pentose Phosphate Pathway	$ \begin{array}{l} [1] \ (12) + 120 \ (2 = 1) \ (11) \ (12) \ (22) + 120 \ (2 = 1) \ (11) \ (12) \ (22) $
R GJPTT R TDPCOH R GALNT R NADHJO R NADH5 R NADH5 R NADH5 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH7 R NADH7 R NADH8 R NADH7 R NADH8 R NADH2 R NADH8 R NADH2 R NADH7 R R NADH7 R R NADH7 R R NADH7 R R NADH7 R R R R R R R R R R R R R R R R R R R	Chro.60524 Chro.3020 Chro.80452 Chro.20206 Chro.50231 or Chro.50322 or Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70218 Chro.70168 Chro.40159 Chro.40159 Chro.40159 Chro.40159 Chro.6082 and Chro.20424 af Chro.20424 and Chro.70559 a Chro.20424 and Chro.70559 c Chro.20424 and Chro.70559 c Chro.20425 Chro.20425 Chro.20231 Chro.20231 Chro.20336 Chro.20336	$\begin{array}{c} 6.3.1.1\\ 6.3.1.2\\ 6.3.5.4\\ 2.7.7.24\\ 4.2.1.46\\ 1.6.5.3\\ 1.6$	Landownia and a second se	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Giycan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation Pantothenate-Vit B5 and CoA biosynthesis Pantothenate-Vit B5 and CoA biosynthesis Pentose Phosphate Pathway Pentose Phosphate Pathway Pentose Phosphate Pathway Pentose Phosphate Pathway Phentose Phosphate Pathway	$ \begin{array}{llllllllllllllllllllllllllllllllllll$
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R GJPTT R TDPCOH R GGAINT R NADH10 R NADH5 R NADH5 R NADH5 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH7 R NADH8 R NADH2 R NADH2 R PPA 1 R PPA 1 R PPA 1 R PPA 2 R PPA 1 R ATPS4r R ATPS4r R ATPS4F R ATPS4F R ATPS5 R ATP51 R APCOAK R PFK 3 R PFK 3 R PFK 3 R PFK 4 R PF	Chro. 60524 Chro. 30020 Chro. 30020 Chro. 30020 Chro. 30026 Chro. 70216 Chro. 70218 Chro. 70168 Chro. 70159 Chro. 20424 and Chro. 70559 a Chro. 20231 Chro. 20231 Chro. 20231 Chro. 20336 Chro. 30373 Chro. 30373 Chro. 30503	$\begin{array}{c} 6.3.1.1 \\ 6.3.1.2 \\ 6.3.1.2 \\ 6.3.1.2 \\ 1.4.2 \\ 2.7.7.24 \\ 4.2.1.46 \\ 1.6.5.3 \\ 1.6.5.5 \\ 1.6.5.5 \\$	Japaradinesynthetase Japaradinesynthetase Japaradinesynthetase Japaradinesynthetase Japaradinesynthese(dutamine-hydrolysing) Japaradinesynthase(dutamine-hydrolysing) Japaradinesynthase(dutamine-hydrolysing) Japaradinesynthase(dutamine-hydrolysing) Japaradinesynthase(dutamine-hydrolysing) Lehtydrogenase(hydrolysing) Lehtydrogenase(manaquinone-8&0,protons) NADHdehydrogenase(menaquinone-8&1,protons) NADHdehydrogenase(menaquinone-8&2,protons) NADHdehydrogenase(demethylmenaquinone-8&2,protons) NADHdehydrogenase(demethylmenaquinone-8&2,Borotons) NADHdehydrogenase(demethylmenaquinone-8&2,Borotons) NADHdehydrogenase(demethylmenaquinone-8&2,Borotons) NADHdehydrogenase(demethylmenaquinone-8&2,Borotons) NADHdehydrogenase(cherthylmenaquinone-8&2,Borotons) NaDHdehydrogenase(cherthylmenaquinone-8&2,Borotons Silfumatekinase Shjkimatekinase(Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nucleotide Sugar Metabolism O-Givcan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation Dentose Phosphate Patimwa Pentose Phosphate Patimwa Phenselalanine, Tvrosine and Tryutophan B Phervylalanine, Tvrosine and Tryutophan B	$ \begin{array}{llllllllllllllllllllllllllllllllllll$
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R GJPTT R TDPCOH R GALNT R NADH10 R ICHH 1 PERIOD R NADH5 R NADH5 R NADH6 R NADH6 R NADH6 R NADH6 R NADH6 R NADH7 R NADH8 R NADH2 R NADH8 R NADH2 R NADH2 R NADH4 R NADH2 R NADH2 R NADH2 R NADH2 R NADH5 R NADH2 R NADH2 R NADH2 R NADH2 R NADH2 R NADH2 R NADH5 R NADH2 R N	Chro. 60524 Chro. 30020 Chro. 80452 Chro. 20206 Chro. 60231 or Chro. 50322 or Chro. 70218 Chro. 70168 Chro. 40159 Chro. 40159 Chro. 40159 Chro. 40159 Chro. 20424 and Chro. 70559 a Chro. 20424 and Chro. 70559 Chro. 20424 and Chro. 70559 Chro. 202424 and Chro. 70559 Chro. 20231 Chro. 20231 Chro. 20231 Chro. 20231 Chro. 20336 Chro. 20336 Chro. 20336 Chro. 30373 Chro. 80609 Chro. 50503 Chro. 50503 Chro. 50503 Chro. 5054 or Chro. 80385	$\begin{array}{c} 6.3.1.1 \\ 6.3.1.2 \\ 6.3.5.4 \\ 2.7.7.24 \\ 4.2.1.46 \\ 1.6.5.3 \\ 1.6.5.5$	abapradinesynthetase abapradinesynthetase (alutaminesynthetase (alutaminesynthetase (alutaminesynthetase (alutaminesynthetase (alutaminesynthetase (alutaminesynthetase (alutaminesynthese (alutaminese (aluta	Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nitrogen Metabolism Nuclectide Sugar Metabolism O-Givcan Biosynthesis Oxidative Phosphorylation Oxidative Phosphorylation Pantothenate-Vit B S and CoA biosynthesis Pentose Phosphate Pathway Pentose Phosphate Pathway	$ \begin{array}{llllllllllllllllllllllllllllllllllll$
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R_ACCOACr	Chro.80425	6.4.1.2	acetyl-CoAcarboxylase, reversible reaction	Propanoate Metabolism	[c] : accoa + atp + hco3 <==> adp + h + malcoa + pi
R IMPD R RNDR2n	Chro.60012 Chro.60090 or Chro.60091	1.1.1.205	IMPdehydrogenase	Purine Metabolism	[c]: h20 + imp + had> h + hadh + xmp
R RNDR4n	Chro.60090 or Chro.60091	1.17.4.1	ribonucleoside-diphosphatereductase(UDP),nuclear	Purine Metabolism	[c] : trdrd + udp> dudp + h2o + trdox
R ADNK2	Chro.20322	2.7.1.20	adenosinekinase	Purine Metabolism	[c] : adn + gtp> adp + gmp + h
R ADNK1	Chro.20322	2.7.1.20	adenosinekinase	Purine Metabolism	[c] : adn + atp> adp + amp + h
R NDPK10	Chro.40275 or Chro.50237 or	2.7.4.6	nucleoside-diphosphatekinase(ATP:dIDP)	Purine Metabolism	[c] : $atp + didp <==> adp + ditp$
R NDPK9	Chro.40275 or Chro.50237 or	2.7.4.6	nucleoside-diphosphatekinase(ATP:IDP)	Purine Metabolism	[c] : atp + idp <==> adp + itp
R NDPK8	Chro.40275 or Chro.50237 or	2.7.4.6	nucleoside-diphosphatekinase(ATP:dADP)	Purine Metabolism	[c] : atp + dadp <==> adp + datp
R NDPK7	Chro.40275 or Chro.50237 or Chro.40275 or Chro.50237 or	2.7.4.6	nucleoside-diphosphatekinase(ATP:dCDP)	Purine Metabolism	[c] : atp + dcdp <==> adp + dctp
R NDPK5	Chro.40275 or Chro.50237 or	2.7.4.6	nucleoside-diphosphatekinase(ATP:dGDP)	Purine Metabolism	[c]: atp + dqdp <==> adp + dqtp
R_NDPK4	Chro.40275 or Chro.50237 or	2.7.4.6	nucleoside-diphosphatekinase(ATP:dTDP)	Purine Metabolism	[c] : atp + dtdp <==> adp + dttp
R NDPK3	Chro.40275 or Chro.50237 or Chro.40275 or Chro.50237 or	2.7.4.6	nucleoside-diphosphatekinase(ATP:CDP)	Purine Metabolism	c : atp + cdp <==> adp + ctp
R NDPK1	Chro.40275 or Chro.50237 or Chro.40275 or Chro.50237 or	2.7.4.6	nucleoside-diphosphatekinase(ATP:GDP)	Purine Metabolism	[c]: atp + ddp <==> adp + dtp
R DGK1	Chro.70250	2.7.4.8	deoxyguanylatekinase(dGMP:ATP)	Purine Metabolism	[c] : atp + dgmp <==> adp + dgdp
R GK1	Chro.70250	2.7.4.8	guanylatekinase(GMP:ATP)	Purine Metabolism	[c]: atp + qmp <==> adp + qdp
R NTD10	Chro.50026	3.1.3.5	5'-nucleotidase(XMP)	Purine Metabolism	[c] : h2o + xmp> pi + xtsn
R NTD12	Chro.50026	3.1.3.5	5'-nucleotidase(dIMP)	Purine Metabolism	[c] : dimp + h2o> din + pi
R NTD9 R NTD8	Chro.50026	3.1.3.5	5'-nucleotidase(GMP)	Purine Metabolism	[c]: qmp + h2o> qsn + pi
R NTD1	Chro.50026	3.1.3.5	5'-nucleotidase(dUMP)	Purine Metabolism	[c]: dump + h2o> duri + pi
R_NTD3	Chro.50026	3.1.3.5	_5'-nucleotidase(dCMP)	Purine Metabolism	[c] : dcmp + h2o> dcyt + pi
R NTD2 R NTD5	Chro.50026	3.1.3.5	5'-nucleotidase(UMP) 5'-nucleotidase(dTMP)	Purine Metabolism	[c] : h2o + ump> pi + uri [c] : dtmp + h2o> pi + thymd
R NTD4	Chro.50026	3.1.3.5	5'-nucleotidase(CMP)	Purine Metabolism	[c]: cmp + h2o> cytd + pi
R NTD7	Chro.50026	3.1.3.5	5'-nucleotidase(AMP)	Purine Metabolism	[c] : amp + h2o> adn + pi
R NTD6	Chro.50026	3.1.3.5	5'-nucleotidase(dAMP)	Purine Metabolism	[c] : damp + h2o> dad-2 + pi
R PDE1	Chro.30269 or Chro.60462	3.1.4.17	3',5'-cyclic-nucleotidephosphodiesterase	Purine Metabolism	[c]: camp + h2o> amp + h
R PDE2	Chro.30269 or Chro.60462	3.1.4.17	3',5'-cyclic-nucleotidephosphodiesterase	Purine Metabolism	[c] : 35cdamp + h2o> damp + h
R PDE3	Chro.30269 or Chro.60462	3.1.4.17	3',5'-cyclic-nucleotidephosphodiesterase	Purine Metabolism	[c] : 35cmp + h2o> h + imp [c] : 35cmp + h2o> cmp + h
R PDE4	Chro.30269 or Chro.60462	3.1.4.17	3',5'-cyclic-nucleotidephosphodiesterase	Purine Metabolism	[c] : 35cqmp + h2o> qmp + h
R AMPDAm	Chro.40214	3.5.4.6	Adenosinemonophosphatedeaminase, mitochondrion	Purine Metabolism	[c] : amp + h + h2o> imp + nh4
K_AMPDAg R NTPP9	Chro 10434 or Chro 70577	3.5.4.6	Auenosinemonophosphatedeaminase,glycosome	Purine Metabolism	[c]: anp + n + nzo> mp + nh4 [c]: h2o + itn> h + imn + nni
R NTPP10	Chro.10434 or Chro.70577	3.6.1.19	Nucleosidetriphosphatepyrophosphorylase(ditp)	Purine Metabolism	[c] : ditp + h2o> dimp + h + ppi
R NTPP11	Chro.10434 or Chro.70577	3.6.1.19	Nucleosidetriphosphatepyrophosphorylase(xtp)	Purine Metabolism	[c] : h2o + xtp> h + ppi + xmp
R GTPH2e	Chro.60194 Chro.60194	3.6.1.5	GTPdiphosphohydrolase	Purine Metabolism	<u>rej : uup + n20> ump + n + pi</u> fe] : adp + h2o> amp + h + pi
R ATPH2e	Chro.60194	3.6.1.5	ATPdiphosphohydrolase	Purine Metabolism	[e] : adp + h2o> amp + h + pi
R UTPH1e	Chro.60194	3.6.1.5	UTPdiphosphohydrolase	Purine Metabolism	[e] : utp + 2 h2o> ump + 2 h + 2 pi
R ATPH1e	Chro.60194	3.6.1.5	ATPdiphosphohydrolase	Purine Metabolism Purine Metabolism	ie) : gtp + 2 h2o> gmp + 2 h + 2 pi
R NDP3ex	Chro.60194	3.6.1.6	nucleoside-diphosphatase(GDP),extracellular	Purine Metabolism	[e] : gdp + h2o> gmp + h + pi
R NDP10ex	Chro.60194	3.6.1.6	nucleoside-diphosphatase(IDP),extracellular	Purine Metabolism	[e] : h2o + idp> h + imp + pi [c] : dadp + h2o> damp + h + pi
R NDP6	Chro.60194	3.6.1.6	nucleoside-diphosphatase(dCDP)	Purine Metabolism	[c]: dcdp + h2o> dcmp + h + pi
R NDP3	Chro.60194	3.6.1.6	nucleoside-diphosphatase(GDP)	Purine Metabolism	[c] : gdp + h2o> gmp + h + pi
R NDP8 R NDP8ex	Chro.60194 Chro.60194	3.6.1.6	nucleoside-diphosphatase(dUDP) nucleoside-diphosphatase(UTP).extracellular	Purine Metabolism Purine Metabolism	[c] : dudp + h2o> dump + h + pi [e] : h2o + utp> h + pi + udp
R NDP3g	Chro.60194	3.6.1.6	nucleoside-diphosphatase(GDP),Golgi	Purine Metabolism	[c]: qdp + h2o> qmp + h + pi
R NDP7er	Chro.60194	3.6.1.6	nucleoside-diphosphatase(UDP),endoplasmicreticulum	Purine Metabolism	[c] : h2o + udp> h + pi + ump
R NDP7ex	Chro.60194 Chro.60194	3.6.1.6	nucleoside-diphosphatase(UDP),extracellular nucleoside-diphosphatase(UDP),Golgiapparatus	Purine Metabolism Purine Metabolism	(e) : n2o + udp> n + pi + ump (c) : h2o + udp> h + pi + ump
R ADSL2r		4.3.2.2	adenylosuccinatelyase	Purine Metabolism	[c] : 25aics <==> aicar + fum
R ADSL1r		4.3.2.2	adenylsuccinatelyase	Purine Metabolism	[c] : dcamp <==> amp + fum
R ADSL1r R ADSL2 R ADSL1		4.3.2.2 4.3.2.2 4.3.2.2	adenylsuccinatelyase adenylosuccinatelyase adenylosuccinatelyase	Purine Metabolism Purine Metabolism Purine Metabolism	[c] : dcamp <==> amp + fum [c] : 25aics> aicar + fum [c] : dcamp> amp + fum
R ADSL1r R ADSL2 R ADSL1 R_ADNCYC	Chro.50255 or Chro.40352	4.3.2.2 4.3.2.2 4.3.2.2 4.6.1.1	adenylsuccinatelyase adenylosuccinatelyase adenylauccinatelyase adenylatecyclase	Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism	[c] : dcamp <==> amp + fum [c] : 25aics> aicar + fum [c] : dcamp> amp + fum [c] : atp> camp + ppi
R ADSL1r R ADSL2 R ADSL1 R ADNCYC R GUACYC P GMPS	Chro.50255 or Chro.40352 Chro.50255 or Chro.30141 or	4.3.2.2 4.3.2.2 4.3.2.2 4.6.1.1 4.6.1.2 6.3.4 1	adenylsuccinatelyase adenylosuccinatelyase adenylosuccinatelyase adenylatecyclase guanylatecyclase GMecynbase	Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism	[c]: dcamp.<==> amp.+fum [c]: 25aics-> aicar+fum [c]: 25aics-> aicar+fum [c]: dcamp> amp.+fum [c]: aitp> camp.+ppi [c]: aitp> camp.+ppi [c]: aitp> aif(aitp> aitp>
R ADSL1r R ADSL2 R ADSL1 R ADNCYC R GUACYC R GMPS R RMPS R RNDR4	Chro.50255 or Chro.40352 Chro.50255 or Chro.30141 or Chro.60090 or Chro.60091	4.3.2.2 4.3.2.2 4.3.2.2 4.6.1.1 4.6.1.2 6.3.4.1 1.17.4.1	adenvisuccinatelyase adenvisuccinatelyase adenviatecyclase quanylatecyclase GMPsynthase Tibonucleoside-diphosphatereductase(UDP)	Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism	[c]: dcamp <=> amp + fum [c]: dcamp <-> amp + fum [c]: dcamp> amp + fum [c]: dcamp> amp + fum [c]: dcamp> amp + fum [c]: sto> 35camp + ppi [c]: sto +-> 35camp + ppi [c]: sto + nh4 + xmp> amp + gmp + 2 h + ppi [c]: tridf + udp> adup + h2o + tridox
R ADSL1r R ADSL2 R ADSL1 R ADNCYC R GMPS R RNDR4 R RNDR3		4.3.2.2 4.3.2.2 4.3.2.2 4.6.1.1 4.6.1.2 6.3.4.1 1.17.4.1 1.17.4.1	adenvisuccinatelyase adenvisuccinatelyase adenvisuccinatelyase adenviatecyclase guanylatecyclase GMPsynthase ribonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(CDP)	Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Pvrimildine Metabolism Pvrimildine Metabolism	$\begin{array}{l} (c): dcamp <=> amp + fum \\ (c): 25ai(cs -> ai(car + fum \\ c): dcamp -> amp + fum \\ (c): atom -> camp + ppi \\ (c): ato -> 35camp + ppi \\ (c): ato -> 35camp + ppi \\ (c): ato -> 35camp + ppi \\ (c): ato + nh4 + xmp -> amp + amp + 2 h + ppi \\ (c): trdrd + udp -> bio + trdox \\ (c): cdp + trdrd -> dcdp + h20 + trdox \\ (c): cdp + trdrd -> dcdp + h20 + trdox \\ \end{array}$
R ADSL1r R ADSL2 R ADSL1 R_ADNCYC R_GMPS R_RNDR4 R_RNDR3 R_RNDR1 R_RNDR2	Chro.50255 or Chro.40352 Chro.50255 or Chro.30141 or Chro.60090 or Chro.60091 Chro.60090 or Chro.60091 Chro.60090 or Chro.60091 Chro.60090 or Chro.60091	4.3.2.2 4.3.2.2 4.3.2.2 4.6.1.1 4.6.1.2 6.3.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1	adenyisuccinatelyase adenyiosuccinatelyase adenyiosuccinatelyase adenyiatecyclase guanyiatecyclase GMPsynthase ribonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(DPP) ribonucleoside-diphosphatereductase(ADP)	Purine Metabolism Purine Metabolism Purine Metabolism Purindium Metabolism Purindium Metabolism Purindium Metabolism	[c] : dcamp <==> amp + fum [c] : 25a(cs -> ac(car + fum [c] : 25a(cs -> ac(car + fum [c] : ato -> camp + ppi [c] : ato -> 35c(amp + rpi [c] : ato +> ath + xmp ->> amp + amp + 2 h + ppi [c] : cird + 1udp ->> dudp + h2a + trdox [c] : cird + 1udq ->> dudp + h2a + trdox [c] : cird + 1udq ->> dudp + h2a + trdox [c] : cird + 1udq ->> dudp + h2a + trdox
R ADSL1r R ADSL2 R ADSL1 R ADSL1 R ADSCYC R GUACYC R GMPS R RNDR4 R RNDR3 R RNDR1 R RNDR2 R TRDR	Chro.50255 or Chro.40352 Chro.50255 or Chro.40352 Chro.50255 or Chro.30141 or Chro.60090 or Chro.60091 Chro.60090 or Chro.60091 Chro.60090 or Chro.60091 Chro.60090 or Chro.6091	4.3.2.2 4.3.2.2 4.3.2.2 4.6.1.1 4.6.1.2 6.3.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.8.1.9	adenvisuccinatelvase adenvisuccinatelvase adenvisuccinatelvase ganylatecyclase GMFSynthase ribonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(DP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(SDP) hiboredosinreductase(NADPH)	Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Pyrimidine Metabolism Pyrimidine Metabolism Pyrimidine Metabolism Pyrimidine Metabolism	[c] : dcamp <==> amp + fum [c] : 25a(s ->> amp + fum [c] : 25a(s ->> amp + fum [c] : dcamp -> amp + fum [c] : atp -> -2 amp + ppi [c] : atp -> -35camp + ppi [c] : atp + nN4 + xmp -> amp + qmp + 2 h + ppi [c] : tridr + udp ->> dudp + h20 + tridox [c] : dcp + tridr -> dcdp + h20 + tridox [c] : adp + tridr ->> dcdp + h20 + tridox [c] : adp + tridr ->> dqdp + h20 + tridox [c] : h + nadph + tridox ->> [c] : h + radph + tridox ->> [c] : h + radph + tridox ->> [c] : h + radph + tridox ->>
R ADSL1r R ADSL2 R ADSL1 R ADSL1 R GUACYC R GUACYC R RNDR3 R RNDR3 R RNDR3 R TRDR R TRDR R TRDR R TRDR R TRDR2	Chro.50255 or Chro.40352 Chro.50255 or Chro.40352 Chro.50255 or Chro.30141 or Chro.60090 or Chro.60091 Chro.60090 or Chro.60091 Chro.60090 or Chro.60091 Chro.20464 Chro.20464	4.3.2.2 4.3.2.2 4.6.1.1 4.6.1.2 6.3.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.8.1.9 1.8.1.9	adenylsuccinatelyase adenylosuccinatelyase adenylatecyclase GMPsynthase ribonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(DP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) Thioredoxin(ubiquinone10)reductase(NADPH) Thioredoxin(ubiquinone10)reductase(NADPH)	Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Pyrimidine Metabolism Pyrimidine Metabolism Pyrimidine Metabolism Pyrimidine Metabolism Pyrimidine Metabolism Pyrimidine Metabolism	[c] : dcamp <=> amp + fum [c] : dcamp <=> amp + fum [c] : dcamp> amp + qmp + 2 h + ppi [c] : tridr + udp> adug + h20 + tridox [c] : dca + tridr> adug + h20 + tridox [c] : ado + tridr> adug + h20 + tridox [c] : ado + tridr> adug + h20 + tridox [c] : h + nadgh + tridox> adug + tridrd [c] : h + nadgh + tridox> adug + q10h2
R ADSL1r R ADSL2 R ADSL2 R ADNCYC R GUACYC R GVACYC R RNDR3 R RNDR3 R RNDR3 R RNDR1 R RNDR2 R TRDR R TRDR2 R TRDR2 R TRDR3 R TNDS	Chro.50255 or Chro.40352 Chro.50255 or Chro.30141 or Chro.60090 or Chro.60091 Chro.60090 or Chro.60091 Chro.60090 or Chro.60091 Chro.60090 or Chro.60091 Chro.20464 Chro.20464 Chro.20464 Chro.20464	43.2.2 43.2.2 43.2.2 4.6.1.1 4.6.1.2 6.3.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.8.1.9 1.8.1.9 1.8.1.9 2.1.1.45	adenvisuccinatelyase adenviosuccinatelyase adenviosuccinatelyase adenviosuccinatelyase adenviosuccinatelyase GMPsynthase Tibonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(CDP) ribonucleoside-diphosphatereductase(DP) ribonucleoside-diphosphatereductase(DP) ribonucleoside-diphosphatereductase(DP) ribonucleoside-diphosphatereductase(SDP) ribonucleoside-diphosphatereductase(SDP) ribonucleoside-diphosphatereductase(NADPH) Thioredoxin(ubiquinone10)reductase(NADH) Thioredoxin(ubiquinone10)reductase(NADH)	Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purinel Metabolism Purindine Metabolism Purindine Metabolism Purindine Metabolism Purindine Metabolism Purindine Metabolism Purindine Metabolism Purindine Metabolism Purindine Metabolism	$ \begin{array}{l} (c): dcamp <=> amp + fum \\ (c): 25a(s ->> aicar + fum \\ (c): 25a(s ->> aicar + fum \\ (c): c): 25a(s ->> aicar + fum \\ (c): (c): 25a(s ->> aicar + fum \\ (c): (c): (c): conterve + fum \\ (c): (c): (c): (c): (c): (c): (c): (c):$
R ADSL1r R ADSL2 R ADSL2 R ADNCYC R GMACYC R GMPS R RNDR4 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R RNDR2 R TRDR2 R TRDR2 R TRDR2 R TRDR3 R TRDR3 R TRDR3 R TRDSf		4.3.2.2 4.3.2.2 4.3.2.2 4.6.1.1 4.6.1.2 6.3.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.8.1.9 1.8.1.9 1.8.1.9 1.8.1.9 2.1.1.45	adenvisuccinatelvase adenvisuccinatelvase adenvisuccinatelvase adenvisuccinatelvase guanvlatecyclase (DMP3vnthase) ribonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) thoredoxinuclouranoe10/reductase(NADH) thymidylatesynthase(Favin-dependent)	Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purinidine Metabolism Purindine Metabolism Purindine Metabolism Purindine Metabolism Purindine Metabolism Purindine Metabolism Purindine Metabolism Purindine Metabolism Purindine Metabolism	[c] : dcamp <=> amp + fum [c] : dcamp - samp + fum [c] : Zasica - samp + fum [c] : dcamp samp + fum [c] : tarb Sacamp + ppi [c] : tarb - + Sacamp + ppi [c] : tarb + nhd + xmm> amp + gmp + 2 h + ppi [c] : tarb + nhd + xmm> amp + tarbax [c] : tarb + tarbd> addp + h2a + trdax [c] : adb + tardd> dadp + h2a + trdax [c] : adb + tardd> dadp + h2a + trdax [c] : adb + tardd> dadp + h2a + trdax [c] : h + nadph + adb - + 2ndb + tarbax [c] : h + nadph + adb> nadb + tarbax [c] : h + nadph + adb> nadb + tarbax [c] : h + nadph + adb> nadb + adbh2 [c] : dum p + mthf -> dthf + dtmp [c] : dum p + mthf -> dtm p + fmn + thf
R ADSL1r R ADSL2 R ADSL2 R ADNCYC R GMPS R RMDR4 R RMDR4 R RNDR4 R RNDR4 R RNDR3 R TRDR R TRDR R TRDR2 R TRDR3 R TRDR3 R TMDSf R TMDSf R TMDSf R TMDSf R TMDSf R TMDSf	Chro.50255 or Chro.40352 Chro.50255 or Chro.40352 Chro.50255 or Chro.30141 or Chro.60090 or Chro.60091 Chro.60090 or Chro.60091 Chro.60090 or Chro.60091 Chro.20464 Chro.20464 Chro.20464 Chro.20464 Chro.40506 or Chro.30116 Chro.40506 or Chro.30116 Chro.3016	4.3.2.2 4.3.2.2 4.3.2.2 4.6.1.1 4.6.1.2 6.3.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.8.1.9 1.8.1.9 2.1.1.45 2.1.1.45 2.4.2.9 2.7.1.21	adenyisuccinatelyase adenyiosuccinatelyase adenyiosuccinatelyase adenyiotecyclase GMPSynthase Tibonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(CDP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(SDP) thioredoxin(ubiquinone10)reductase(NADPH) Thioredoxin(ubiquinone10)reductase(NADPH) thymidylatesynthase(Taiwin-dependent) uracilphosphonibosyltransferase(r) uracilphosphonibosyltransferase(r)	Purine Metabolism Purinel Metabolism Purindine M	[c] : dcamp <=> amp + fum [c] : dcamp -> amp + fum [c] : 25a(s-> > amp + fum [c] : dcamp -> amp + fum [c] : atp ->> 35cqmp + ppi [c] : atp ->> 35cqmp + ppi [c] : tot +> 35cqmp + npi [c] : tot +> adp ->> dudp + n20 + trdox [c] : tot += udp ->> dudp + n20 + trdox [c] : dop + trdd ->> dedp + h20 + trdox [c] : dop + trdd ->> dedp + h20 + trdox [c] : dop + trdd ->> dedp + h20 + trdox [c] : dop + trdd ->> dedp + h20 + trdox [c] : h + nadph + td0 -> nadp + trdd [c] : h + nadph + td0 ->> nadp + td10h2 [c] : dump + mthf ->> dhf + dtmp [c] : dump + mthf ->> dhf + dtmp [c] : dump + mthf ->> dhf + dtmp + fm + thf [c] : np + udx <=>> ppi + ump
R ADSL1r R ADSL2 R ADSL2 R ADNCYC R GUACYC R GMP5 R RNDR4 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R TRDR R TRDR2 R TRDR2 R TRDR2 R TRDR2 R TRDR3 R TND5 R TMD5 R TM		4.3.2.2 4.3.2.2 4.3.2.2 4.6.1.2 6.3.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.17.4.1 1.8.1.9 1.8.1.9 1.8.1.9 2.1.1.45 2.1.1.45 2.4.2.9 2.7.1.21 2.7.1.21	adenylsuccinatelyase adenylosuccinatelyase adenylosuccinatelyase adenylatecyclase GMPsynthase Tibonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) Thioredoxin(ubiquinone10)reductase(NADPH) Thioredoxin(ubiquinone10)reductase(NADPH) Thioredoxin(ubiquinone10)reductase(NADPH) thymidylatesynthase thymidylatesynthase thymidylatesynthase(Flavin-dependent) uraciphosphotbosyltransferase(r) thymidylate(STP:Uthymidine)	Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Pyrimidine Metabolism	[c] : dcamp <=> amp + fum [c] : dcamp <=> amp + fum [c] : 25a(s->> aica + fum [c] : 2ba(s->> aica + fum [c] : dcamp -> aimp + fum [c] : dta ->> 35camp + ppi [c] : dta +> 35camp + ppi [c] : tridt + udp ->> alug + h20 + tridox [c] : dta + tridd ->> dcdp + h20 + tridox [c] : dap + tridd ->> dcdp + h20 + tridox [c] : dap + tridd ->> ddp + h20 + tridox [c] : dap + tridd ->> ddp + h20 + tridox [c] : dap + tridd ->> ddp + h20 + tridox [c] : dap + tridd ->> adp + h20 + tridox [c] : h + nadghh + td10 ->> nadp + td10h2 [c] : h + nadgh + td10 ->> nadp + td10h2 [c] : dump + mihtf ->> dth + dtmp [c] : dump + mihtf ->> dth + dtmp [c] : stpp + ura <==> ppi + ump [c] : stp + tura <=>> adp + ttmp + hn [c] : stp + tura ->> adp + ttmp
R ADSL1r R ADSL2 R ADSL2 R ADNCYC R GMPS R RNDR4 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R RNDR4 R RNDR3 R RNDR3 R RNDR4 R TRDR3 R TRDR2 R TRDR2 R TRDR5 R TMDSf R TMDSf R TMDSf R TMDSf R UPPFTF R TMDK1 R UPRIX2 R UPRIX2 R UPRIX2		$\begin{array}{r} 4.3.2.2 \\ 4.3.2.2 \\ 4.3.2.2 \\ 4.3.2.2 \\ 4.5.1.1 \\ 4.5.1.2 \\ 6.3.4.1 \\ 1.17.4.1 \\ 1.17.4.1 \\ 1.17.4.1 \\ 1.17.4.1 \\ 1.17.4.1 \\ 1.17.4.1 \\ 1.18.1.9 \\ 1.1.145 \\ 2.1.1.45 \\ 2.1.1.45 \\ 2.7.1.48 \\ 2.7.1.48 \\ 2.7.1.48 \\ 2.7.1.48 \\ 2.7.1.48 \end{array}$	adenyisuccinatelyase adenyiosuccinatelyase adenyiosuccinatelyase adenyiatecyclase guanyiatecyclase (MPSynthase ribonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(CDP) ribonucleoside-diphosphatereductase(CDP) thioredoxin(ubiquinone10)reductase(NADPH) Thioredoxin(ubiquinone10)reductase(NADPH) Thioredoxin(ubiquinone10)reductase(NADPH) thymidyiatesynthase (flavin-dependent) turadiphosphorbose(flavin-dependent) turadiphosphorbose(flavin-dependent) turadiphosphorbose(flavin-dependent) turadiphosphorbose(flavin-dependent) urdinekinase(ATP:thymidine)	Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purine Metabolism Purindine Metabolism	[c] (i diamp <==> amp + fum [c] (i diamp -<=> amp + fum [c] 25a(cs -> alcar + fum [c] (i diamp> amp + fum [c] (i diamp> amp + fum [c] (i diamp> amp + mp] + 2mp + 2 h + pp] [c] (i diamp> add + sump> amp + amp + 2 h + pp] [c] (i diamp> add + h2a + trdox [c] (i diamp + trdd> add + h2a + trdox [c] (i diamp + trdd> add + h2a + trdox [c] (i diamp + trdd> add + h2a + trdox [c] (i h + add h + trdd> add + h2a + trdox [c] (i h + add h + trdd> add + trdox [c] (i diamp + trdd> add + trdox [c] (i h + add h + trdd> add + trdox [c] (i diamp + trdd> add + trdomp + fun [c] (i diamp + trdm> add + h + ump [c] (i add + un -> add + h + ump [c] (i add + un -> add + h + ump [c] (i add + un -> add + h + ump
R ADSL1r R ADSL2 R ADSL2 R ADNCYC R GMPS R RNDR4 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R TRDR2 R TRDR2 R TRDR3 R TRDR3 R TRDR3 R TRDR3 R TMDSf R UMPK5		$\begin{array}{r} 4.3.2.2\\ 4.3.2.2\\ 4.3.2.2\\ 4.5.1.2\\ 4.6.1.2\\ 6.3.4.1\\ 1.17.4.1\\ 1.17.4.1\\ 1.17.4.1\\ 1.17.4.1\\ 1.17.4.1\\ 1.17.4.1\\ 1.17.4.1\\ 1.17.4.1\\ 1.1.1.4.1.9\\ 1.1.1.4.1.9\\ 1.1.1.4.5\\ 2.1.1.4.5\\ 2.1.1.4.5\\ 2.7.1.21\\ 2.7.1.4.8\\ 2.7.4.14\\ 2.7.4.14\\ 2.7.4.14\end{array}$	adenvisuccinatelvase adenvisuccinatelvase adenvisuccinatelvase adenvisuccinatelvase GMPsynthase ribonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(CDP) ribonucleoside-diphosphatereductase(CDP) ribonucleoside-diphosphatereductase(CDP) ribonucleoside-diphosphatereductase(CDP) ribonucleoside-diphosphatereductase(CDP) ribonucleoside-diphosphatereductase(CDP) ribonucleoside-diphosphatereductase(CDP) ribonucleoside-diphosphatereductase(CDP) ribonucleoside-diphosphatereductase(CDP) ribonucleoside-diphosphatereductase(CDP) thioredoxin(ubiquinone 10)reductase(NADH) thymidiylatexynthase(Ravin-dependent) uracilphosphoribosyttransferase(r) thymidinekinase(ATP:Uridine) urdinekinase(ATP:Uridine) vctidylatekinase(dTP)	Purine Metabolism Purindine	[c] : dcamp <=> amp + fum [c] : dcamp -<=> amp + fum [c] : dcamp> amp + fum [c] : dcamp> amp + fum [c] : dcp> acc amp + ppi [c] : atp +-> acc amp + ppi [c] : atp + nh4 + xmp> amp + qmp + 2 h + ppi [c] : atp + nh4> acdp + h2o + trdox [c] : adp + trdd> acdp + h2o + trdox [c] : adp + trdd> adp + h2o + trdox [c] : adp + trdd> adp + h2o + trdox [c] : adp + trdd> adp + h2o + trdox [c] : adp + trdd> adp + h2o + trdox [c] : adp + trdd> adp + h2o + trdox [c] : h + nadph + td0> nadp + tldh2 [c] : h + nadph + td0> nadp + tldh2 [c] : h + nadph + td0> nadp + tldh2 [c] : dump + mhf> dmp + fum + thf [c] : dump + mhf> dhf + dtmp [c] : atp + trdm> adp + h + mp [c] : atp + trdm> adp + h + mp [c] : atp + trdm> adp + h + mp [c] : atp + trdm> adp + h + mp [c] : atp + trdm -=> adp + dcdp [c] : datp = tmp <=> adp + dcdp
R ADSL17 R ADSL2 R ADSL2 R ADNCYC R GMPS R RNDR4 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R TRDR R TRDR R TRDR R TRDR5 R TMDS5 R TMD55 R		$\begin{array}{r} 4.3.2.2\\ 4.3.2.2\\ 4.3.2.2\\ 4.5.1.2\\ 4.6.1.2\\ 6.3.4.1\\ 1.17.4.1\\ 1.17.4.1\\ 1.17.4.1\\ 1.17.4.1\\ 1.17.4.1\\ 1.17.4.1\\ 1.17.4.1\\ 1.8.1.9\\ 1.8.1.9\\ 1.8.1.9\\ 1.8.1.9\\ 2.1.1.45\\ 2.1.1.45\\ 2.4.2.9\\ 2.7.1.48\\ 2.7.1.48\\ 2.7.1.48\\ 2.7.4.14\\ 2.7.4.14\\ 2.7.4.14\\ 2.7.4.14\end{array}$	adenyisuccinatelyase adenyiosuccinatelyase adenyiosuccinatelyase adenyiosuccinatelyase gamylatecyclase GMPSynthase Tibonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) Thioredoxin(ubiquinone10)reductase(NADPH) Thioredoxin(ubiquinone10)reductase(NADPH) thymidylatesynthase(Taivin-dependent) uracilphosphonibosyltransferase(r) thymidinekinase(ATP:Urumiline) urdinekinase(ATP:Urumiline) urdinekinase(ATP:Urumiline) urdinekinase(ATP) UMPKinase(ATP) UMPKinase(ATP) UMPKinase(CMP) UMPKinase(C	Purine Metabolism Purineline Metabolism Purindine M	[c] : dcamp <=> amp + fum [c] : dcamp -> amp + fum [c] : 25a(s-> ack + fum [c] : dcamp -> admp + fum [c] : atp -> 35cqmp + ppi [c] : atp -> 35cqmp + ppi [c] : atp +> 35cqmp + ppi [c] : atp + ndq -> 3 dcdp + h20 + trdox [c] : dcd + trdd -> dcdp + h20 + trdox [c] : dcd + trdd -> dcdp + h20 + trdox [c] : dcd + trdd -> dcdp + h20 + trdox [c] : dcd + trdd -> dddp + h20 + trdox [c] : dcd + trdd -> dddp + h20 + trdox [c] : dcd + trdd -> dddp + h20 + trdox [c] : dcd + trdd -> dddp + h20 + trdox [c] : dcd + trdd -> dddp + h20 + trdox [c] : h + nadbh + ttd0 -> nadp + trdd [c] : h + nadbh + ttd0 -> nadp + trdd [c] : h + nadbh + ttd0 -> nadp + trdnd [c] : dum + mthf -> dhf + dtmp [c] : dum + nthf -> dhf + dtmp + fm [c] : atp + trdm -> adp + thmp + fm [c] : atp + trdm -> adp + h + ump [c] : atp + um -> adp + h + ump [c] : atp + um <=> adp + h + ump [c] : atp + um <=> addp + dcdp [c] : cmp + dc <=>> addp + dcdp
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R ADSL17 R ADSL2 R ADSL2 R ADNCYC R GMPS R GMPS R RNDR4 R RNDR3 R TNDS R TNDS R TMDSf R TMDSf R TMDSf R TMDSf R UPRTr R UPRTr R UPRTS R CYTK9 R CYTK9 R CYTK9 R CYTK9 R CYTK9 R CYTK9 R CYTK6 R CYT		$\begin{array}{c} 4.3.2.2\\ 4.3.2.2.2\\ 4.3$	adenvisuccinatelvase adenvisuccinatelvase adenvisuccinatelvase adenvisuccinatelvase guanylatecyclase guanylatecyclase guanylatecyclase guanylatecyclase guanylatecyclase inbonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) ribonucleoside-diphosphatereductase(ADP) thioredoxin(ubiquinone10)reductase(NDPH) thioredoxin(ubiquinone10)reductase(NDPH) thymidiylatesynthase(Faluri-dependent) uracliphosphoribosyltransferase(r) thymidinekinase(ATP:Undine) vctidylatekinase(CMP)	Purine Metabolism Purineline Metabolism Purindine M	[c] : dcamp <=> amp + fum [c] : dcamp -> amp + fum [c] : dcamp -> amp + fum [c] : dcamp -> amp + fum [c] : dtp ->> 3dcamp + ppi [c] : dtp +> 35camp + ppi [c] : dtp + m4 + xmp -> amp + qmp + 2 h + ppi [c] : dtp + m4 + xmp -> amp + qmp + 2 h + ppi [c] : dtp + trdd ->> dcdp + h2o + trdox [c] : ddp + trdd ->> dcdp + h2o + trdox [c] : ddp + trdd ->> dddp + h2o + trdox [c] : ddp + trdd ->> dddp + h2o + trdox [c] : ddp + trdd ->> dddp + h2o + trdox [c] : ddp + trdd ->> dddp + h2o + trdox [c] : dh + nadhh + trd0 ->> nadp + trdrd [c] : h + nadhh + trd0 ->> nadp + trdrd [c] : h + nadh + trd0 ->> nadp + trdrd [c] : h + nadh + trd0 ->> nadp + trdrd [c] : dtp + trdm ->> dhf + dtmp [c] : dtp + trdm ->> dhf + dtmp [c] : dtp + trdm ->> adp + trdm + thf [c] : atb + trdm ->> adp + trdm + h [c] : atb + trdm ->> adp + th - trdm [c] : atb + trdm ->> adp + th - trdm [c] : atb + trdm ->> adp + dtmp + h [c] : atb + trdm >=> adp + dcdp [c] : dtp + dtmp <==>> ddp + ddp [c] : cmp + dtp <==> cdp + ddp [c] : cmp + dtp <==> cdp + dcdp [c] : cmp + dtp <==> cdp + dcdp [c] : cmp + dtp <==> cdp + dcdp [c] : cmp + dtp <==> 2dp + dcdp [c] : cmp + dtp <==> 2dp + dcdp
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R. ADSL17 R. ADSL2 R. ADSL2 R. ADSL2 R. ADNCYC R. GMP5 R. RNDR4 R. SNDR4 R. SNDR4 R. SNDR3 R. SN		$\begin{array}{r} 4.3.2.2\\ 4.3.2$	adenyisuccinatelyase adenyisuccinatelyase adenyiosuccinatelyase adenyiosuccinatelyase (MPSynthase ribonuclosside-diphosphatereductase(UDP) ribonuclosside-diphosphatereductase(DDP) ribonuclosside-diphosphatereductase(CDP) ribonuclosside-diphosphatereductase(CDP) ribonuclosside-diphosphatereductase(CDP) ribonuclosside-diphosphatereductase(CDP) ribonuclosside-diphosphatereductase(CDP) ribonuclosside-diphosphatereductase(NADPH) Thioredoxin(ubicatione10)reductase(NADPH) thymidivitases(Tase(NADPH) thymidivitases(Tase(NADPH) uracilphosphoribosytransferase(r) thymidivitases(ATP:Uridine) urdinekinase(ATP:Uridine) urdinekinase(ATP:Uridine) urdinekinase(ATP:Uridine) vrtidylatekinase(CMP) vrti	Purine Metabolism	[c] : dcamp <=> amp + fum [c] : dcamp -> amp + mp] [c] : tab >> 35cmm + pp] [c] : tab + trid + xmm -> amp + amp + 2 h + pp] [c] : tab + trid + xmm -> amp + amp + 2 h + pp] [c] : tab + trid -> addp + h2a + tridax [c] : adp + tridd -> addp + h2a + tridax [c] : adp + tridd -> addp + h2a + tridax [c] : adp + tridd -> addp + h2a + tridax [c] : adp + tridd -> addp + h2a + tridax [c] : h + radph + q10 -> andp + tridd [c] : h + radph + q10 -> andp + tridd [c] : h + radph + q10 -> andp + tridd [c] : h + radph + q10 -> andp + tridd [c] : h + radph + q10 -> andp + tridd [c] : tab + tridd -> dhf + dtmp [c] : adp + tridd -> adp + tridm + thf [c] : tab + tridd -> adp + tridm + thf [c] : tab + tridd -> adp + tridm + thf [c] : tab + tridd -> adp + tridm + thf [c] : tab + tridm -> adp + tridm + thf [c] : tab + tridm -> adp + tridm + thf [c] : tab + tridm -> adp + tridm + thf [c] : tab + tridm -> adp + th ump [c] : tab + tridm -> adp + th ump [c] : tab + tridm -> adp + th ump [c] : tab + tridm -> adp + th ump [c] : tab + tridm ->= adp + dcdp [c] : tab + tridm ->= adp + dcdp [c] : cmp + dtb <==> 2 dch + ddp [c] : cmp + dtb <==> 2 dch + ddp [c] : cmp + dtb <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump <==> 2 dch + udp [c] : dtb + ump
R ADSL1F R ADSL1 R ADSL2 R ADSL2 R ADSL2 R ADNCYC R GUACYC R GUACYC R GUACYC R GUACYC R GNDS R RNDR4 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R RNDR3 R RNDR4 R TRDR2 R TRDR2 R TRDR2 R TRDR2 R TRDR2 R TRDR2 R TRDR3 R TRDR3 R TRDR3 R TRDR4 R TRDR4 R TRDR5 R TTDF5 R CYTK2 R UMPK3 R UMPK4 R UMPK4 R OTTK10 R CYTK10 R CYTK10 R CYTK12 R OTTK10 R CYTK13 R CYTK13 R CYTK14 R UMPK4 R DUMPK4 R DUMPK4 R DUMPK4 R DUMPK5 R AP4AH1 R DUMPK5 R AP4AH1 R UDTPOP R AP4AH1 R UDTPOP R AP4AH1 R UDTPOP R AP4AH1 R UDTPOP R AP4AH1 R DUMPS R AP4AH1 R DUMPS R AP4AH1 R MDH12 R MDH3 R ACALD R ACS2 M ACS2 C TS2 R ACS2 R ACS		$\begin{array}{r} 4.3.2.2\\ 4.3.2\\ 4.3$	adenyisuccinatelyase adenyisuccinatelyase adenyisuccinatelyase adenyiatecyclase Guanyiatecyclase GuBSynthase ribonucleoside-diphosphatereductase(UDP) ribonucleoside-diphosphatereductase(DP) ribonucleoside-diphosphatereductase(DP) ribonucleoside-diphosphatereductase(DP) thioredoxin(ubiquinone10)reductase(NADPH) Thioredoxin(ubiquinone10)reductase(NADPH) Thioredoxin(ubiquinone10)reductase(NADPH) thymidylatesynthase thymidylatesynthase(Favin-dependent) uracilphosphorbosyltransferse(r) thymidylatesynthase thymidylatesynthase(GP) urdinekinase(GPF:Urdine) urdinekinase(GPF:Urdine) urdinekinase(GPF:Urdine) urdinekinase(GPF:Urdine) urdinekinase(CPF) urdinekinase(CPF) urdinekinase(CPF) urdinekinase(CPF) urdinekinase(CPF) urdinekinase(CPF) urdidylatekinase(CPP) urdidylatekinase(CPP) urdidylatekinase(CPP) uthykinase(CPP) uthykinase(CPP) uthykinase(CPP) uthykinase(CPP) uthykinase(CPP) uthykinase(CPP) uthykinase(CPP) uthykinase(CPP) uthykinase(CPP) uthykinase dUMPkinase dUMPkinase dUMPkinase dUMPkinase dUMPkinase dUMPkinase dUMPkinase dUMPkinase dUMPkinase dUMPkinase dUMPkinase dUMPkinase a-Mercaptolactate:NAD-toxidoreductase xatabelydrogenase (uspinopshatase xithyinase(MADP) malitecnyme(NADP) malitecnyme	Purine Metabolism Purindine	[c] : damp <=> amp + fum [c] : damp - s amp + fum [c] : damp - s amp + fum [c] : damp - s amp + fum [c] : damp - damp + ppi [c] : damp + damp + amp + 2 h + ppi [c] : damp + damp - s amp + amp + 2 h + ppi [c] : damp + damp - s amp + amp + 2 h + ppi [c] : damp + damp - s amp + amp + 2 h + ppi [c] : damp + damp - s amp + amp + 2 h + ppi [c] : damp + damp - s admp + h2 a + trdox [c] : damp + damp - s admp + h2 a + trdox [c] : damp + damp - s admp + h2 a + trdox [c] : h + addh + td0 - s - nada + al0h2 [c] : h + nadh + td0 - s - nada + al0h2 [c] : damp + damp - s admp + damp + fam + thf [c] : damp - famh2 - s admp + damp + fam + thf [c] : damp - famh2 - s admp + damp + fam [c] : damp - famh2 - s admp + damp + fam [c] : damp - tamp - s admp + damp + fam [c] : damp + damp - s admp + damp + fam [c] : damp + damp - s admp + damp [c] : adm + damp <=> admp + damp [c] : admp + damp <==> admp + damp [c] : damp + damp <==> admp + damp [c] : admp + damp



R_RDH3a	Chro.40258	1.1.1.105	retinoldehydrogenase(11-cis,NADPH)	Retinol-Vit A Metabolism	[c] : nadp + retinol-cis_DASH_11 <==> h + nadph + retinal-11_DASH_cis
R RDH1a	Chro.40258	1.1.1.105	retinoldehydrogenase(all-trans,NADPH)	Retinol-Vit A Metabolism	[c] : nadp + retinol <==> h + nadph + retinal
R RDH2a	Chro.40258	1.1.1.105	retinoldehydrogenase(9-cis,NADPH)	Retinol-Vit A Metabolism	[c] : nadp + retinol-9 DASH cis <==> h + nadph + retinal-cis DASH 9
R RDH1	Chro.40258	1.1.1.105	retinoldehydrogenase(all-trans)	Retinol-Vit A Metabolism	[c] : nad + retinol <==> h + nadh + retinal
R RDH3	Chro.40258	1.1.1.105	retinoldehydrogenase(11-cis,NADH)	Retinol-Vit A Metabolism	[c] : nad + retinol-cis DASH 11 <==> h + nadh + retinal-11 DASH cis
R RDH2	Chro.40258	1.1.1.105	retinoldehydrogenase(9-cis,NADH)	Retinol-Vit A Metabolism	[c]: nad + retinol-9 DASH cis <==> h + nadh + retinal-cis DASH 9
R RDH4	Chro.40258	1.1.1.105	retinoldehydrogenase(13-cis,NADH)	Retinol-Vit A Metabolism	[c] : nad + retinol-cis DASH 13 <==> h + nadh + retinal-cis DASH 13
R RBFSb	Chro.80106	2.5.1.9	riboflavinsynthase	Riboflavin Metabolism-Vit B2	[c] : 2 dmlz> 4r5au + ribflv
R RBFSa	Chro.80106	2.5.1.9	riboflavinsynthase	Riboflavin Metabolism-Vit B3	[c]: 4r5au + db4p> dmlz + 2 h2o + pi
R ACP1 LPAREN FM	Chro.20071 or Chro.80016 or	3.1.3.2	acidphosphatase(FMN)	Riboflavin Metabolism-Vit B4	[c] : fmn + h2o> pi + ribflv
R SULR	Chro.40087	1.8.2.2	sulfitereductase(NADPH2)	Selenoamino acid metabolism	[c]: 3 h2o + h2s + 3 nadp <==> 5 h + 3 nadph + so3
R SEAHCYSHYD	Chro.30017	3.3.1.1	Se-Adenosylselenohomocysteinehydrolase	Selenoamino acid metabolism	[c]: h2o + seahcys> adn + selhcys
R SIAASE		3.2.1.18	sialidase	Sphingoglycolipid Metabolism	[c]: 2 h2o + s2l2n2m2mn> 2 acnam + l2n2m2mn
R UDPGDr	Chro.80111	1.1.1.22	UDPglucose6-dehydrogenase	Starch and Sucrose Metabolism	[c]: h2o + 2 nad + udpg <==> 3 h + 2 nadh + udpglcur
R GLCP	Chro.60284	2.4.1.1	glycogenphosphorylase	Starch and Sucrose Metabolism	[c] : alvcoaen + pi> a1p
R GLPASE2	Chro.60284	2.4.1.1	glycogenphosphorylase(amyls->glc-D)	Starch and Sucrose Metabolism	[c] : alvan3 + 7 h2o> Tvr-aan + 7 alc-D
R GLPASE1	Chro.60284	2.4.1.1	alvcogenphosphorvlase(glvgn2->dxtrn)	Starch and Sucrose Metabolism	[c] : glygn2 + 3 pi> dxtrn + 3 g1p
R TRE6PS	Chro.80565	2.4.1.15	alpha,alpha-trehalose-phosphatesynthase(UDP-forming)	Starch and Sucrose Metabolism	[c] : g6p + udpg> h + tre6p + udp
R GBEZ	Chro.60381	2.4.1.18	1.4-alpha-glucanbranchingenzyme	Starch and Sucrose Metabolism	[c] : 14glun> glycogen + h2g
R GLBRAN	Chro.60381	2.4.1.18	1,4-alpha-glucanbranchingenzyme(glygn1->glygn2)	Starch and Sucrose Metabolism	[c] : alvan1> alvan2
R AMALT1	Chro.60114	2.4.1.25	Amvlomaltase(maltotriose)	Starch and Sucrose Metabolism	[c] : mait + maittr> glc-D + maitttr
R AMALT2	Chro.60114	2.4.1.25	Amylomaltase(maltotetraose)	Starch and Sucrose Metabolism	[c] : malt + maitttr> glc-D + maitpt
R AMALT3	Chro.60114	2.4.1.25	Amylomaltase(maltopentaose)	Starch and Sucrose Metabolism	[c] : malt + maltpt> glc-D + malthx
R AMALT4	Chro.60114	2.4.1.25	Amylomaltase(maltohexaose)	Starch and Sucrose Metabolism	[c] : malt + malthx> glc-D + malthp
R AMY2e	Chro.80574 or Chro.50082 or	3.2.1.1	alpha-amylase, extracellular(glygn2->glygn4)	Starch and Sucrose Metabolism	[e] : qlyqn2 + 8 h2o> 8 qlc-D + qlyqn4
R AMY1e	Chro.80574 or Chro.50082 or	3.2.1.1	alpha-amylase.extracellular(strch1->strch2)	Starch and Sucrose Metabolism	[e] : 8 h2o + strch1> 8 glc-D + strch2
R GLCGSD	Chro 80574 or Chro 70613 or	3213	ducan1 4-alpha-ducosidase	Starch and Sucrose Metabolism	[c] : alvcogen + b2o> alc-D
R GLOBBAN	Chro 60114	3 2 1 33	alvcogendebranchingenzyme	Starch and Sucrose Metabolism	[c]: dytrn + h2o> a c-D + a van3
R PGI3	Chro 20336	5319	alucose-6-nhosphateisomerase	Starch and Sucrose Metabolism	[c] : g6p-4 <==> f6p
R PGI2	Chro 20336	5319	alucose-6-phosphateisomerase	Starch and Sucrose Metabolism	[c] : g6p-A <==> g6p-B
R PGI1	Chro 20336	5319	alucose-6-phosphateisomerase	Starch and Sucrose Metabolism	[c] : g6p-B <==> f6p
R DXPRI	0110120350	1 1 1 267	1-deoxy-D-xylulosereductoisomerase	Sterol Biosynthesis	[c]: dxy[5n + h + nadnh> 2me4n + nadn
R IPDDI	•	5332	isonentenvl-dinbosnbateD-isomerase	Sterol Biosynthesis	[c] : indn <==> dmnn
R DMATT	Chro 40285	2511	dimethylallyltranstransferase	Ternenoid Biosynthesis	[c] : dmpn + indn> ardn + nni
R GRTT	Chro 40285	2 5 1 10	geranyltranstransferase	Terpenoid Biosynthesis	[c] : $ardp + ipdp> frdp + ppi$
R SOLS	Chro. 10227	2.5.1.21	Squalenesynthase	Terpenoid Biosynthesis	$[c]: 2 \operatorname{frdp} + h + n \operatorname{adph} -> n \operatorname{adp} + 2 \operatorname{pni} + \operatorname{sol}$
R H2Ot			H2Otransportviadiffusion	Transport, Extracellular	$h2o[e] \leq => h2o[c]$
R CYSt2r				Transport, Extracellular	cvs-l[e] + h[e] <==> cvs-l[c] + h[c]
R MFTt2r				Transport, Extracellular	h[e] + met-l[e] <==> h[c] + met-l[c]
R GINt2r				Transport Extracellular	a[n-1][e] + b[e] <==> a[n-1][c] + b[c]
R II Et2r				Transport, Extracellular	h[e] + i e-l[e] <==> h[c] + i e-l[c]
R FUIt2r				Transport, Extracellular	h[e] + h[e] < => h[e] + h[e]
R SIII abc				Transport, Extracellular	atp[c] + b2o[c] + so4[c] -> adp[c] + b[c] + b[c] + so4[c]
R PROt2r				Transport, Extracellular	h[e] + pro-l[e] <==> h[c] + pro-l[c]
R ARGt2r				Transport, Extracellular	arg - [e] + b[e] < = > arg - [c] + b[c]
R ASPt2r				Transport, Extracellular	asp-l[e] + h[e] <==> asp-l[c] + h[c]
R ALAt2				Transport, Extracellular	ala-l[e] + b[e] -> ala-l[c] + b[c]
R HISt2r				Transport, Extracellular	h[e] + h[e] <==> h[c] + h[e]
R LYSt2r				Transport, Extracellular	h[e] + h[e] < => h[e] + h[e] + h[e]
R SERt2r				Transport, Extracellular	h[e] + sect[e] <==> h[e] + sect[e]
R THRt2				Transport, Extracellular	h[e] + thr-l [e]> h[c] + thr-l [c]
P TPP+2r				Transport, Extracellular	b[e] + trad[e] <=> b[c] + trad[c]
D TVD+2r				Transport, Extracellular	h[e] + h[e] <> h[e] + h[e] + h[e]
R VALE2r				Transport, Extracellular	h[e] + yal- [e] <=> h[e] + yal- [e]
R PIt2				Transport, Extracellular	h[e] + n[e] < => h[c] + n[c]
P CMPtrane				Transport, Extracellular	cmp[e] + b[e]> cmp[e] + b[e]
R AMPtrans				Transport, Extracellular	amp[a] + h[a] -> amp[a] + h[c]
R CMPtranc				Transport, Extracellular	$amp[e] + h[e] \rightarrow amp[e] + h[e]$
				Transport, Extracellular	
R GLCLII				Transport, Extracellular	gic-b[e] <==> gic-b[c]
R COZL				Transport, Extracellular	ph4[o] <==> ph4[o]
				Transport, Extracellular	hin4[e] <> hin4[c]
D TODTOS	Chro 70176	6112	Tryptophanyl-tPNAsynthetase	Tryptophan metabolism	[c] : ato ± troatro ± troat -> amo ± poi ± trotroa
R ALCD2m	Chro 80199 or Chro 80199	1 1 1 1	alcoholdebydrogenase(ethanol) mitochondrial	Tyrosine metabolism	[c] : atob + pad <> acald + b + padb
R DOBARMO	Chro.00199 01 Chro.00198	1 14 17 1	depamineheta meneowigenase	Tyrosine metabolism	[c] , con i nau <> acau + II + IIauii [c] ; cch i dopp c2 -> dbdocch b2c prophr
R CEEDS	Chro 70551	1 2 1 41	autamate E comialdebydedebydragonace	Urop Cycle and Metabolism of Arrian Carry	Ic] - ascure + acya + 02> anadsec + 1120 + 1170 + 1170
N 03502	CIII0.70331	1.2.1.41	giucamate-o-semialdenydedenydrogenase	Urea Cycle and Metabolism of Arrian Care	<pre>[c] . glupp + n + ndun> glupsd + ndu + pi [c] . glupp + b + podpb -> glupsc + podp + pi </pre>
D CECD	Chro 70EE1			Used Lyde and meladolisti of Amino Grou	$101, 00000 \pm 0 \pm 04000 = 2.000584 \pm 0400 \pm 01$
R G5SD	Chro.70551	2 7 2 11	glutamate5-semialdenydedenydrogenase	Uran Cycle and Metabolism of Arrian Cray	
R G5SD R GLU5K	Chro.70551 Chro.70551 or Chro.20246	2.7.2.11	glutamate-5-semialdenydedenydrogenase	Urea Cycle and Metabolism of Amino Grou	[c] : atp + glu-L> adp + glu5p
R G5SD R GLU5K R OIVD2 R OIVD3	Chro.70551 Chro.70551 or Chro.20246	1.2.1.41 2.7.2.11 1.2.4.4	glutamate-5-semaldenydedenydrogenase glutamate5-kinase R 2 oxoisovalerate dehydrogenase acylating 3 meth	Urea Cycle and Metabolism of Amino Grou Valine, Leucine, and Isoleucine Biosynthes	[c]: atp + glu-L> adp + glu5p [c]: 1.0 3mob + 1.0 coa + 1.0 nad> 1.0 co2 + 1.0 ibcoa + 1.0 nadh [c]: 1.0 3mob + 1.0 coa + 1.0 nad> 1.0 grbcoa + 1.0 co2 + 1.0 nadh
R G5SD R GLU5K R OIVD2 R OIVD3 P LEUTRS	Chro.70551 Chro.70551 or Chro.20246	1.2.1.41 2.7.2.11 1.2.4.4 1.2.4.4 6.1.1.4	glutamate-3-semialdenydedenydrodenase glutamate-5-kinase R 2 oxoisovalerate dehydrogenase acylating 3 meth Jaucol+RNsvntbetase	Urea Cycle and Metabolism of Amino Grou Valine, Leucine, and Isoleucine Biosynthes Valine, Leucine, and Isoleucine Biosynthes Valine, Leucine, and Isoleucine Biosynthes	[c]: atp + qlu-L> adp + qlu5p [c]: 1.0 3mob + 1.0 coa + 1.0 nad> 1.0 co2 + 1.0 ibcoa + 1.0 nadh [c]: 1.0 3mop + 1.0 coa + 1.0 nad> 1.0 2mbcoa + 1.0 co2 + 1.0 nadh [c]: atp + luu + ± traaleu> amp + lautra + pni
R G5SD R GLU5K R OIVD2 R OIVD3 R LEUTRS R ILETRS	Chro.70551 Chro.70551 or Chro.20246 Chro.50330 or Chro.50331 Chro.30434	1.2.1.41 2.7.2.11 1.2.4.4 1.2.4.4 6.1.1.4 6.1.1.5	diutanate's-semaioenydeverydrogenase diutanate's-kinase R 2 oxoisovalerate dehydrogenase acylating 3 meth R 2 oxoisovalerate dehydrogenase acylating 3 meth Leucyl-tRNAsynthetase Isoleucyl-tRNAsynthetase	Urea Cycle and Metabolism of Amino Grou Valine, Leucine, and Isoleucine Biosynthe Valine, Leucine, and Isoleucine Biosynthe Valine, Leucine, and Isoleucine Biosynthes	[c]: atp + qlu-L> adp + qlu5p [c]: 1.0 3mob + 1.0 coa + 1.0 nad -> 1.0 co2 + 1.0 ibcoa + 1.0 nadh [c]: 1.0 3mob + 1.0 coa + 1.0 nad -> 1.0 2mbcoa + 1.0 co2 + 1.0 nadh [c]: atp + leu-L + traaleu> amp + leutrna + pni [c]: atp + leu-L + traaleu> amp + ileutra + pni



Appendix B: Gap Analysis Results

REACTION IDs	ENZYME NAME	PATHWAY	EC NUMBER	REACTION ADDED THROUGH GAP ANALYSIS
While integrating prote	omic data, following highlighted reaction that were inser	ted through Gap Analysis algorithm	were later	found to be existing in oocyst stage of parasite
	hence r	not included in the figure 8, gap and	alysis reacti	on classification
R BIOMASS	biomass	Biomass		[c]: 0.257980584 ala-L + 0.176597196 arg-L + 0.218152121 asn-L + 0.230278549 asp-L + 0.04
R UAG4E	R UDP N acetylglucosamine 4 epimerase	Aminosugar Metabolism	5.1.3.7	[c] : 1.0 uacgam> 1.0 uacgala
R MECDES	2-C-methyl-D-erythritol2.4-cyclodiphosphatesynthase	Biosynthesis of Steroids	4.6.1.12	[c] : 2n4c2me> 2mecdn + cmn
R_IPDDI	isopentenyl-diphosphateD-isomerase	Biosyhthesis of Steroids	5.3.3.2	[c] : ipdp <==> dmpp
R DXPS	1-deoxy-D-xylulose5-phosphatesynthase	Biosynthesis of Steroids	2.2.1.7	[c] : g3p + h + pyr> co2 + dxyl5p
R MEPCT	2-C-methyl-D-erythritol4-phosphatecytidylyltransferase	Biosynthesis of Steroids	2.7.7.60	[c] : 2me4n + ctn + h> 2p4c2me + adp + n [c] : 2me4n + ctn + h> 4c2me + nni
R KAS2	R b ketoacyl synthetase n C140	Fatty Acid Biosynthesis	2.3.1.41	[c] : 1.0 accoa + 17.0 h + 6.0 malcoa + 12.0 nadph> 6.0 co2 + 7.0 coa + 5.0 h2o + 12.0 nadp
R KAS8	R b ketoacyl synthetase palmitate n C160	Fatty Acid Biosynthesis	2.3.1.41	[c]: 1.0 accoa + 20.0 h + 7.0 malcoa + 14.0 nadph> 7.0 co2 + 8.0 coa + 6.0 h2o + 1.0 hdca
R KAS141	R b ketoacyl synthetase n C141	Fatty Acid Biosynthesis	2.3.1.41	$[c]: 1.0 \operatorname{accoa} + 23.0 \operatorname{h} + 6.0 \operatorname{malcoa} + 16.0 \operatorname{malcph}> 6.0 \operatorname{co2} + 9.0 \operatorname{coa} + 7.0 \operatorname{n20} + 16.0 \operatorname{malcoa}$
R KAS7	R b ketoacyl synthetase n C161	Fatty Acid Biosynthesis	2.3.1.41	[c] : 1.0 accoa + 19.0 h + 7.0 malcoa + 13.0 nadph> 7.0 co2 + 8.0 coa + 6.0 h2o + 1.0 hdcea
R KAS17	R b ketoacyl synthetase n C181	Fatty Acid Biosynthesis	2.3.1.41	[c] : 1.0 accoa + 22.0 h + 8.0 malcoa + 15.0 nadph> 8.0 co2 + 9.0 coa + 7.0 h2o + 15.0 nadp
R KAS130iso	R b ketoacyl synthetase branched(iso) C100	Fatty Acid Biosynthesis	2.3.1.41	[c]: 11.0 h + 1.0 ivcoa + 4.0 malcoa + 8.0 nadph -> 4.0 co2 + 5.0 co2 + 1.0 dca + 2.0 h20 + 0.
R_KAS1	R_b_ketoacyl_synthetaseIso_C140_	Fatty Acid Biosynthesis	2.3.1.41	[c] : 14.0 h + 1.0 ibcoa + 5.0 malcoa + 10.0 nadph> 5.0 co2 + 6.0 coa + 1.0 fa1 + 4.0 h2o +
R KAS3	R b ketoacyl synthetase Iso C150	Fatty Acid Biosynthesis	2.3.1.41	[c]: 14.0 h + 1.0 ivcoa + 5.0 malcoa + 10.0 nadph> 5.0 co2 + 6.0 coa + 1.0 fa3 + 4.0 h20 +
R KAS11	R b ketoacyl synthetase Iso C100	Fatty Acid Biosynthesis	2.3.1.41	$[c]: 17.0 \text{ h} + 1.0 \text{ ibcoa} + 6.0 \text{ malcoa} + 12.0 \text{ malcbin} \longrightarrow 6.0 \text{ coa} + 7.0 \text{ coa} + 1.0 \text{ rad} + 5.0 \text{ rad} + 1.0 \text{ rad} + $
R KAS180iso	R b ketoacyl synthetase Iso C180	Fatty Acid Biosynthesis	2.3.1.41	[c] : 20.0 h + 1.0 ibcoa + 7.0 malcoa + 14.0 nadph> 7.0 co2 + 8.0 coa + 1.0 ocdcaiso + 6.0 h
R KASS	R b ketoacyl synthetase Iso C161	Fatty Acid Biosynthesis	2.3.1.41	[c]: 16.0 h + 1.0 ibcoa + 6.0 malcoa + 11.0 nadph> 6.0 co2 + 7.0 coa + 1.0 fa5 + 5.0 h20 + 1.0 ibcoa + 6.0 malcoa + 11.0 nadph> 6.0 co2 + 7.0 coa + 1.0 fa9 + 5.0 h20 + 1.0 ibcoa + 1.0 ibcoa + 6.0 malcoa + 1.0 ibcoa
R KAS4	R b ketoacyl synthetase Anteiso C150	Fatty Acid Biosynthesis	2.3.1.41	$[c]: 1.0 \text{ 2mbcoa} + 14.0 \text{ h} + 5.0 \text{ malcoa} + 10.0 \text{ nadph} \rightarrow 5.0 \text{ co2} + 7.0 \text{ coa} + 1.0 \text{ na} + 5.0 \text{ nz} + 1.0 \text{ na} + 1.0 \text{ na}$
R KAS12	R b ketoacyl synthetase Anteiso C170	Fatty Acid Biosynthesis	2.3.1.41	[c] : 1.0 2mbcoa + 17.0 h + 6.0 malcoa + 12.0 nadph> 6.0 co2 + 7.0 coa + 1.0 fa12 + 5.0 h2
R KAS10 R MAN1PT2r	R b ketoacyl synthetase Anteiso C171	Fatty Acid Biosynthesis	2.3.1.41	[c]: 1.0 2mbcoa + 16.0 h + 6.0 malcoa + 11.0 nadph> 6.0 co2 + 7.0 coa + 1.0 fa10 + 5.0 h2 [c]: adp + b + map1p <> adpmapp + pi
R PLA2 2	phospholipaseA2	Glycerophospholipid Metabolism	3.1.1.4	[c]: h2o + pchol hs> Rtotal2 + h + lpchol hs
R G3PCT	R glycerol 3 phosphate cytidylyltransferase	Glycerophospholipid Metabolism	2.7.7.39	[c] : 1.0 ctp + 1.0 qlyc3p + 1.0 h> 1.0 cdpqlyc + 1.0 ppi
R_CDGPI_CI	R_CDPdiacylglycerolsn_glycerol_3_phosphate_3_phosphatidylt R_Phosphatidylglycerophosphate_phosphobydrolase	Glycerophospholipid Metabolism	2.7.8.5	[c] : 1.0 cdpdag_CI + 1.0 glyc3p> 1.0 cmp + 1.0 h + 1.0 pglyp_CI
R PAP CT	R phosphatidic acid phosphatase	Glycerophospholipid Metabolism	3.1.3.4	[c] : 1.0 12dag3p CT + 1.0 h2o> 1.0 12dgr CT + 1.0 pi
R GLUK	Glucokinase	Glycolysis/Gluconeogenesis	2.7.1.2	[c] : atp + glc-D> adp + g6p-B + h
R G3POA CI	R glycerol 3 phosphate O acyltransferase R lysylphosphatidylglycerol synthesis	Miscellaneous		[c]: 1.0 glyc3p + 0.051 dcacoa + 0.022 trdacoa + 0.023 fa1coa + 0.0092 tdcoa + 0.022 ttdcecoa [c]: 1.0 atp + 1.0 lys-l + 1.0 pgly CT> 1.0 amp + 1.0 b + 1.0 lysylpgly CT + 1.0 ppi
R UGT CT	R UDP glucosyltransferase diglucosyl	Miscellaneous		[c] : 1.0 12dgr CT + 2.0 udpg> 1.0 d12dg CT + 2.0 h + 2.0 udp
R UGT1 CT	R UDP glucosyltransferase monoglucosyl	Miscellaneous		[c]: 1.0 12dgr CT + 1.0 udpg> 1.0 h + 1.0 m12dg CT + 1.0 udp
R UGI2 CI R LIPO1524 CT	R UDP glucosyltransferase triglucosyl R lipoteichoic acid synthesis p24 linked glucose substit	Miscellaneous		[c]: 1.0 12dgr CI + 3.0 udpg> 3.0 h + 1.0 t12dg CI + 3.0 udp[c]: 24.0 cdpglyc + 1.0 d12dg CT + 24.0 udpg> 24.0 cmp + 48.0 h + 1.0 lipo1 24. CT + 24.0
R LIPO2S24 CT	R lipoteichoic acid synthesis n24 linked N acetylqlucos	Miscellaneous		[c]: 24.0 cdpglyc + 1.0 d12dg CT + 24.0 uacgam> 24.0 cmp + 48.0 h + 1.0 lipo2 24 CT + 24.0 uacgam> 24.0 cmp + 48.0 h + 1.0 lipo2 24 CT + 24.0 uacgam> 24.0 cmp + 48.0 h + 1.0 lipo2 24 CT + 24.0 uacgam> 24.0 cmp + 48.0 h + 1.0 lipo2 24 CT + 24.0 uacgam> 24.0 cmp + 48.0 h + 1.0 lipo2 24 CT + 24.0 uacgam> 24.0 cmp + 48.0 h + 1.0 lipo2 24 CT + 24.0 uacgam> 24.0 cmp + 48.0 h + 1.0 lipo2 24 CT + 24.0 uacgam> 24.0 cmp + 48.0 h + 1.0 lipo2 24 CT + 24.0 uacgam> 24.0 cmp + 48.0 h + 1.0 lipo2 24 CT + 24.0 uacgam + 24.
R LIPO3S24 CT	R lipoteichoic acid synthesis n24 unliked D alanine su	Miscellaneous		[c]: 24.0 ala-D + 24.0 atp + 24.0 cdpqlyc + 1.0 d12dg CT + 24.0 h2o> 24.0 amp + 24.0 cmp
R_LIPO4S24_CI R_TECA1S45	R_lipoteichoic_acid_synthesisn24linked_unsubstituted	Miscellaneous		$[c]: 24.0 \text{ cdpglyc} + 1.0 \text{ d12dg}_CI \longrightarrow 24.0 \text{ cmp} + 24.0 \text{ h} + 1.0 \text{ lpo4}_24_CI$
R TECA2S45	R glycerol teichoic acid n45 unlinked D ala substituted	Miscellaneous		[c] : 45.0 ala-D + 45.0 atp + 45.0 cdpglyc + 45.0 h2o + 1.0 uacgam + 1.0 uacmam> 45.0 amp
R TECA3S45	R glycerol teichoic acid n45 unlinked glucose substitut	Miscellaneous		[c]: 45.0 cdpglyc + 1.0 h2o + 1.0 uacgam + 1.0 uacmam + 45.0 udpg> 45.0 cmp + 1.0 gtca3
R TEICH45	R minor teichoic acid synthesis n30 R teichuronic acid n45 unlinked GalNAc GlcA repeated	Miscellaneous		[c]: 30.0 h20 + 30.0 uacqala + 30.0 udpq> 60.0 h + 1.0 tcam CI + 30.0 udp + 30.0 ump [c]: 45.0 uacqala + 45.0 udpq/cur <==> 45.0 h + 1.0 teich 45 CT + 45.0 udp + 45.0 ump
R UAGPT3	R UDP N acetylglucosamine N acetylmuramyl pentapeptide	Miscellaneous		[c] : 1.0 uacgam + 1.0 uagmda> 1.0 h + 1.0 uaagmda + 1.0 udp
R PPTGS CT	R Peptidoglycan subunit synthesis	Miscellaneous		[c] : 1.0 uaagmda> 1.0 h + 1.0 peptido CT + 1.0 udcpdp
R GGTT	R geranvlgeranvltransterase	Miscellaneous		[c] : 1.0 grap + 1.0 ipap> 1.0 grap + 1.0 ppi [c] : 1.0 grap + 1.0 ipap> 1.0 pendp + 1.0 ppi
R PPTT	R trans pentaprenyltranstransferase	Miscellaneous		[c] : 1.0 ipdp + 1.0 pendp> 1.0 hexdp + 1.0 ppi
R HEXTT	R trans hexaprenyltranstransferase	Miscellaneous		[c] : 1.0 hexdp + 1.0 ipdp> 1.0 hepdp + 1.0 ppi
R 2S6HCCi	R 2 succinyl 6 hydroxy 2 4 cyclohexadiene 1 carboxylate	Miscellaneous		[c]: 1.0 chor < -> 1.0 chor <-> 1.0 2 shchc + 1.0 co2 + 1.0 pyr
R SUCBZS	R O succinylbenzoate CoA synthase	Miscellaneous		[c] : 1.0 2shchc> 1.0 h2o + 1.0 sucbz
R SUCBZL	R o succinylbenzoate CoA ligase	Miscellaneous		[c] : 1.0 atp + 1.0 coa + 1.0 sucbz> 1.0 amp + 1.0 ppi + 1.0 sbzcoa
R DHNAOT7	R 1 4 dihydroxy 2 naphthoate octaprenyltransferase	Miscellaneous		[c] : 1.0 dhna + 1.0 hepdp + 1.0 nad> 1.0 2dmmg7 + 1.0 co2 + 1.0 nadh + 1.0 ppi
R AMMQT7	R S adenosylmethione2 demthylmenaquinone methyltransfer	Miscellaneous		[c] : 1.0 2dmmq7 + 1.0 amet + 1.0 nadph> 1.0 ahcys + 1.0 mql7 + 1.0 nadp
R H2CO3D2	carboxylicaciddissociation	Miscellaneous		[c]: h + hco3 <==> h2co3 $[c]: 2mecdn + h -> h2mb4n + h2n$
R CLPNS2 CT	R cardiolipin synthase	Miscellaneous	2.7.8	[c] : 2.0 pqly CT> 1.0 cdlp CT + 1.0 qlyc
R UPP3S	uroporphyrinogen-IIIsynthase	Porphyrin and chlorophyll metabolism	4.2.1.75	[c] : hmbil> h2o + uppg3
R ADSL2r	adenylosuccinatelyase	Purine Metabolism Purine Metabolism	4.3.2.2	[c] : 25aics <==> aicar + fum
R_ADSL2	adenylosuccinatelyase	Purine Metabolism	4.3.2.2	[c] : 25aics> aicar + fum
R ADSL1	adenylosuccinatelyase	Purine Metabolism	4.3.2.2	[c] : dcamp> amp + fum
R GMPS	GMPsynthase cytidylatekinase(dCMP)	Purine Metabolism	6.3.4.1	[c] : atp + nh4 + xmp> amp + gmp + 2 h + ppi
R UMPK5	UMPkinase(dATP)	Pyrimidine Metabolism	2.7.4.14	[c]: datp + ump <==> dadp + udp
R CYTK9	cytidylatekinase(CMP,dCTP)	Pyrimidine Metabolism	2.7.4.14	[c] : cmp + dctp <==> cdp + dcdp
R CYTKS	cytidylatekinase(CMP,dATP) cytidylatekinase(dCMP)	Pyrimidine Metabolism Pyrimidine Metabolism	2.7.4.14	c : cmp + datp <==> cdp + dadp
R CYTK7	cytidylatekinase(CMP,UTP)	Pyrimidine Metabolism	2.7.4.14	[c]: cmp + utp <==> cdp + udp
R CYTK6	cytidylatekinase(CMP,CTP)	Pyrimidine Metabolism	2.7.4.14	[c] : cmp + ctp <==> 2 cdp
R LIMPK3	cytidylatekinase(CMP) LIMPkinase(LITP)	Pyrimidine Metabolism Pyrimidine Metabolism	2.7.4.14	[c] : upp + utp <==> 2 udp
R UMPK2	UMPkinase(CTP)	Pyrimidine Metabolism	2.7.4.14	[c]: ctp + ump <==> cdp + udp
R_UMPK7	UMPkinase(dGTP)	Pyrimidine Metabolism	2.7.4.14	<pre>[c] : dgtp + ump <==> dgdp + udp</pre>
R UMPK6	UMPkinase(GTP)	Pyrimidine Metabolism	2.7.4.14	[c]: dcp + ump <==> dcdp + udp
R CYTK11	cytidylatekinase(dCMP,dGTP)	Pyrimidine Metabolism	2.7.4.14	[c]: dcmp + dqtp <==> dcdp + dqdp
R CYTK10	cytidylatekinase(CMP,dGTP)	Pyrimidine Metabolism	2.7.4.14	[c] : cmp + dqtp <==> cdp + dqdp
R CYTK13	cytidylatekinase(dCMP,dATP) cytidylatekinase(dCMP,dCTP)	Pyrimidine Metabolism	2.7.4.14	c : datp + dctp <==> dadp + dcdp c : dcmp + dctp <==> 2 dcdp
R CYTK14	cytidylatekinase(dCMP,UTP)	Pyrimidine Metabolism	2.7.4.14	[c] : dcmp + utp <==> dcdp + udp
R UMPK	UMPkinase	Pyrimidine Metabolism	2.7.4.14	[c] : atp + ump <==> adp + udp
R CBPS	appanyurolase,asymmetricaliy carbamoyl-phosphatesynthase(olutamine-hydrolysing)	Pyrimidine Metabolism Pyrimidine Metabolism	6.3.5.5	c : ap+a + 20> amp + atp + 2 n c : 2 atp + alp-L + h20 + hco3> 2 adp + cbn + alu-L + 2 h + ni
R SIAASE	sialidase	Sphingoglycolipid Metabolism	3.2.1.18	[c] : 2 h2o + s2l2n2m2mn> 2 acnam + l2n2m2mn
R_H2Ot	H2Otransportviadiffusion	Transport, Extracellular		h2o[e] <==> h2o[c]
R DOPABMO	dopaminebeta-monooxygenase	Tyrosine metabolism	1.14.17.1	<pre>[cys-u[e] + ii]e] <==> cys-u[c] + n[c] [c] : ascb-L + dopa + o2> dhdascb + h2o + prophr</pre>
R OIVD2	R 2 oxoisovalerate dehydrogenase acylating 3 methyl 2 o	Valine, Leucine, and Isoleucine Biosyn	1.2.4.4	[c] : 1.0 3mob + 1.0 coa + 1.0 nad> 1.0 co2 + 1.0 ibcoa + 1.0 nadh
R OIVD3	R 2 oxoisovalerate dehydrogenase acylating 3 methyl 2 o	Valine, Leucine, and Isoleucine Biosyn	1.2.4.4	[c]: 1.0 3mop + 1.0 coa + 1.0 nad> 1.0 2mbcoa + 1.0 co2 + 1.0 nadh

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Appendix C: Predicted Essential Reactions in the Model

REACTION IDs	ENZYME NAME	PATHWAY	EC NUMBER	GENE IDs	REACTION
R biomass target	Biomass Rxn	Biomass Objective			[c]: 0.257980584 ala-L + 0.176597196 arg-L + 0.218152121 asn-L + 0.230278549 asp-L + 0.0
R G3POA CT	R glycerol 3 phosphate O acyltransfer				[c] : qlyc3p + 0.051 dcacoa + 0.022 trdacoa + 0.023 fa1coa + 0.0092 tdcoa + 0.022 ttdcecoa +
R LYSLG CT	R lysylphosphatidylqlycerol synthesis				[c] : atp + lys-L + pqly CT> amp + h + lysylpqly CT + ppi
R UGT CT	R UDP glucosyltransferase diglucosyl				[c] : 12dgr CT + 2.0 udpg> d12dg CT + 2.0 h + 2.0 udp
R UGT1 CT	R UDP glucosyltransferase monogluco				[c]: 12dgr CT + udpg> h + m12dg CT + udp
R UGT2 CT	R UDP glucosyltransferase triglucosyl				[c] : 12dgr CT + 3.0 udpg> 3.0 h + t12dg CT + 3.0 udp
R AGPATr CT	R 1 acylglycerol 3 phosphate O acylti		2.3.1.51	Chro.80165	[c]: 1ag3p CT + 0.051 dcacoa + 0.022 trdacoa + 0.023 fa1coa + 0.0092 tdcoa + 0.022 ttdceco
R PHCYT CT	R phosphatidate cytidylyltransferase		2.7.7.41	Chro.70059 o	[c] : $12dag3p$ CT + ctp + h> cdpdag CT + ppi
R CLPNS2 CT	R cardiolipin synthase		2.7.8		[c] : 2.0 pgly CT> cdlp CT + glyc
R CDPDSP CT	R CDPdiacylglycerol serine O phosphat		2.7.8.8	Chro.70250	[c] : cdpdag CT + ser-L> cmp + h + ps CT
R PSDC CT	R phosphatidylserine decarboxylase		4.1.1.65	Chro.30247	[c] : ps CT> co2 + psetha CT
R_P5CD	_1-pyrroline-5-carboxylatedehydrogenas	Arginine and Proline Metabolism	1.5.1.12	Chro.60426 o	[c] : 1pyr5c + 2 h2o + nad> glu-L + h + nadh
R PRO1x	prolineoxidase(L-proline,NAD)	Arginine and Proline Metabolism	1.5.1.2	Chro.60426	[c] : nad + pro-L> 1pyr5c + 2 h + nadh
R KAS12	R b ketoacyl synthetase Anteiso C17	Fatty Acid Biosynthsis	2.3.1.41		[c] : 2mbcoa + 17.0 h + 6.0 malcoa + 12.0 nadph> 6.0 co2 + 7.0 coa + fa12 + 5.0 h2o + 12
R KAS100iso	R b ketoacyl synthetase branched(ise	Fatty Acid Biosynthsis	2.3.1.41		[c]: 8.0 h + ibcoa + 3.0 malcoa + 6.0 nadph> 3.0 co2 + 4.0 coa + dca + 2.0 h2o + 6.0 nadp
R KAS130iso	R b ketoacyl synthetase branched(ise	Fatty Acid Biosynthsis	2.3.1.41		[c] : 11.0 h + ivcoa + 4.0 malcoa + 8.0 nadph> 4.0 co2 + 5.0 coa + trdca + 3.0 h2o + 8.0 na
R KAS1	R b ketoacyl synthetase Iso C140	Fatty Acid Biosynthsis	2.3.1.41		[c]: 14.0 h + ibcoa + 5.0 malcoa + 10.0 nadph> 5.0 co2 + 6.0 coa + fa1 + 4.0 h2o + 10.0 n
R KAS6	R b ketoacyl synthetase Iso C160	Fatty Acid Biosynthsis	2.3.1.41		[c]: 17.0 h + ibcoa + 6.0 malcoa + 12.0 nadph> 6.0 co2 + 7.0 coa + fa6 + 5.0 h20 + 12.0 n
R_KAS180iso	R_b_ketoacyl_synthetaseIso_C180_	Fatty Acid Biosynthsis	2.3.1.41		[c] : 20.0 h + ibcoa + 7.0 malcoa + 14.0 nadph> 7.0 co2 + 8.0 coa + ocdcaiso + 6.0 h2o + 1
R KAS7	R b ketoacyl synthetase n C161	Fatty Acid Biosynthsis	2.3.1.41		[c] : accoa + 19.0 h + 7.0 malcoa + 13.0 nadph> 7.0 co2 + 8.0 coa + 6.0 h2o + hdcea + 13.
R KAS8	R b ketoacyl synthetase palmitate	Fatty Acid Biosynthsis	2.3.1.41		[c] : accoa + 20.0 h + 7.0 malcoa + 14.0 nadph> 7.0 co2 + 8.0 coa + 6.0 h2o + hdca + 14.0
R KAS2	R b ketoacyl synthetase n C140	Fatty Acid Biosynthsis	2.3.1.41		[c] : accoa + 17.0 h + 6.0 malcoa + 12.0 nadph> 6.0 co2 + 7.0 coa + 5.0 h2o + 12.0 nadp +
R FACOAL170 anteiso	R fatty acid CoA ligase anteiso C17	Fatty Acid Biosynthsis	6.2.1.3	Chro.50052 o	[c] : atp + coa + fa12 <==> amp + fa12coa + ppi
R FACOAL100	R fatty acid CoA ligase Iso C100	Fatty Acid Biosynthsis	6.2.1.3	Chro.50052 o	[c] : atp + coa + dca <==> amp + dcacoa + ppi
R FACOAL130	R fatty acid CoA ligase Iso C130	Fatty Acid Biosynthsis	6.2.1.3	Chro.50052 o	[c] : atp + coa + trdca <==> amp + trdacoa + ppi
R FACOAL140 ISO	R fatty acid CoA ligase Iso C140	Fatty Acid Biosynthsis	6.2.1.3	Chro.50052 o	c]: atp + coa + fa1 <==> amp + fa1coa + ppi
R FACOAL160 ISO	R fatty acid CoA ligase Iso C160	Fatty Acid Biosynthsis	6.2.1.3	Chro.50052 o	c]: atp + coa + fa6 <==> amp + fa6coa + ppi
R FACOAL180 ISO	R fatty acid CoA ligase Iso C180	Fatty Acid Biosynthsis	6.2.1.3	Chro.50052 o	c] : atp + coa + ocdcaiso <==> amp + ppi + strcoaiso
R FACOAL161	fatty-acidCoAligase(hexadecenoate)	Fatty Acid Biosynthsis	6.2.1.3	Chro.50052 o	c]: atp + coa + hdcea <==> amp + hdcoa + ppi
R GLNS	glutaminesynthetase	Glutamate metabolism	6.3.1.2	Chro.60524	c : atp + glu-L + nh4> adp + gln-L + h + pl
R G3PD1ir	glycerol-3-phosphatedenydrogenase(NA	Glycerolipid Metabolism	1.1.1.8	Chro.20028	[c]: dhap + h + hadh> glyc3p + had
R CDGPT CT	R CDPdiacylglycerolsn glycerol 3 phos	Glycerophospholipid Metabolism	2.7.8.5		[c]: cdpdag CI + glyc3p> cmp + h + pglyp CI
R PGPPH CI	R Phosphatidylqlycerophosphate phosp	Glycerophospholipid Metabolism	3.1.3.2/		c]: h20 + pglyp Cl> pgly Cl + pi
R PAP CI	R prospraticic acid prospratase	Giverophospholipid Metabolism	3.1.3.4	Ch	[c] : 120ag3p CI + n20> 120gr CI + pi
R GAPD	glyceraldehyde-3-phosphatedehydrogen	Glycolysis/Gluconeogenesis	1.2.1.12	Chro.60434 o	$ c : g_{3p} + nad + p_{1} <==> 13dpg + n + nadn$
R PYK	pyruvatekinase	Glycolysis/Gluconeogenesis	2.7.1.40	Chro.10234	c : adp + n + pep> atp + pyr
R_FBA	fructose-bisphosphateaidolase	Glycolysis/Gluconeogenesis	4.1.2.13	Chro.10335	[c]: rap <=> anap + gsp
R ENU	enolase	Giycolysis/Gluconeogenesis	4.2.1.11	Chro.50184	c : 2pg <=> nzo + pep
R PGM	phosphoglyceratemutase	GIVCOIVSIS/GIUCONEOGENESIS	5.4.2.1	Chro.10196 0	[c]: 2pg <==> 3pg
R NADK	NADKINASE	NAD Metabolism	2.7.1.23	Chro. 60000 c	[c]: atp + nad> adp + n + nadp
R RINDR4	nbonucleoside-diphosphatereductase(ot	Purine Metabolism	2.7.1.20	Chiro.60090 0	[c]: $udd + udp = -3 udp + 1120 + ud0x$
R ADNKZ	adenosinekinase	Purine Metabolism	2.7.1.20	Chro.20322	c : aon + gtp> aop + gmp + n
R NDPK4	nucleoside-dipnosphatekinase(ATP:dTDP	Purine Metabolism	2.7.4.0	Chro. 40275 0	c : atp + dtap <==> adp + dttp
R_GRI	guanyiatekinase(GMP:ATP)	Purine Metabolism	2.7.4.0	Chro E0026	[c]: atp + ginp <=> adp + gip
P NTDS	5-nucleotidace(AMP)	Purine Metabolism	2125	Chro 50026	[c] : dtmp + h2p> pi + thymd
R NIDS	3 - HUCIEOUUASE(UTMP)	Purimidine Metabolism	3.1.3.3	Chro 60000 e	c; cump + fizo> pi + triving
	ribonucleoside-diphosphatereductase(GL	Pyrimiding Motabolism	1.17.4.1	Chro 60000 c	$\frac{ c : qup + trara -> uqup + n20 + traox}{ c : qup + trade +$
	ribonucleoside-diphosphatereductase(AL	Pyrimiding Matabalism	1.17.4.1	Chro 60000 a	[c] : cdp + trdrd -> dcdp + h2p + trdpy
	thiorodoviproductoco(NADPH)	Pyrimiding Matabalism	1.1/.4.1	Chro 20464	[c] : b + padpb + trday -> padp + trday
	dTMDkinaco	Pyrimiding Matabalism	2740	Chro 50400	Ic] : ata + dtapa <==> ada + dtda
	dCMPdoaminaco	Pyrimidine Metabolism	2.7.4.9	Chro 20204	$[c]: dcmp + b + b^{2}p < ==> dcmp + pb4$
N DUPIEDA	uchirucaninase	rymmume metabolisili	J.J.4.1Z	CIII 0.20294	101 . domp = 11 = 120 <==> dump = 1119



Appendix D: Optimization result of oocyst and sporozoite stage data with nodel iNV213

Gene IDs	EC Numbers	Enzyme	Pathway	Reaction
Reaction pre	esent in oocyst	stage only		
Chro 40402	2 7 1 107	P disculaturaret kinara		[c] + 12der CT + etc. > 12dec2n CT + edc. + h
Chro 60435	2.7.1.107	hexokinase	Glycolysis/Gluconeogenesis	[c] : atn + a(c-D)> adn + b + a6n
Chro.40330	1.2.1.31	L-aminoadipate-semialdehydedehydrogenase(NADPH)	Lysine Biosynthesis	[c]: L2aadp + atp + h + nadph> L2aadp6sa + amp + nadp + ppi
Chro.40330	1.2.1.31	L-aminoadipate-semialdehydedehydrogenase(NADH)	Lysine Biosynthesis	[c] : L2aadp6sa + h2o + nad> L2aadp + 2 h + nadh
Chro.40159	3.6.1.1	inorganicdiphosphatase	Oxidative Phosphorylation	[c] : h2o + ppi> h + 2 pi
Chro.50026	3.1.3.5	5'-nucleotidase(UMP)	Purine Metabolism	[c] : h2o + ump> pi + uri
Chro.50026	3.1.3.5	5'-nucleotidase(AMP)	Purine Metabolism	[c] : amp + h2o> adn + pi
Chro.20322	2.7.1.20	adenosinekinase	Purine Metabolism	[c]: adn + qtp> adp + qmp + h
Chro.50398 o	2.7.1.21	thymidinekinase(ATP:thymidine)	Pyrimidine Metabolism	c : atp + thymd> adp + dtmp + h
Chro 10216 0	2.7.1.48	uridinekinase(ATP:Uridine)	Pyrimidine Metabolism	c : atp + url> adp + n + ump
Chro 50389	4 1 1 31	phosphoepolpyruvatecarboxylase	Pyruvate Metabolism	[c]: co2 + b2o + pep> b + oaa + pi
Chro.50314	1.1.1.38	malicenzyme(NAD)	Pyruvate Metabolism	[c]: mal-l + nad> co2 + nadh + pyr
Chro.50314	1.1.1.40	malicenzyme(NADP)	Pyruvate Metabolism	[c] : mal-L + nadp> co2 + nadph + pyr
Reactions pr	resnt in sporoz	oite stage only		
Ch + 60101		Glucokinase	Glycolysis/Gluconeogenesis	c : atp + qlc-D> adp + q6p-B + h
Chro.60194	3.6.1.6	nucleoside-diphosphatase(GDP)	Nucleotide Salvage Pathway	c : qdp + h2o> qmp + h + pi
Chro 60104	2616	Glucose-6-phosphatelsomerase	Puring Matabalism	$[c]: dodp + b 2a \rightarrow domp + b + pi$
Chro 60194	3616	nucleoside-diphosphatase(dLIDP)	Purine Metabolism	[c] : dudp + h20> dump + h + pi
Chro.60194	3.6.1.6	nucleoside-diphosphatase(UDP)	Purine Metabolism	[c] : h20 + udp> h + pi + ump
	2.7.4.14	cytidylatekinase(dCMP)	Pyrimidine Metabolism	[c]: ctp + dcmp <==> cdp + dcdp
Chro.20336	5.3.1.9	glucose-6-phosphateisomerase	Starch and Sucrose Metabolism	[c] : g6p-A <==> g6p-B
Chro.20336	5.3.1.9	glucose-6-phosphateisomerase	Starch and Sucrose Metabolism	[c] : g6p-A <==> f6p
Chro.20336	5.3.1.9	glucose-6-phosphateisomerase	Starch and Sucrose Metabolism	[c] : q6p-B <==> f6p
		a fa haifa dha ata a a		
Reactions co	ommonly prese	nt in both the stages		
		nbosnboglyceratekinase	Carbon Eixation	[c]: 3ng + atg <==> 13dgg + adg
		triose-nhosphateisomerase	Eructose and Mannose Metabolism	$[c]: dban \leq => n3n$
		phosphoglyceratekinase	Glycolysis/Gluconeogenesis	[c]: 3pg + atp <==> 13dpg + adp
		pyruvatedecarboxylase	Glycolysis/Gluconeogenesis	[c]: h + pyr> acald + co2
		enolase	Glycolysis/Gluconeogenesis	[c] : 2pg <==> h2o + pep
		phosphoglyceratemutase	Glycolysis/Gluconeogenesis	[c] : 2pq <==> 3pq
		glucose-6-phosphateisomerase	Glycolysis/Gluconeogenesis	[c] : q6p <==> f6p
		glyceraldehyde-3-phosphatedehydrogenase	Glycolysis/Gluconeogenesis	[c]: q3p + nad + pi <==> 13dpq + h + nadh
	•	pyruvatekinase	Glycolysis/Gluconeogenesis	<pre>[c]: adp + h + pep> atp + pyr</pre>
	•	fructoro hisphasphatealdelase	Glycolysis/Gluconeogenesis	[c]: elon + nau <==> acalu + n + naun
	•	nbosnbofructokinase alvcosome	Glycolysis/Gluconeogenesis	[c]: atp + ffp> adp + fdp + b
		adenylosuccinatelyase	IMP Biosynthesis	[c]: 25aics> aicar + fum
		adenylosuccinatelyase	Nucleotides	[c] : dcamp> amp + fum
		phosphofructokinase	Pentose Phosphate Pathway	[c]: atp + f6p> adp + fdp + h
		adenylosuccinatelyase	Purine Metabolism	[c] : 25aics <==> aicar + fum
		nucleoside-diphosphatekinase(ATP:dADP)	Purine Metabolism	<pre>[c] : atp + dadp <==> adp + datp</pre>
		nucleoside-diphosphatekinase(ATP:dCDP)	Purine Metabolism	[c] : atp + dcdp <==> adp + dctp
	ŀ	nucleoside-diphosphatekinase(ATP: GDP)	Purine Metabolism	c : atp + dqdp <==> adp + dqtp
	·	nucleoside-diphosphatekinase(ATP:UDP)	Purine Metabolism	[c]: atp + cup <==> adp + ctp
	1.	adenylsuccinatelyase	Purine Metabolism	[c]: dcamp <==> amp + fum
	Ľ	nucleoside-diphosphatekinase(ATP:GDP)	Purine Metabolism	[c]: atp + qdp <==> adp + qtp
		guanylatekinase(GMP:ATP)	Purine Metabolism	[c]: atp + gmp <==> adp + gdp
	1.	UMPkinase(CTP)	Pyrimidine Metabolism	[c]: ctp + ump <==> cdp + udp
		UMPkinase(dGTP)	Pyrimidine Metabolism	[c] : dqtp + ump <==> dqdp + udp
		UMPkinase	Pyrimidine Metabolism	[c]: atp + ump <==> adp + udp
	·	UMPkinase(dCTP)	Pyrimidine Metabolism	c : dctp + ump <=> dcdp + udp
	·	cytidylatekinase(dCMP)	Pyrimidine Metabolism	c : atp + dcmp <==> adp + dcdp
	·	cytidylatekinase(CMP,0CTP)	Pyrimidine Metabolism	[c]: cmp + dctp <==> cdp + dcdp
	ŀ	cytidylatekinase(CMPTITP)	Pyrimidine Metabolism	[c]: cmp + utp <==> cdp + udp
-	Ľ	cytidylatekinase(CMP.CTP)	Pyrimidine Metabolism	[c]: cmp + ctp <==> 2 cdp
		cytidylatekinase(CMP)	Pyrimidine Metabolism	[c]: atp + cmp <==> adp + cdp
		UMPkinase(UTP)	Pyrimidine Metabolism	[c] : ump + utp <==> 2 udp
l		UMPkinase(dATP)	Pyrimidine Metabolism	<pre>[c] : datp + ump <==> dadp + udp</pre>
		UMPkinase(GTP)	Pyrimidine Metabolism	[c]: qtp + ump <==> qdp + udp
	•	cytidylatekinase(dCMP,dGTP)	Pyrimidine Metabolism	c : dcmp + dqtp <==> dcdp + dqdp
	•	cytidylatekinase(CMP,dGTP)	Pyrimidine Metabolism	c : cmp + dqtp <==> cdp + dqdp
	·	cytigylatekinase(gCMP,gATP)	Pyrimidine Metabolism	$\frac{ c : ualp + acmp <==> aaap + acdp}{ c : dcmp + dctp <==> 2 dcdp}$
	1	cytidylatekinase(dCMP1ITP)	Pyrimidine Metabolism	[c]: dcmp + utp <==> 2 dcdp + udp
-	Ľ	malatedehydrogenase(otherdirection)	Pyruvate Metabolism	[c]: h + nadh + oaa> mal-l + nad
		L-lactatedehydrogenase	Pyruvate Metabolism	[c] : lac-L + nad <==> h + nadh + pvr
		malatedehydrogenase	Pyruvate Metabolism	[c] : mal-L + nad <==> h + nadh + oaa
		H2Otransportviadiffusion	Transport, Extracellular	h2o[e] <==> h2o[c]
		alcoholdehydrogenase(ethanol),mitochondrial	Tyrosine metabolism	[c] : etoh + nad <==> acald + h + nadh
1	1		1	$[a]c-D[e] \leq => a[c-D[c]$



VITA

Niti Vanee was born on December 20, 1984 in Kanpur, India and she is currently a citizen of Republic of India. Niti received her school education in India and graduated with Bachelors in Technology from College of Engineering and Technology IILM, India in 2006, majoring in Biotechnology.

She is a member of the honor society of Phi Kappa Phi and most outstanding graduate student of Masters of Sciences in Bioinformatics with a GPA of 3.86.

