

Metagenómica en HPC

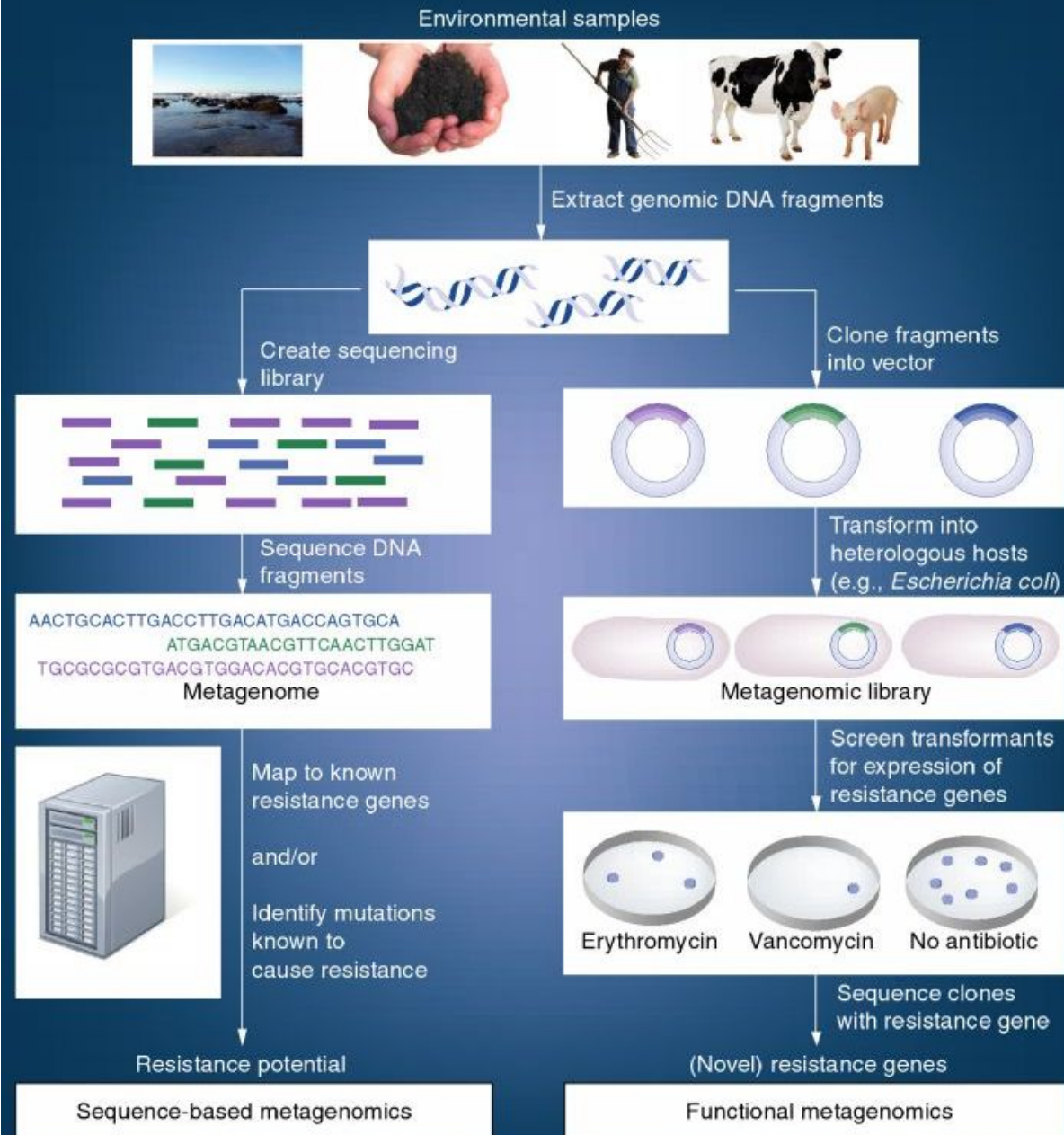
Biomedicina,
Santiago 17 Octubre 2014
Dante Travisany

Temas

- Introducción
- Pipeline LBMG
- Ejemplo en el HPC
- Aproximación por Red
- Reconstrucción

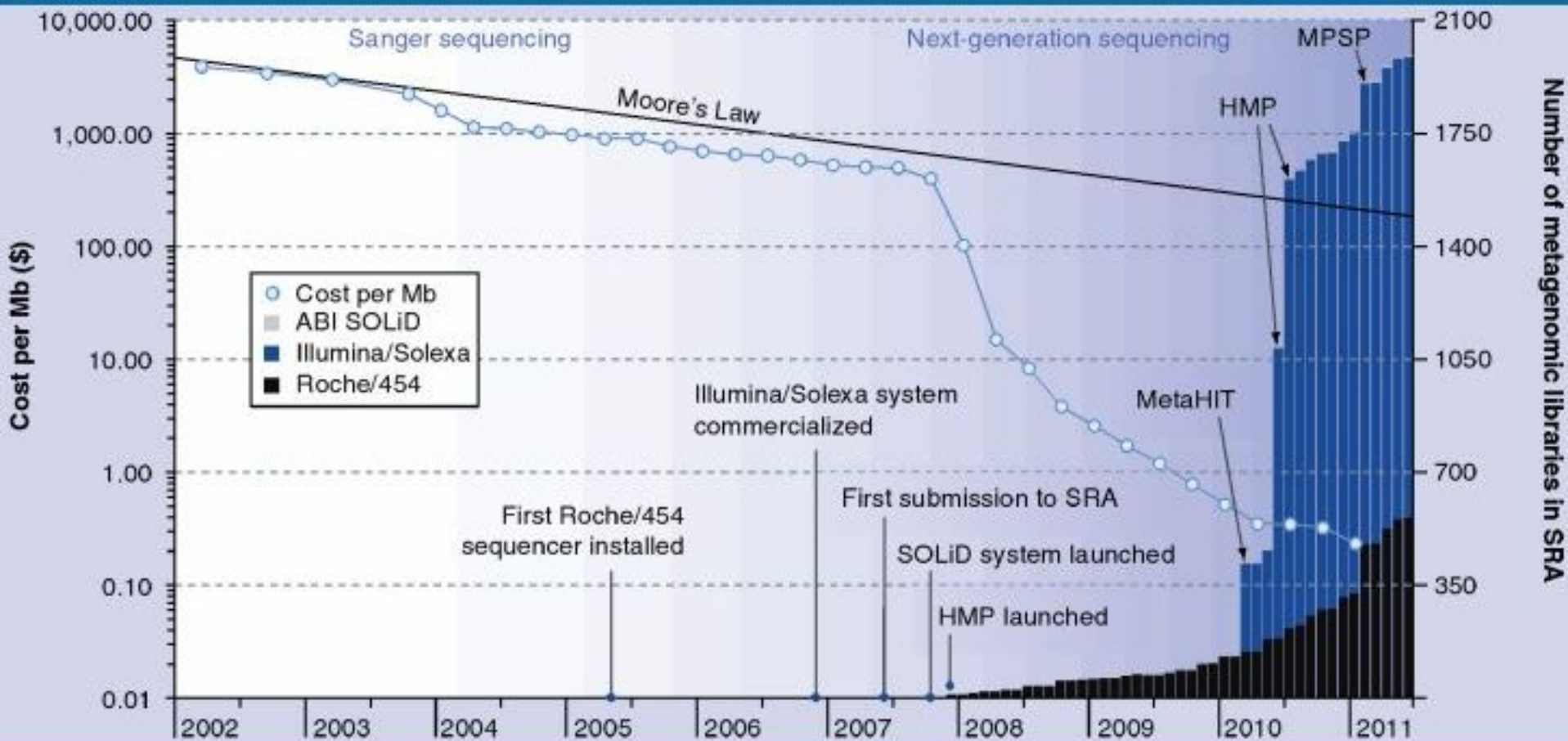
Introducción





Introducción

Medscape



Source: Future Microbiol © 2012 Future Medicine Ltd

HMP



NIH HUMAN MICROBIOME PROJECT

Current News

- May 2014
Poster and Booth at ASM 2014
- April 2014
HMP DACC Releases New Collection of Data
- December 2013
New Datasets available: Phase II and Demo 16S and WGS

[More News Items](#)

Publications

- Metagenomics reveals sediment microbial community response to Deepwater...
- Evidence of extensive DNA transfer between bacteroidales species withi...
- The placenta harbors a unique microbiome....

[More Publications](#)

Partner Resources

The screenshot shows the HMP DACC website. At the top is a dark blue navigation bar with links: REFERENCE GENOMES, MICROBIOME ANALYSIS, IMPACTS ON HEALTH, TOOLS & TECHNOLOGY, ETHICAL IMPLICATIONS, OUTREACH, and HMPDACC DATA BROWSER. A 'Login' button and a search bar are on the right. Below the navigation bar is a light gray banner with a welcome message and two buttons: 'GET DATA' and 'GET TOOLS'. The main content area features a large image of a human torso with a glowing green microbiome overlay. Below this image is a section titled 'Areas of Interest' with a sub-section 'Impacts on Health' containing text about demonstration projects. At the bottom, there is a link for 'DACC Member Organizations'.

Welcome to the Data Analysis and Coordination Center (DACC) for the National Institutes of Health (NIH) Common Fund supported Human Microbiome Project (HMP). This site is the central repository for all HMP data. The aim of the HMP is to characterize microbial communities found at multiple human body sites and to look for correlations between changes in the microbiome and human health. More information can be found in the menus above and on the [NIH Common Fund site](#).

[GET DATA](#)

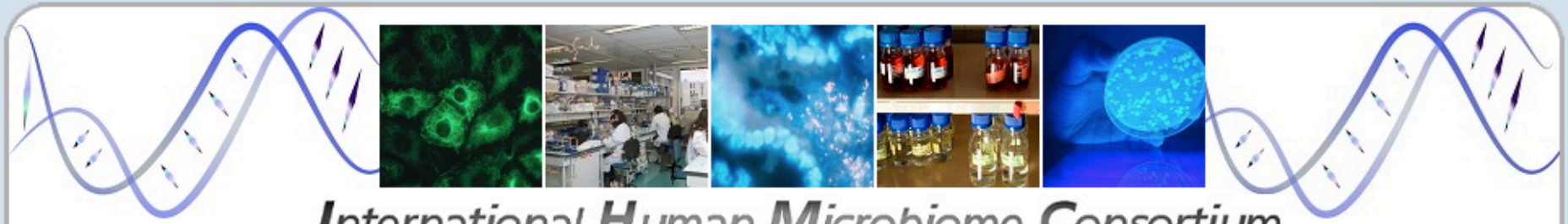
[GET TOOLS](#)

Areas of Interest

Impacts on Health
Demonstration projects to determine the relationship between human health and changes in the human microbiome through the use of 16S and whole metagenome sequencing of clinical samples of interest...

[DACC Member Organizations](#)

IHMC



International Human Microbiome Consortium

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► Programs

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Menu

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[Application](#)

[Past meetings](#)

[Paris 2005](#)

[Rockville, MD 2007](#)

[Jouy en Josas 2008](#)

[Heidelberg 2008](#)

[Shenzhen 2010](#)

[Vancouver 2011](#)

[Paris 2012](#)

Research Programs

MetaGenoPolis

2012-2019 Financed by the french initiative "Investissements d'Avenir"
www.mgps.eu

Coordinator: S.D. Ehrlich (INRA - France) Partners: INRA-MICALIS, Université Catholique de Lyon (Thierry Magnin), Cardiometabolism and Nutrition Institute (Karine Clément)

MetaGenoPolis (MGP) has a strategic goal to demonstrate the impact of the human gut microbiota on health and disease, by making available cutting-edge metagenomics technology, quantitative and functional, to the medical, academic and industrial communities. The approach is built upon the knowledge gathered by the EC FP7 MetaHIT project, such as the establishment of a broad gene catalogue of the human intestinal metagenome, discovery of the three human enterotypes, characterization of microbiota in two chronic diseases, obesity and inflammatory bowel disease and the pilot high-throughput functional metagenomics screens.

International Human Microbiome Standards - IHMS

Login

Username:

Password:

[Forgot your password?](#)

IHMC Presentation



MetaHIT



Metagenomics of the Human Intestinal Tract

Home	Paris 2012	Live News	Project	WPs	Our Team	Publications	Conf 2010	Media	Links	Intranet
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► [Home](#)

[Search](#) [Legal mention](#) [Site map](#)

Menu

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[Objectives](#)

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[Microbial profiling](#)

[Data analysis](#)

[Function analysis](#)

[Technology transfer](#)

[Coordination](#)

[WPs](#)

[Sequencing](#)

[Tool](#)

Welcome to MetaHIT website

MetaHIT is a project financed by the European Commission under the 7th FP program. The consortium gathers 13 partners from academia and industry, a total of 8 countries. Its total cost has been evaluated at more than 21,2 million € and the funding requested from the European Commission has been set with an upper limit of 11,4 million €. The project will last from January 1, 2008 until June 30, 2012.

Grant agreement ref.: HEALTH-F4-2007-201052

Starting date: January 1st, 2008

MetaHIT in brief!



Metagenomics of the Human Intestinal Tract
European research project

Budget

22 million euros

The 4 year program was financed in large part by the European Union under the 7th (7th Framework Programme).

Laboratories

8 countries
14 research & industrial

Institutions are involved in the consortium, with more than 50 research teams and companies between Europe and China.

The microbiota

The microbiota is an ecosystem composed of billions of bacteria that make up a vast "forest" (more 10¹⁴ cells). These bacteria colonize our digestive tract to form our intestinal microbiota (2kg for adults). MetaHIT focuses on the digestive tract since it is where the largest and most diversified bacterial community lives in our body.

INTRODUCTION

Since 2008, researchers with the European consortium MetaHIT have been studying the microbial diversity of the microbiota present in the human intestine.

RESEARCH

Observations
chronic

Research themes

Medicine: With the study of the

DEFINITION

follow us on



News

May 15, 2012

we just uploaded a **series of interviews** given during the International Human Microbiome Congress in Paris

Contact

[contact\(aro\)metahit.eu](mailto:contact(aro)metahit.eu)

MetaHIT
scientific coordinator:



Metagenomics
of the Human Intestinal Tract
European research project

INTRODUCTION

Since 2008, researchers with the European consortium MetaHIT have been analyzing the collected genomes of the microorganisms present in our intestine : the microbiota.

RESEARCH

Little understood until now, the intestinal microbiota interests researchers as an avenue of inquiry to explain the evolution of chronic diseases.

FINDINGS

The MetaHIT consortium published two major findings in the scientific journal Nature : an established catalog of bacterial genes in the intestine; and the discovery of enterotypes.

PERSPECTIVES

MetaHIT opens avenues for further efforts in the field of human microbiome research : early detection of chronic diseases, personalized medicine and more healthful food.

Budget

22 million euros

The 4 year program was financed in large part by the European Union under the FP7 (7th Framework Programme).

Laboratories

**8 countries
14 research & industrial**

institutions are involved in the consortium, with more than 50 researchers and cooperation between Europe and China.

The microbiota



The microbiota is an ecosystem composed of billions of bacteria that make up a veritable "organ." Within 24 hours of birth, these bacteria colonize our digestive tract to form our intestinal microbiota (2kg for adults). MetaHIT focuses on the digestive tract since it is where the largest and most diversified bacterial community lives in our body.

Observations



Observations made in the past 50 years cannot be solely explained by variations of our genome.

Research themes



Nutrition. Better knowledge of the intestinal microbiota of individuals will enable the nutritional needs to adapt to everyone's specific nutrient needs.

Medicine. With the study of the microbiota and the established catalogue of genes, we can have an unprecedented overview of the microbiota in healthy individuals and in patients. With the discovery of enterotypes we can imagine the upcoming development of new diagnostic or even prognostic tools for human health.

DEFINITION



*Enterotypes

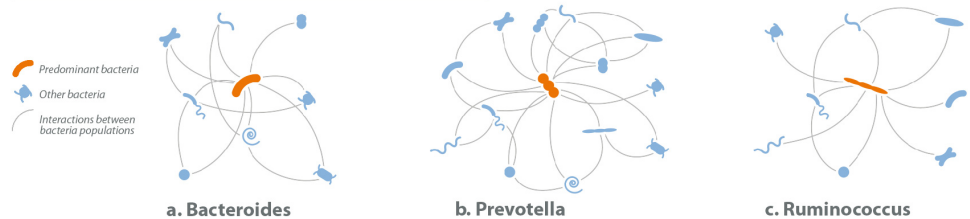
There are three in the world's population, each characterized by a predominant bacterial population.

Genome sequencing

3,3 million genes

The gut bacterial gene catalog, which can be compared to a *molecular scanner*, was established by metagenomic high throughput sequencing and allows the observation of the human gut microbiome.

Discovery of the 3 enterotypes*



Chronic diseases



Disturbances in the microbiota can be early warning signs for certain diseases like Crohn's disease or diabetes.

Nutritional impact

If it is possible to reveal early warning signs of obesity, one can imagine nutritional intervention and diet advice being used to reestablish a healthy microbiota. The possibility of intervening directly in the flora, in the case of disturbance to the intestinal ecosystem, could also be envisioned.

Personalized medicine



Classification by enterotype will help in the development of diagnostic tools able to reveal cases where a planned treatment would not be effective, and to adapt it accordingly.

You are what you ~~EAT~~ HOST



obes maketh man



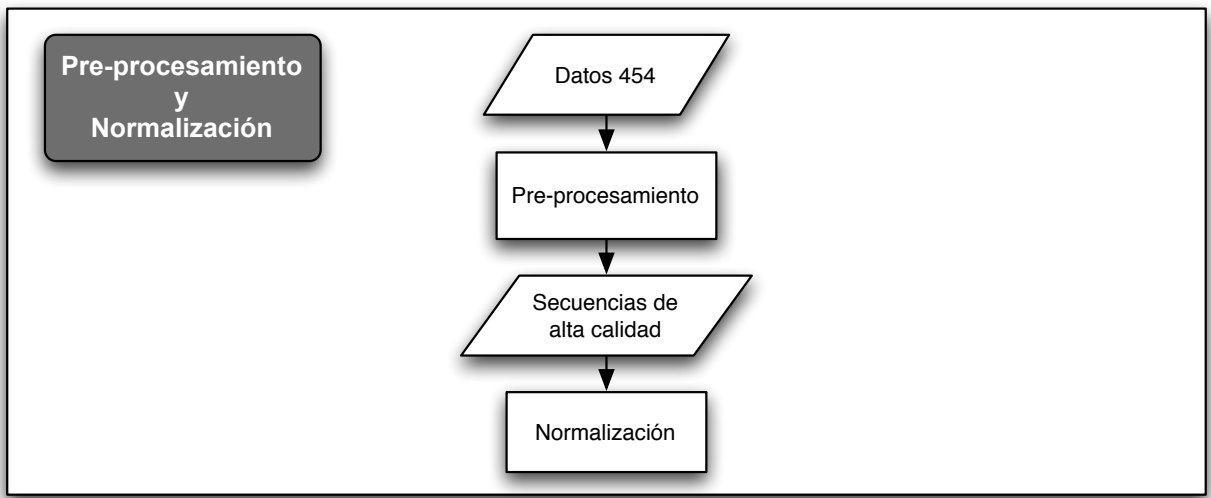
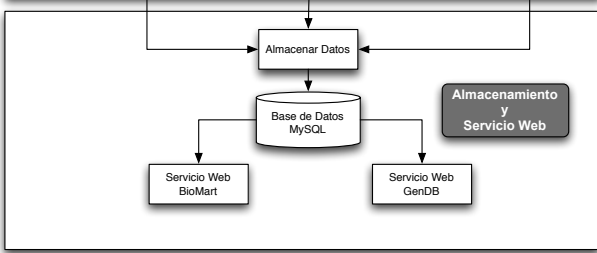
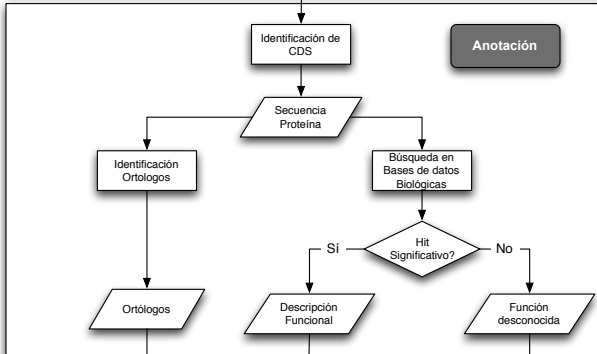
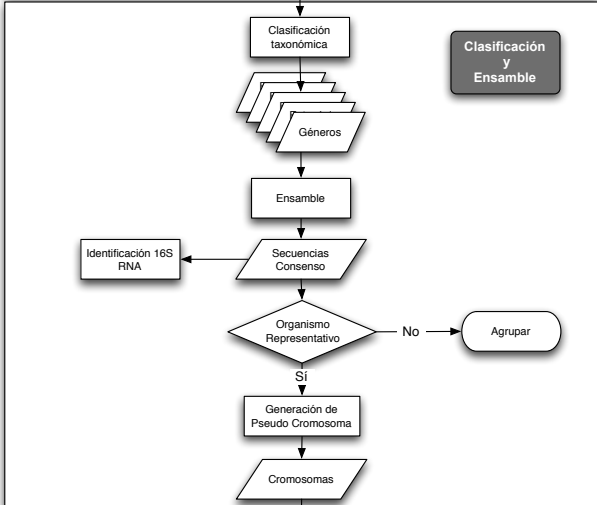
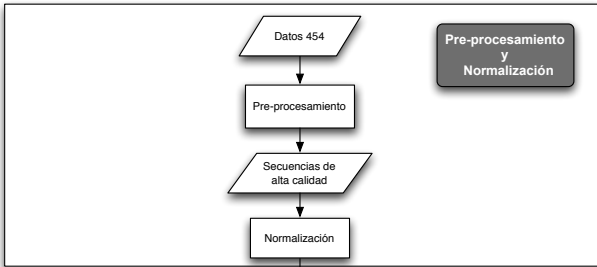
Impacts on Health

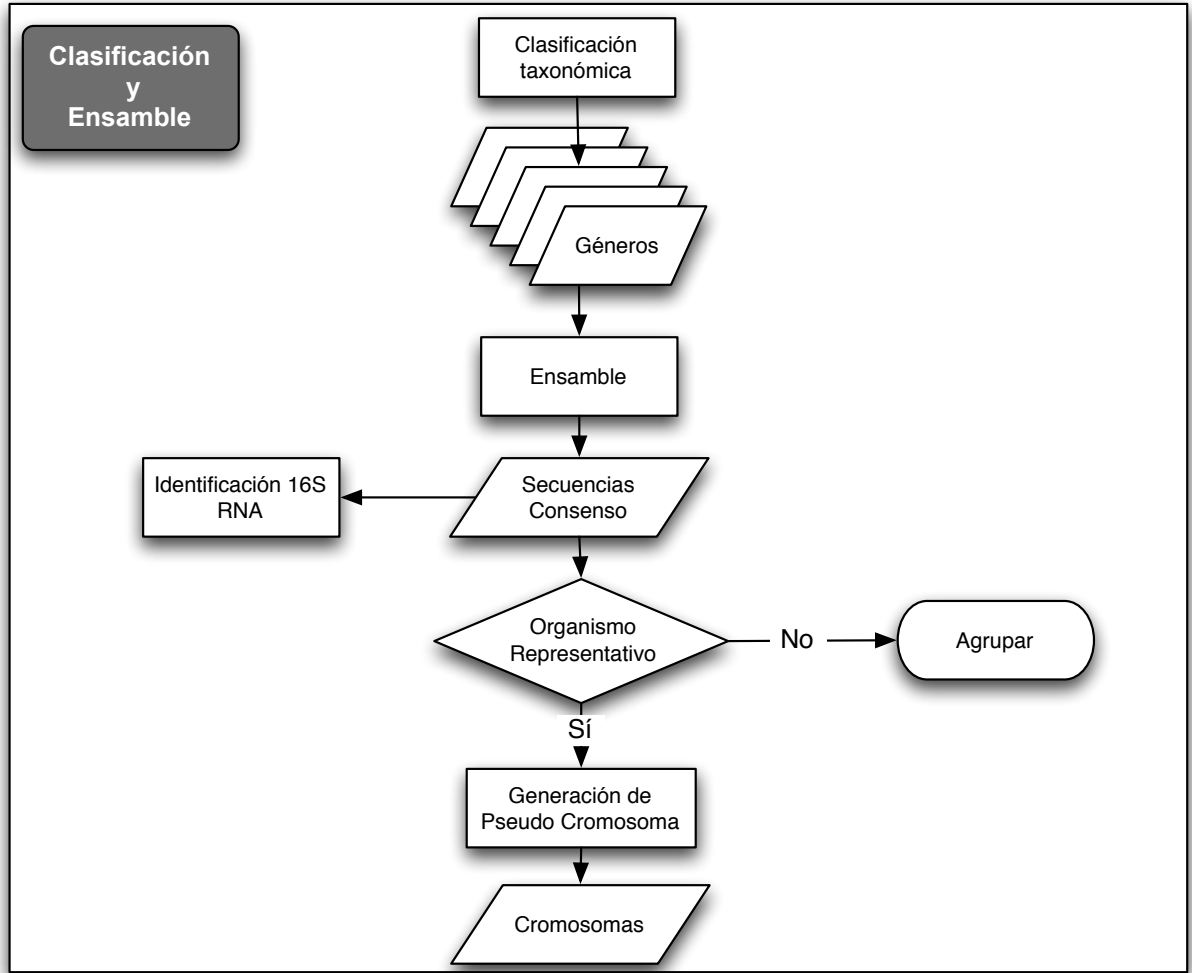
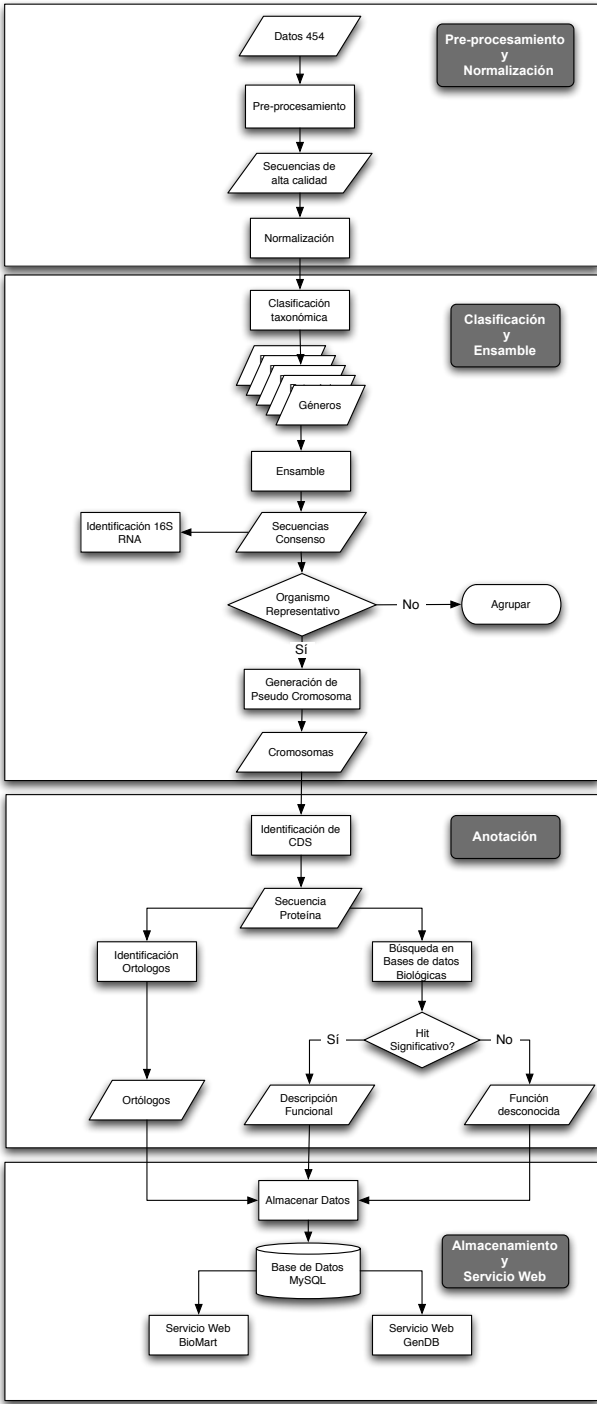
Fifteen demonstration projects have been funded to demonstrate hypothesized correlations between the microbiome and human health and disease. These investigator-initiated projects will leverage advances made by the HMP's large scale sequencing efforts, e.g. tool & technology development and protocol standardization, to examine the relationship between changes in the human microbiome and diseases of interest.

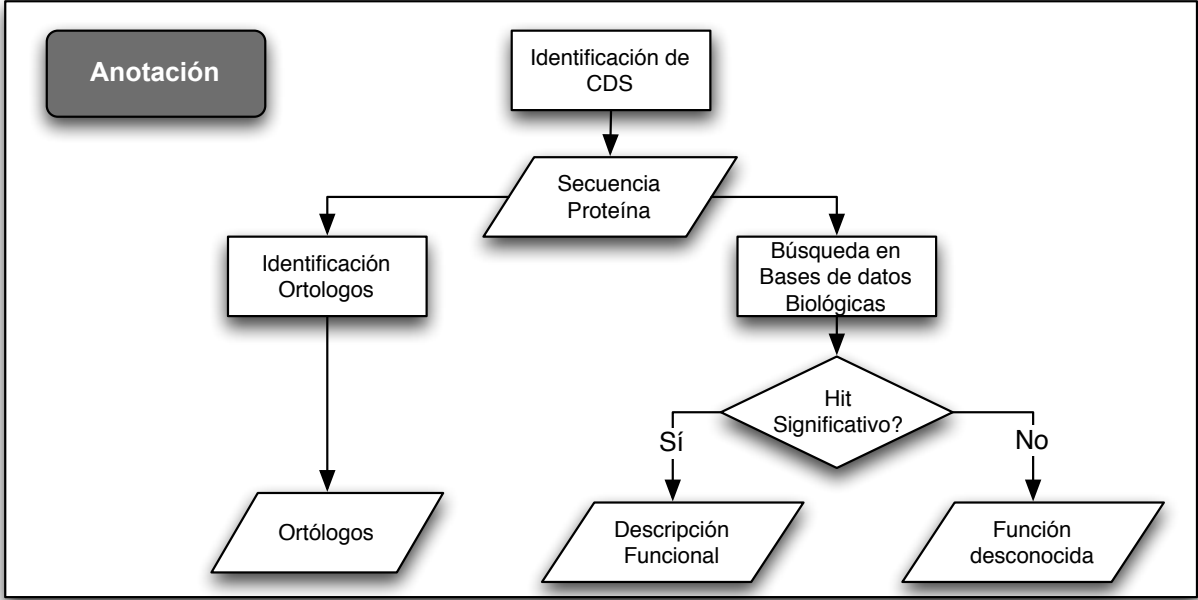
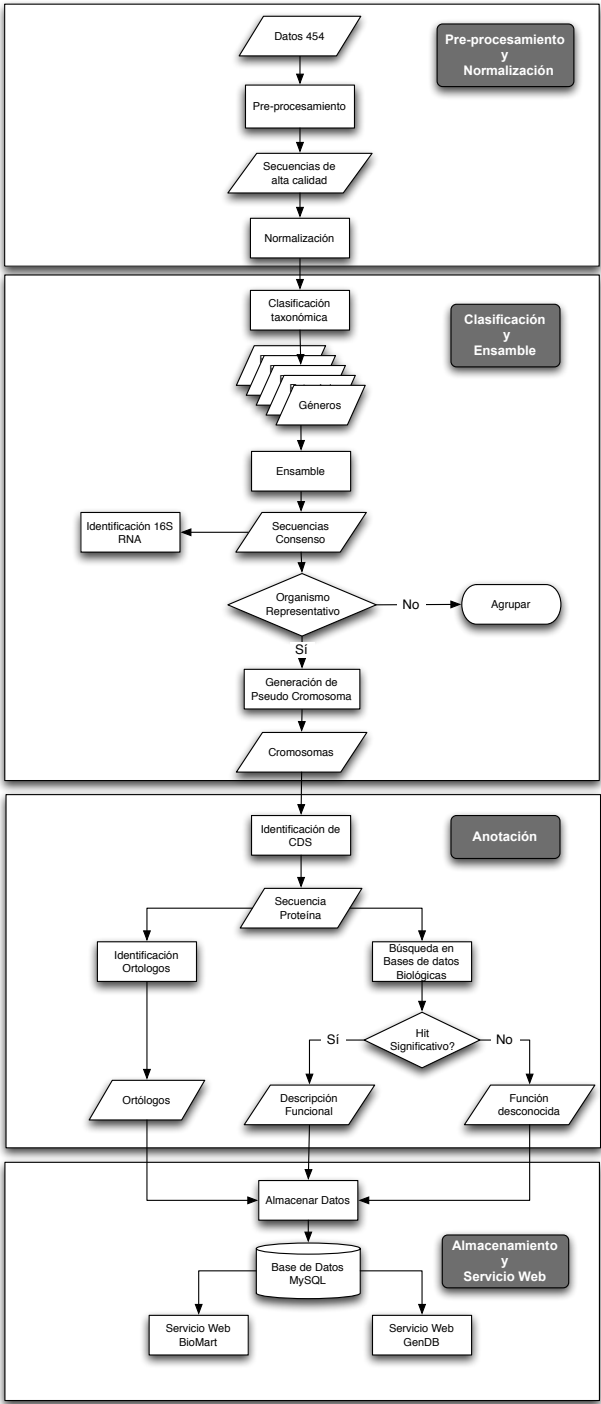
More information can be found by clicking on each project. Like the data being generated by the larger initiative, Demonstration project data is being submitted to public and controlled access areas of the NCBI sequence read archives.

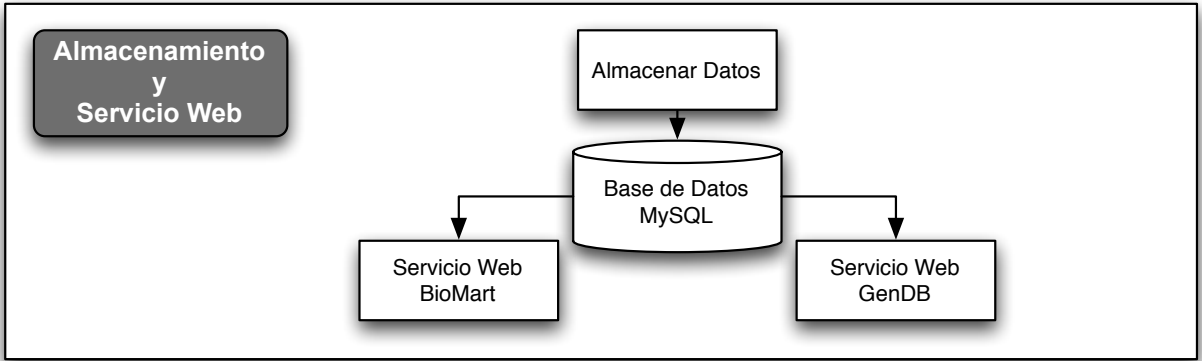
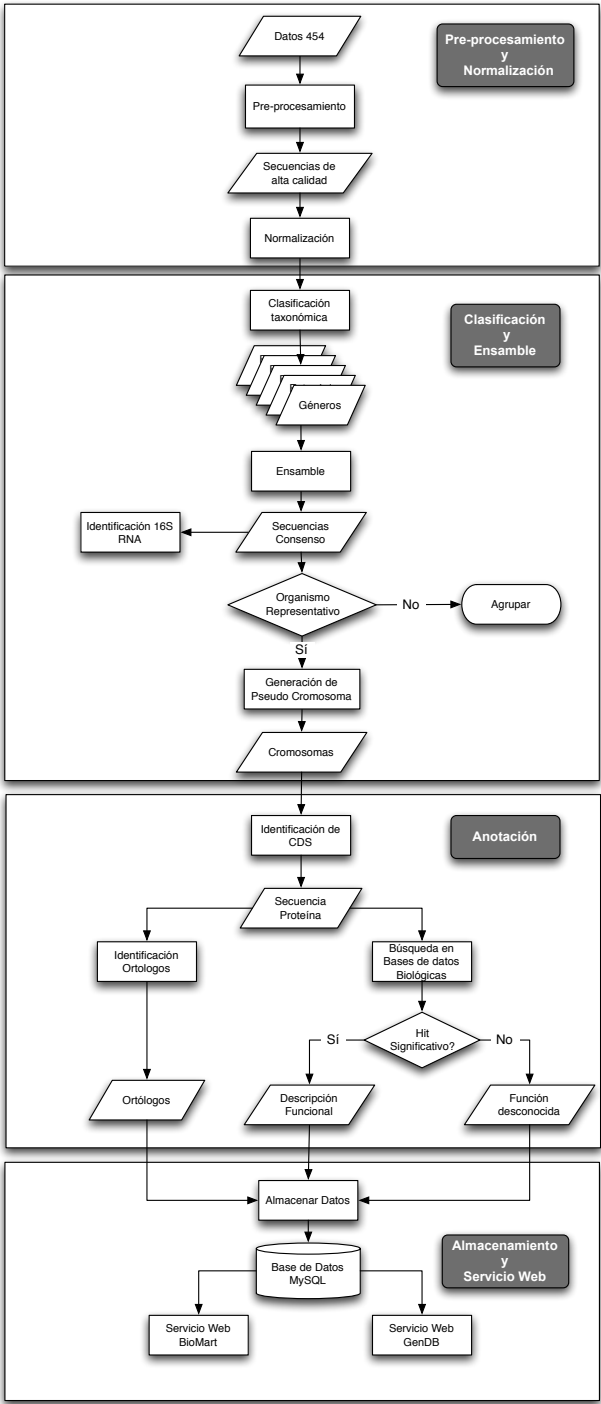
NCBI's HMP Demonstration Projects.

	Project Title	Principal Investigator(s)	Institution(s)
▶	Evaluation of the cutaneous microbiome in psoriasis	Martin J Blaser	New York University School of Medicine
▶	The Vaginal Microbiome: Disease, Genetics and the Environment	Cynthia Nau Cornelissen, Lindon J Eaves, Jerome Frank Strauss, Gregory A Buck	Virginia Commonwealth University
▶	Diet, Genetic Factors, and the Gut Microbiome in Crohn's Disease	Frederic D Bushman, James D Lewis, Gary D Wu	University of Pennsylvania
▶	The Role of the Gut Microbiota in Ulcerative Colitis	Eugene B Chang, Folker Meyer, Thomas M Schmidt, Mitchell L Sogin, James M Tiedje, Vincent B Young	University of Michigan at Ann Arbor
▶	Urethral Microbiome of Adolescent Males	Dennis J Fortenberry	Indiana University-Purdue University at Indianapolis
▶	The Thrifty Microbiome: The Role of the Gut Microbiota in Obesity in the Amish	Alan R Shuldiner, Claire M Fraser	University of Maryland Baltimore
▶	Metagenomic Analysis of the Structure and Function of the Human Gut Microbiota in Crohn's Disease	Claire M Fraser	University of Maryland Baltimore
▶	Effect of Crohn's Disease Risk Alleles on Enteric Microbiota	Ellen Li	Washington University
▶	Metagenomic study of the human skin microbiome associated with acne	Huiying Li	University of California Los Angeles







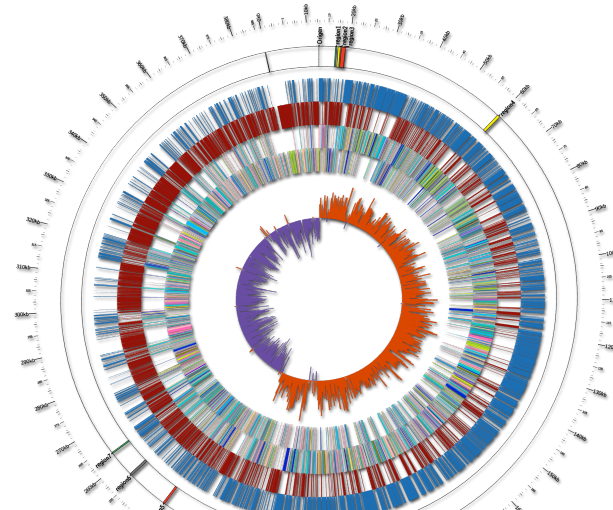
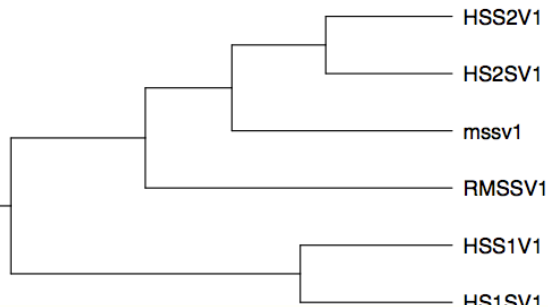


Datos 454

Pre-procesamiento
y
Normalización

Hierarchical Clustering Plot

data type:Kegg Pathway (EC) | level:super-pathway | distance matrix:bray | cluster method:average



Filter

Help *

Filter

Browse Kegg Pathways (EC)

Metabolism [2,331 hits]

Carbohydrate Metabolism [1,442 hits]

Energy Metabolism [867 hits]

Oxidative phosphorylation (pathway) [79 hits]

ubiquinol---cytochrome-c reductase. (1.10.2.2) (enzyme) [2 hits]

succinate dehydrogenase (ubiquinone). (1.3.5.1) (enzyme) [5 hits]

succinate dehydrogenase. (1.3.99.1) (enzyme) [4 hits]

NADH:ubiquinone reductase (H+-translocating). (1.6.5.3) (enzyme)

NADH dehydrogenase. (1.6.99.3) (enzyme) [2 hits]

NADH dehydrogenase (quinone). (1.6.99.5) (enzyme) [31 hits]

cytochrome-c oxidase. (1.9.3.1) (enzyme) [12 hits]

polyphosphate kinase. (2.7.4.1) (enzyme) [3 hits]

inorganic diphosphatase. (3.6.1.1) (enzyme) [4 hits]

H+/K+-exchanging ATPase. (3.6.3.10) (enzyme) [0 hits]

H+-transporting two-sector ATPase. (3.6.3.14) (enzyme) [16 hits]

H+-exporting ATPase. (3.6.3.6) (enzyme) [0 hits]

Photosynthesis (pathway) [22 hits]

Photosynthesis - antenna proteins (pathway) [235 hits]

Carbon fixation in photosynthetic organisms (pathway) [54 hits]

Carbon fixation pathways in prokaryotes (pathway) [323 hits]

Methane metabolism (pathway) [232 hits]

Nitrogen metabolism (pathway) [65 hits]

Sulfur metabolism (pathway) [19 hits]

Lipid Metabolism [1,404 hits]

Nucleotide Metabolism [332 hits]

Amino Acid Metabolism [1,169 hits]

Metabolism of Other Amino Acids [364 hits]

Glycan Biosynthesis and Metabolism [1,486 hits]

Metabolism of Cofactors and Vitamins [1,521 hits]

Metabolism of Terpenoids and Polyketides [1,401 hits]

Biosynthesis of Other Secondary Metabolites [1,852 hits]

Xenobiotics Biodegradation and Metabolism [1,617 hits]

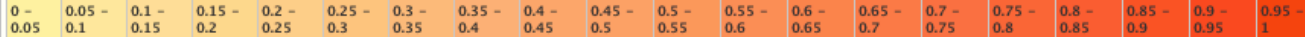
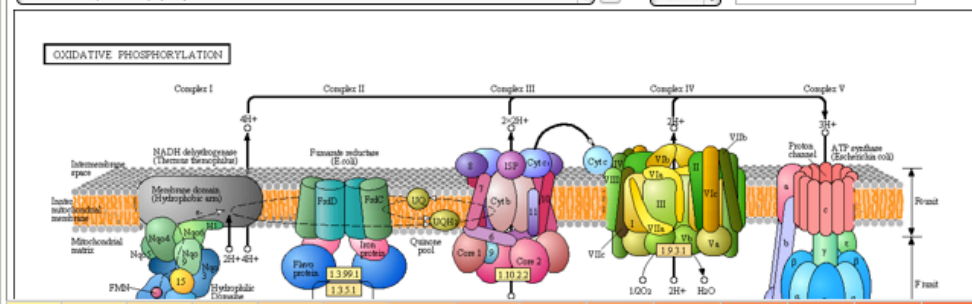
Genetic Information Processing [107 hits]

Pathway Classification

Oxidative phosphorylation

Reference pathway (EC)

100%



Enzymes Distribution

Rank	Enzymes	#Hits	%Hits	Bar Chart (% Found Enzymes)
1	NADH dehydrogenase (quinone). (1.6.99.5)	31	39.24 %	
2	H+-transporting two-sector ATPase. (3.6.3.14)	16	20.25 %	
3	cytochrome-c oxidase. (1.9.3.1)	12	15.19 %	
4	succinate dehydrogenase (ubiquinone). (1.3.5.1)	5	6.33 %	
5	inorganic diphosphatase. (3.6.1.1)	4	5.06 %	
6	succinate dehydrogenase. (1.3.99.1)	4	5.06 %	
7	polyphosphate kinase. (2.7.4.1)	3	3.8 %	
8	NADH dehydrogenase. (1.6.99.3)	2	2.53 %	
9	ubiquinol---cytochrome-c reductase. (1.10.2.2)	2	2.53 %	
10	H+-exporting ATPase. (3.6.3.6)	0	0 %	
11	H+/K+-exchanging ATPase. (3.6.3.10)	0	0 %	
12	NADH:ubiquinone reductase (H+-translocating). (1.6.5.3)	0	0 %	

Servicio Web
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GenDB

Herramienta 3

de