Future ISICR Meetings

Oct. 6 - 11, 2002
Torino, Italy
Joint ISICR/ICS/SLB/ECS
www.marionegri.it/cyto2002/

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Oct. 26 - 30, 2003
Cairns, Australia

•

Oct. 21-25, 2004
San Juan, Puerto Rico
(Joint with ICS)

ISICR WWW Site

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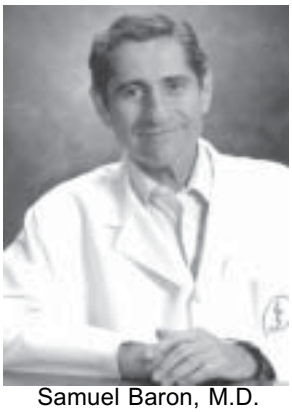
ISICR

INTERNATIONAL SOCIETY FOR INTERFERON AND CYTOKINE RESEARCH

August 2002
Volume 9, No. 3

An Interview with Dr. Samuel Baron
Thomas Tan


Samuel Baron, M.D.

Dr. Samuel Baron received his B.A. and M.D. from New York University. After postdoctoral research at the University of Michigan, he spent 20 years at the NIH. He served as Chairman of the Dept. of Microbiology and Immunology, Univ of Texas Medical Branch in Galveston for 22 years and is currently Professor, Department of Microbiology and Immunology and Internal Medicine at the Univ of Texas Medical Branch, Galveston. A long time ISICR member, Dr. Baron served as ISICR President (1992-1993) and was elected to honorary membership in 1998. He is currently ISICR Treasurer and serves on the ISICR Advisory Board and Board of Directors.
-- T.T.

You received both your BA in Biology and MD from New York University. Were you born in New York? I was born and lived in New York City for 25 years before moving to Ann Arbor, Michigan for postdoctoral training.

Were your parents born in the States? If not, did they settle down and find jobs here right away? My parents were born in Russia and immigrated to New York City when they were teenagers. They worked in the garment industry and raised 4 children.

Did your parents have a large formative influence on you? I believe that my parents influenced me greatly by placing a high value on education, social justice, and intellectual freedom.

When did you first become interested in science or Virology? Who was your role model in science? As an adolescent, I was fortunate in having some excellent science teachers who encouraged me to pursue my interest in science. My readings in fiction (e.g. *Arrowsmith*), science fiction, and non-fiction (*Microbe Hunters*) provided additional creative, idealistic role models. My later role models were various faculty, colleagues, and scientists that I was fortunate to work with – many are currently members of the IFN/Cytokine society.

see *Baron,* page 4

ISICR MEMBER, DR. SIDNEY PESTKA, RECEIVES U.S. NATIONAL MEDAL OF TECHNOLOGY

(Adapted from a Press Release from the University of Medicine and Dentistry of New Jersey-Robert Wood Johnson Medical School)

Dr. Sidney Pestka, professor and chairman of the Department of Molecular Genetics, Microbiology and Immunology at Robert Wood Johnson Medical School of the University of Medicine and Dentistry of New Jersey was awarded the National Medal of Technology.

President George W. Bush presented this award for scientific and technologic accomplishment to four individuals and one corporate recipient during a White House ceremony in June.

Dr. Pestka was cited for his "for pioneering achievements that led to the development of the biotechnology industry, to the first recombinant interferons for the treatment of cancers, leukemias, viral diseases such as hepatitis B and C, and multiple sclerosis; to fundamental technologies leading to other biotherapeutics; and for basic scientific discoveries in chemistry, biochemistry, genetic engineering and molecular biology from protein biosynthesis to receptors and cell signaling."

Dr. Pestka receives medal from President Bush.

The National Medal of Technology, which is the nation's highest achievement for technology, was established by Congress in 1980 and is administered by the U.S. Department of Commerce. It recognizes men and women who embody the spirit of American innovation and have advanced the nation's global competitiveness. The medal recognizes groundbreaking contributions that help commercialize technologies, create jobs, improve productivity and stimulate the nation's growth and development.

In congratulating Dr. Pestka, Dr. Harold L. Paz, dean of UMDNJ-Robert Wood Johnson Medical School, said "Dr. Pestka has been a leader among academicians in bringing achievements in research from concept to basic research to practical application. He has fostered new industries in multiple areas, and developed new medicines for previously untreatable diseases."

The award is based on a series of achievements that began in 1969 when Dr. Pestka began a project to determine what interferon was. He was enticed by the failure of numerous scientists to define interferon - a substance that held the possibility of curing viral diseases that had challenged the ingenuity of medicine for centuries. Such diseases – hepatitis, influenza, Ebola, Dengue, Yellow Fever, West Nile, and even the common cold – can be pandemics or dreaded fevers that kill over 90 percent of those infected.

"The possibility that a single medicine could treat all viral diseases was alluring," Dr. Pestka said, "After taking a few months to evaluate the scientific basis and potential of interferon, I decided to take the substantial risk and commit resources to pursue this research."

Seventeen years later, his dream was fulfilled when the interferon he developed was approved by the U.S. Food and Drug Administration (FDA) in 1986. During this period, Dr. Pestka made a remarkable series of discoveries and developments, often bucking prevailing beliefs and designing innovative solutions to problems along the way to success.

His achievements brought a portfolio of groundbreaking patents for Hoffmann-La Roche where he did the work at the Roche Institute of Molecular Biology. Dr. Pestka's efforts led to the commercialization of interferons to treat viral diseases, cancers and multiple sclerosis in the U.S. and around the world. His discoveries created new products and numerous jobs in the manufacture, production and treatment of diseases with interferon. The market for interferon today is over a $5 billion.

In addition to interferon's commercial impact, there was no general antiviral therapy available before Dr. Pestka began his work on interferon; today, interferon is the first and only general antiviral therapy. Interferon is used to treat hepatitis B and C, diseases which have been diagnosed in more than 300 million people worldwide. Interferons are used for the treatment of cancers such as malignant melanoma and bladder cell carcinoma, some leukemias, AIDS-related Kaposi's sarcoma, and multiple sclerosis. Interferon is a major product of several U.S. companies and foreign companies, including Schering-Plough, Hoffmann-La Roche, Amgen, Biogen and Berlex.

Dr. Pestka's breakthroughs have made an enormous impact on the biotechnology and pharmaceutical industries and on the development of new biotherapeutics for medicine. His work is the basis of several U.S. and more than 100 foreign patents. Dr. Pestka has been professor and chairman of the Department of Molecular Genetics, Microbiology and Immunology at UMDNJ-Robert Wood Johnson Medical School in Piscataway since 1986. ISICR

Clinical Trials

Study ID Numbers 199/16459; MSKCC-01128; NCI-G01-2049 Bexarotene and **Interferon alfa** in Treating Patients With Cutaneous T-Cell Lymphoma Memorial Sloan-Kettering Cancer Center, New York, New York Contact: David J. Straus 212-639-8365

Study ID Numbers 199/12531; MDA-DM-96296; NCI-G97-1206 **Interferon alfa** in Treating Patients With Recurrent Unresectable Meningiomas and Malignant Meningiomas University of Texas - MD Anderson Cancer Center, Houston, Texas, Contact: Wai-Kwan Alfred Yung 713-794-1285

Study ID Numbers 020193; 02-C-0193 A Phase II Study of Pegylated **Interferon Alfa 2b** (PEG-Intron™ (Trademark)) in Children with Diffuse Pontine Gliomas National Cancer Institute (NCI), Bethesda, Maryland Contact: Patient Recruitment and Public Liaison Office 1-800-411-1222 prpl@mail.cc.nih.gov

Study ID Numbers 020072; 02-DK-0072 **Gamma Interferon** Therapy for Chronic Hepatitis C National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK), Bethesda, Maryland Contact: Patient Recruitment and Public Liaison Office 1-800-411-1222 prpl@mail.cc.nih.gov

Study ID Numbers 1100-471 Phase II Trial of Monoclonal Antibody (J591) in Combination with Low-Dose Subcutaneous **Interleukin-2** New York Presbyterian Hospital Medical Oncology/Urology Clinics, New York, New York Contact: Marta Cobham, R.N. 212-746-2920

Study ID Numbers ACTG A5102; AACTG A5102; Substudy AACTG A5109s A Study to See Whether **Interleukin-2** Used with Potent Anti-HIV Drugs Allows for Longer Breaks in Anti-HIV Drug Treatment Stanford Univ Med Ctr, Stanford, California, Contact: Debbie Slamowitz 650-723-2804

Study ID Numbers 199/16280; COG-ANBL0032; COG-P9842 Isotretinoin With or Without Monoclonal Antibody, **Interleukin 2**, and **Sargramostim**

New ISICR Members

The ISICR welcomes the following new members to the society. We look forward to their active participation in the Annual Meeting and on those ISICR committees that they wish to serve. (Please contact ISICR President Dr. Keiko Ozato regarding committee membership. Volunteers are always welcome and needed!!!).

Mukesh K. Agarwal
Cleveland, OH

Jesper B. Anderson
Aarhus, Denmark

Iain L. Campbell
La Jolla, CA

Judith A. Connett
St. Louis, MO

Samuel J. Cutler
Melbourne, Australia

M Jane Ehrke
Buffalo, NY

Eileen M Foy
Dallas, TX

Jun Ichi Fujisawa
Moriguchi Osake, Japan

Miki Hiroi
Sakado Saitama, Japan

Dong-Liang Hu
Hirosaki Amori, Japan

Irene I Lan Hwang
Toronto, Canada

Donald M Nicolsow
Midlothian, UK

Venky Ramakrishna
Charlottesville, VA

Hirotake Sakuraba
Hirosaki Aomori, Japan

Sanae Sasaki
Hirosaki Amori, Japan

Hiroshi Sashinami
Hirosaki Amori, Japan

Lynnette H. Shorts
Frederick, MD

Edward G. Spack
Brisbane, CA

Jianping Wang
La Jolla, CA

Zdenek Zidek
Prague, Czeh Slovak

Famous Quotes

"Wisdom doesn't necessarily come with age. Sometimes age just shows up all by itself."

Tom Wilson

~

"Every person is a fool for at least five minutes a day; wisdom consists in not exceeding the limit."

Elbert Hubbard

Baron, from page 1

My interest in Virology began when I was a student at NYU School of Medicine. I volunteered as a student in the Department of Microbiology and thus I began my studies in immunopathogenesis of infectious diseases.

Whose lab did you work in at the University of Michigan and what was your research project? During postdoctoral training at the University of Michigan, I worked in the Virology lab under the general guidance of Thomas Francis, Jr., who demonstrated the efficacy of the Salk vaccine in human trials. The laboratory also studied influenza virus and its vaccines. My research contribution, at that time, was the demonstration that genetic recombination occurs among animal viruses. This was published simultaneously with Burnet in Australia.

Was there anybody else around that time that had a very large influence on you? At the University of Michigan there were a number of excellent colleagues who strongly influenced me by teaching me the tools and concepts of virology and immunology as well as emphasizing novelty, significance, and seeking definitive answers to hypotheses.

What was your experience at NIH like? And what made you choose to move to UTMB? At the NIH, I had the freedom to engage in truly exciting studies of polio vaccine, immunity to viruses and interferon. While at the NIH, I spent a sabbatical year (1959) in London with Alick Isaacs and his colleagues, who influenced me greatly. Perhaps my most important contributions were the new concepts of innate and adaptive immunity that was first published in Advances in Virus Research in1963. In Isaac's lab the scientific values of novelty, simplicity, decisiveness, as well as enthusiasm, were emphasized. In 1975, I moved to UTMB because, at that particular time, there was an unusual opportunity to establish a strong Department of Microbiology and Immunology.

You received the Samuel Baron Distinguished Professorship in Microbiology. How did you feel about receiving an honor named after you? The naming of a professorship after me was very gratifying in that it recognized important career contributions.

What are currently your concerns and priorities for your department at UTMB? I stepped down from the Chair of Microbiology after 22 years and am currently involved in the studies of the immunopathogenesis and host defenses during HIV and smallpox infections. In a recent publication, we explained why oral transmission of HIV is rare. Unexpectedly, this is due to a new defense mechanism in saliva. I am also studying the role of interferon during poxvirus infections, including the prevention and treatment of smallpox using cell culture and animal models.

How long have you worked in the IFN field? How did you come to this work? I began working in the interferon field in 1959 during my sabbatical year in London, when I worked with Alick Isaacs (who was the co-discoverer of interferon with Lindenmann). It was there that we focused on the potential of IFN as a natural defense and therapy. These studies addressed the challenge of providing sufficient evidence to convince a skeptical scientific community.

Are you pleased with the directions we are heading in interferon research? Are you still optimistic about the therapeutic potential of IFN in viral infections? In my view, the interferon field seems to be headed in positive directions. As a biologist, I would like to see more cellular and whole animal studies being done to help determine the validity and significance of the many molecular findings. As noted, my current studies support the therapeutic potential of IFN and IFN inducers to combat a bioterroist attack with smallpox virus. In addition, we are studying the therapeutic potential of innate defenses against HIV. Thus I continue to be optimistic about the potential of IFN.

What do you see as the major differences between doing research today as compared with your early days? As we all recognize, we currently have many new tools, increased support, and many excellent scientists. Rapid communication and transportation have facilitated and accelerated worldwide collaboration. An important concern is the fact that scientists must divert so much of their creative time writing grants and seeking support.

What is your wife's name? My wife is Phyllis G. Baron, a reading teacher and wise confidant for over 50 years.

How old are your children? My 5 children whose ages range from 38-48, are engaged in science, public policy, law, and remodeling homes. We are fortunate to have 11 grandchildren who seem to be heading in the right direction.

What are some of your interests or hobbies? Outside the laboratory, my interests include the theater, travel, keeping abreast of developments in politics, economics, and the physical and social sciences, including the philosophical considerations.

What kind of priorities do you have in life, what goals today? My priorities are to continue to contribute through new knowledge by trying to ask new and significant questions and answer them decisively. Being a caring and interested spouse, father, and grandfather are of equally high priority. I am pleased with the variety of interests and rapidly expanding opportunities available to all of us.

What do you think is your greatest accomplishment?
I believe my most important scientific accomplishment has been my research on new concepts of nonspecific or innate immunity during viral infections. I believe that my research is that area provided the first clear delineation of the separate roles of innate and adaptive immunity during recovery from viral infections. In providing the specific examples below, I recognize the inclination of most of us to overstate our roles, and that other scientists have made parallel discoveries. These examples are research done in collaboration with outstanding scientists. They are: the body's initial IFN defense against viruses is clearly distinct from the specific immune defense and precedes it by several days; deletion of IFN substantially increases the virulence of viruses; IFN can circulate in plasma and provide systemic protection against viremia; the IFN system can be activated within minutes; the IFN-protected cell can account for the elimination of the large numbers of viruses from infected tissues during recovery from infection; IFN modulates chronic virus infections like rubella and LDV; induction of IFN by bacteria; inhibition of bacterial infection by IFN; IFN inhibits myasthenia gravis in an animal model; IFN modulates humoral immunity; the IFN system matures in the developing embryo; protein translation and protein kinase are mechanisms of IFN action; identification of viral molecular triggers of IFN production; and a new definition of the RNA load during HIV infections. It is pleasing to know that some of these concepts are now part of the accepted body of knowledge.

Another important accomplishment is that I, along with others helped keep the interferon field progressing during the years when it was rejected by many scientists.

Outside of science, my most satisfying accomplishments are my happy and intellectually fulfilling 50-year marriage, as well as seeing my children grow into fine, successful, contributing adults and parents.

What advice would you pass along to young scientists today? My basic advice to young scientists is to keep in mind that great advances in society most often are brought about by introducing new concepts — contagion, microbes, immunity, evolution, antibiotics, electromagnetism, astronomy and genetics, to name a few. It may be important to note that while some of these discoveries are costly and complex, many seminal discoveries are inexpensive and simple. Passion for the work and joy of discovery may be important prerequisites for the job because there are many bumps along the road. ISICR

Are you looking for partners to help with your research or to have a new product tested in basic research labs? The ISICR newsletter will now include a new feature on "Partnerships.' Any Academic, Government or Commercial organization that is looking for research partners is encouraged to send us a description of the type of partnerships desired. Those descriptions deemed suitable for the newsletter will be included in the upcoming issue. Note that we will not include fee for service requests nor will we post advertisements of company products.

Impact of Salivary Cytokine Contamination on Cytokine ELISAs

Data provided courtesy of R & D Systems, Minneapolis, Minnesota

A number of studies have documented the presence of endogenous levels of cytokines and related molecules within saliva.1-3 When an analyte is present within an operator's saliva, a cough, sneeze, or even speaking while running an ELISA can affect the overall results. For example, cytokines derived from saliva may impact assay precision. As a result, it is important to take the necessary precautions to prevent saliva-borne analyte contamination of the plate.

R&D Systems' Quantikine® ELISA development team routinely screens saliva samples during the assay development process. During the development process for the Quantikine human CCL28 ELISA, the potential effects of cytokine contamination from operator saliva on assay performance was assessed (see figure 1). These results underscore the importance of taking the necessary precautions to prevent salivary cytokine contamination when running these ELISAs.

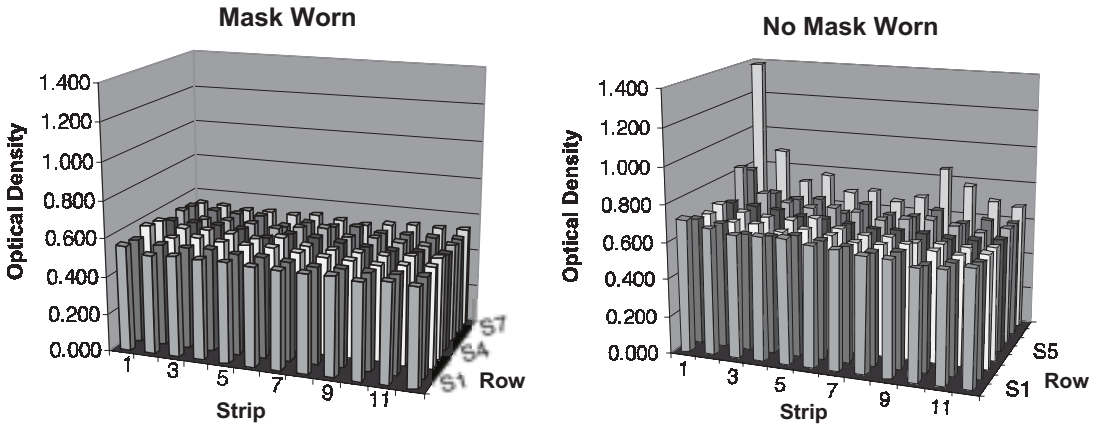


Figure 1. The plate on the left was run by an operator wearing a mask, while the plate on the right was run by an operator without a mask and talking while running the assay (note: both plates were run with the same mid-level standard).

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Levels of Additional Analytes Found in Saliva

Analyte	Mean (pg/mL)	Range (pg/mL)
IL-8	817	122 – 1,590
IP-10	729	292 – 1,340
MMP-7	14,700	3,800 – 28,300
MMP-9	201,000	102,000 – 543,000
PDGF-AA	353	86 – 745
TIMP-1	121,000	46,000 – 208,000
TIMP-2	16,000	10,000 – 22,000
sVEGF R1	280	119 – 577
CCL28	47,846	21,900 – 68,200

Clinical Trials, cont'd.

Following Stem Cell Transplantation in Treating Patients With Neuroblastoma Children's Hospital Los Angeles, Los Angeles, California Contact: Robert Charles Seeger 323-669-5618

Study ID Numbers 199/16483; NBI-3001-ST-0101; NCI-V02-1692; UARIZ-HSC-01196; UCLA-0108085 Intravenous **Interleukin-4 PE38KDEL Cytotoxin** in Treating Patients With Recurrent or Metastatic Kidney Cancer, Non-Small Cell Lung Cancer, or Breast Cancer Arizona Cancer Center, Tucson, Arizona, Contact: Linda Garland 520-626-3434; Jonsson Comprehensive Cancer Center, UCLA, Los Angeles, California, Contact: Robert Alan Figlin 310-825-5788

Study ID Numbers 010155; 01-I-0155 **Anti-Interleukin-5 Antibody** to Treat Hypereosinophilic Syndrome National Institute of Allergy and Infectious Diseases (NIAID), Bethesda, Maryland, Contact: Patient Recruitment and Public Liaison Office 1-800-411-1222 prpl@mail.cc.nih.gov

A Multicenter, Randomized, Double-Blind, Placebo-Controlled, Dose-Escalating, Safety and Exploratory Pharmacogenomic Study of Orally Administered Recombinant Human **Interleukin Eleven (rhIL-11)** in Patients With Mild to Moderate Left-Sided Ulcerative Colitis. Contact: Daniel Pambianco, MD, Charlottesville Medical Research, Charlottesville, VA Tel: 804-817-8484

Study ID Numbers 199/15809; UCCRC-9845; NCI-1192 Vaccine Therapy Plus **Interleukin-12** in Treating Patients With Metastatic Prostate Cancer That Has Not Responded to Hormone Therapy University of Chicago Cancer Research Center, Chicago, Illinois Contact: Thomas F. Gajewski 773-702-4601

Study ID Numbers 199/16378; WCCC-CO-9771; NCI-T98-0025; WCCC-HSC-1998-257 **Interleukin-12** Gene Therapy in Treating Patients With Skin Metastases University of Wisconsin Comprehensive Cancer Center, Madison, Wisconsin Contact: Paul M. Sondel 608-263-9069

Study ID Numbers 000168; 00-D-0168 **Etanercept** (Enbrel) to Treat Pain and Swelling After Third Molar Extraction National Institute of Dental And Craniofacial Research (NIDCR), 9000 Rockville Pike Bethesda, Maryland Contract: Patient Recruitment and Public Liaison Office 1-800-411-1222 prpl@mail.cc.nih.gov

Study ID Numbers 199/14117; ACOSOG-Z0020 Melphalan With or Without **Tumor Necrosis Factor** in Treating Patients With Advanced Melanoma of the Arm or Leg University of Pennsylvania Cancer Center, Philadelphia, Pennsylvania Contact: Douglas L. Fraker 215-662-7866 ISICR

THANK YOU

Mrs. Vivian Milstein and the Milstein Foundation

for your continuing support of the ISICR!!!

Reviews of Interest

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ISICR

Center for Computational Biology
http://www.cudenver.edu/ccb/

The Human Genome Project has transformed molecular biology into an information science. A science that was once data poor now has so much data that new methods of computation are needed to obtain useful information from the data banks that have emerged. Content-based searches for proteins, genes, and other elements require large-scale modeling, analysis and algorithm design. To meet this new challenge, The University of Colorado at Denver and the UC Health Sciences Center have launched the Center for Computational Biology (CCB).

This is an interdisciplinary structure, bringing together researchers in biology and other natural sciences, medicine, computer science, mathematics, and statistics. The CCB acts as matchmaker in arranging new collaborations. The CCB has a second mission: to create courses and programs in computational biology, drawing from resources at CU-Denver and the Health Sciences Center.

While the primary missions are research and education, the CCB approach fosters unification in at least three dimensions. First, research and education is integrated, giving new opportunities to students and faculty. Secondly, UCD and HSC have strengthened their ties by forming this partnership and working collaboratively, bringing complementary strengths to the projects. Third, connections with industry and government serves to unify efforts to share knowledge with those who can bring research results to people. Please visit our website and participate in our activities, notably our workshops.

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CpG islands
http://www.uscnorris.com/cpgislands

We are pleased to announce the availability of our search algorithm for CpG islands which can be accessed at http://www.uscnorris.com/cpgislands. Sequences of up to 50kb can be submitted and CpG islands parameters selected to search for CpG islands. The program is easy to use and the default values (%GC >55%, ObsCpG/ExpCpG >0.65, length >500bp) are the ones described in our paper [Takai and Jones, PNAS 99(6): 3740-5, 2002], but can be easily modified. Please contact takai_d@ccnt.hsc.usc.edu if you experience any problems.

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GENE QUANTIFICATION
http://www.wzw.tum.de/gene-quantification/

Main focus of GENE QUANTIFICATION web page is to describe and summarize all technical aspects involved in quantitative gene expression analysis using real-time (RT-) PCR. (specificity, sensitivity, reproducibility, intra- and inter-assay variations, etc.)

The GENE QUANTIFICATION web page illustrates the usefulness of a reliable quantification strategy, and the difference between absolute vs. relative quantification assays in real-time (RT-) PCR.

RT-PCR is the technique of choice for analysing mRNA in extremely low abundance. Real-time RT-PCR using SYBR Green I detection combines the ease and necessary exactness to be able to produce reliable as well as rapid results.

To obtain high accuracy and reliability in RT and real-time PCR highly Defined quantification strategies and methods are needed.

http://www.wzw.tum.de/gene-quantification/ content:

- Real-time (RT-) PCR and optimisation !!!
- Available real-time PCR platforms
- Description of quantification strategies in real-time (RT-) PCR
- Description of absolute quantification and relative quantification
- REST © (Relative Expression Software Tool ©)
- Housekeeping Gene problematic in real-time PCR (under construction !!)
- Verification of array results via kinetic RT-PCR (under construction !!)
- Comparison of real-time RT-PCR versus competitive RT-PCR
- Download of software tools (e.g. REST ©)
- Summary of relevant literature
- Summary of relevant links

Dr. Michael W. Pfaffl
http://www.wzw.tum.de/gene-quantification/

iProClass Integrated Protein Classification Database
http://pir.georgetown.edu/iproclass/

The iProClass is an integrated resource that provides comprehensive family relationships and structural/functional features of proteins, with rich links to various databases. It currently consists of more than 210,000 non-redundant proteins organized with more than 29,000 superfamilies, 2600 domains, 1300 motifs, 280 post-translational modification sites, and links to more than 30 databases of protein families, structures, functions, genes, genomes, literature, and taxonomy. Protein and superfamily summary reports provide rich annotations, including membership information with length, taxonomy, and keyword statistics, full family relationships, comprehensive enzyme and PDB cross-references, and graphical feature display. The iProClass is implemented in Oracle 8i object-relational system, and can facilitate classification-driven annotation for protein sequences and complete genomes, and support structural/functional genomics and proteomics research.

The database has three major features:
integration, comprehensiveness, and annotation, as outlined below. Example protein and superfamily summary reports are available at: http://pir.georgetown.edu/iproclass/RPTPex.html and http://pir.georgetown.edu/iproclass/RPTFex.html

See *WWW*, page 10

WWW, from page 9

A. Integration:
- Integration of superfamily, domain and motif classifications
- Integration of protein sequence, function, and structural classes

B. Comprehensiveness:
- Protein Sequence Data: non-redundant PIR and SwissProt proteins (>210,000 total, 58% PIR unique, 32% PIR-SwissProt redundant, 10% SwissProt unique)
- Family and Alignment Data: PIR superfamilies (>29,000) MIPS families and ProtFam alignments (>100,000) PIR homology domains and PIR-ALN alignments (>380) Pfam domains (>2250) ProSite motifs and ProClass motif alignments (>1300) PIR-RESID post-translational modifications (>280) PIR-ASDB FASTA similarity clusters of all PIR proteins (>195,000)
- Cross-References: Links to >30 databases of Protein Sequence: PIR-PSD, SwissProt, TrEMBL, GenPept Family: PIR-ASDB, PIR-ALN, MIPS-ProtFam, ProClass, Pfam, ProSite, Blocks, Prints, COG, MetaFam Protein Enzyme/Pathway: KEGG, BRENDA, WIT, EcoCyc Protein Structure and Structural Class: PDB, SCOP, CATH, PIR-RESID Genes/Genome: GenBank/ EMBL/DDBJ, TIGR, UWGP, SGD, Flybase, MGI, GDB, OMIM

Literature: Medline
Taxonomy: NCBI Taxonomy

C. Annotation: Annotated protein entries and curated sets of PIR superfamilies/homology domains, Pfam domains, ProSite/ProClass motifs, and PIR post-translational modification sites

The current version of iProClass (beta-release, 10/2000) is based on the PIR-International Protein Sequence Database (PIR-PSD) Release 66.0 (09/00), SwissProt 39.0 (05/00), TrEMBL 14.0 (06/00), Pfam 5.4 (06/00), BLOCKS 12.0 (06/00), PRINTS 27.0 (04/00), PROSITE 14.0 (07/99), PDB (07/00), and COG (01/00).

The work is supported in part by NSF Grant# DBI-9974855 and NIH Grant#P41 LM05798.

Please contact Cathy Wu at wuc@nbrf.georgetown.edu for any comments, and for inquiries regarding obtaining free copies of the iProClass database or setting up reciprocal links or mirror sites.

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JMV Molecular Viewer
http://www.ks.uiuc.edu/Development/jmv/

The Theoretical Biophysics Group at the University of Illinois is proud to announce an exciting new feature of BioCoRE, a Biological Collaborative Research Environment. BioCoRE is freely accessible at the Theoretical Biophysics Group website and development is supported by the NIH National Center for Research Resources.

JMV
http://www.ks.uiuc.edu/Development/jmv/

Version 1.0 can now be accessed from within BioCoRE.

JMV, a molecular viewer written using Java and Java 3D, can be used to view molecular files stored within the BioFS, BioCoRE's shared filesystem. JMV provides several molecular representations, multiple coloring styles, lighting controls, and stereoscopic rendering capabilities. Version 1.0 of JMV is currently only available within BioCoRE, and a standalone release is upcoming.

In addition, several other BioCoRE components have seen key improvements recently:

* certificates)
* BioCoRE job management can now upload files to the remote supercomputer center of your choice before submitting a job. This allows researchers to keep their input files in the BioCoRE shared filesystem and let BioCoRE automatically stage the files.

For details, please visit the BioCoRE website at http://www.ks.uiuc.edu/Research/biocore/.

The Theoretical Biophysics group encourages BioCoRE users to be closely involved in the development process through reporting bugs, contributing fixes, periodical surveys and via other means. Questions or comments may be directed to biocore@ks.uiuc.edu.

Mouse Genome Data
http://www.ncbi.nlm.nih.gov./genome/guide/mouse/

The Mouse Genome Sequencing Consortium (MGSC) has recently released the assembly of the mouse (strain C57BL/6J) Whole Genome Sequence (WGS) data. This assembly contains sequence data corresponding to 6.4X coverage (if the genome is 3 Gb) to 7.7X coverage (if the genome is 2.5 Gb). Based on initial estimates this asssembly appears to be of very high quality.

This assembly, can be accessed at the following Web sites:

Access to this assembly can be obtained in several ways (Note this assembly is generally referred to as MGSC version 3 or the Feb. 2002 freeze):

- http://genome.ucsc.edu/
- http://www.ncbi.nlm.nih.gov./genome/guide/mouse/ (Blast against MGSCv3)
- http://www.ensembl.org/Mus_musculus/

For those interested in doing Comparative genomics the following sites should be investigated:

- http://www-gsd.lbl.gov/vista/
- http://bio.cse.psu.edu/pipmaker/

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301-402-3044

(More) Famous Quotes

"The tragedy of life is what dies inside a man while he lives."

A. Einstein

~

"A person that learns from their mistakes is smart. A person that learns from other people's mistakes is smarter."

Unknown

PFAM RELEASE 7.0
http://www.sanger.ac.uk/Software/Pfam/

Pfam is a collection of protein domain family alignments which were constructed semi-automatically using profile hidden Markov models. Pfam families contain functional annotation and cross-references to other databases. Query sequences can be searched against the Pfam library of profile hidden Markov models at the web sites below.

Pfam 7.0 contains 3360 families. 69% of proteins in SWISSPROT 40 and TrEMBL 18 have at least one match to a Pfam family.

For interactive access and searching see URLs

- http://www.sanger.ac.uk/Software/Pfam
- http://pfam.wustl.edu
- http://www.cgr.ki.se/Pfam

The release is also available in flat file by anonymous ftp:

- ftp://ftp.sanger.ac.uk/pub/databases/Pfam/
- ftp://ftp.genetics.wustl.edu/pub/Pfam/
- ftp://ftp.cgr.ki.se/pub/data/Pfam/

The Pfam HMM library is compatible with HMMER2 software, available from http://hmmer.wustl.edu/ and also the Wise2 software, available from http://www.sanger.ac.uk/Software/Wise2/.

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Protein annotation
http://www.bmm.icnet.uk/3dgenomics/

The database has a focus on protein structure (SCOP doamins). These are the main features:

- general overview of the annotation status of a particular genome
- assignment of SCOP superfamilies to genomes
- comparison of occurence and frequencies of SCOP superfamilies in different genomes
- SCOP superfamilies in globular parts of membrane proteins in different genomes
- PFAM, SwissProt, PIR assignments + text search of annotation
- annotation of protein from human disease genes
- a detaild report for each processed protein sequence, including:
- prediction of transmembrane, coiled-coil and low complexity regions
- signal peptides
- SCOP, PFAM, PDB, SwissProt+PIR assignments
- Prosite pattern matches
- detection of internal repeats
- Position Specific Sequence Profiles (from PSI-BLAST)
- secondary structure prediction
- search for homologous sequences using BLAST, PSI-BLAST, IMPALA or 3D-PSSM and filter the restuls for one ore more taxonomic groups, source databases or genomes
- access alignments (mutiple alignnment style or pairwise alignments)
- sequence searches + alignments are precompiled and easy to access (I hope ;-)

See ***WWW***, page 13

cDNA resources

Sources of mouse and human full-length cDNAs

1. **Origene -** (www.origene.com). 10 000 full-length human cDNA clones based on the annotated NCBI RefSeq database.
2. Stratagene - GeneConnection collection (www.stratagene.com). 26 000 human cDNA clones (16 000 unique clusters) - 50% of the clones estimated to be 'full length'. A small collection of 435 expression-tested Myc and His epitope tagged clones is also available.
3. Mammalian Gene Collection (http://mgc.nci.nih.gov/). This presently contains 9 000 human and 4 000 mouse full-length cDNAs.
4. ResGen (Invitrogen) - (http://www.resgen.com/full_length/index.php3).
    a. 35 000 clones representing ~ 10 000 unique human genes. 70% of the clones are estimated to be full-length. All clones are provided in a Gateway™ modified mammalian expression vector.
    b. GeneStorm - 2 500 fully sequenced and expression tested cDNAs in a mammalian expression system. Tagged with a V5 epitope.
5. RIKEN - (http://www.gsc.riken.go.jp/e/FANTOM/). A mouse cDNA library containing 21 076 full-length enriched clones.
6. Harvard Institute of Proteomics - FLEXGene Database. (http://www.hip.harvard.edu/): An ongoing project that aims at creating a complete repository of all human ORFs.
7. American Type Culture Collection - (www.atcc.org): It maintains a repository of cDNAs deposited by individual investigators in addition to cell lines.
8. The German Human cDNA Project (DHGP) (http://mips2.gsf.de/proj/cDNA/) A consortium of eight German sequencing laboratories that aim at identifying and sequencing 3 000-4 000 full-length human cDNA clones in the near future.
9. FLJ clones (NEDO) – (http://www.nedo.go.jp/bio-e/). Currently houses 12 000 human cDNAs.
10. Upstate Biotechnology (www.upstatebiotech.com) and Invivogen (www.invivogen.com): Both of these companies provide expression-tested cDNAs of various signaling and related molecules.
11. Human Unidentified Gene-Encoded (HUGE) database -(http://www.kazusa.or.jp/huge/). ~ 2 000 long (>4 kb) cDNAs. A highly annotated database.

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WWW, from page 11

The web-site is a side-product of ongoing research projects in our lab, but it's free to access. The web-resource is still under construction and may change in future.

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http://www.bmm.icnet.uk

Web Portal
www.Molbio.org

There is a new web portal for all things related to molecular biology and bioinformatics (including the related fields of cell biology, biochemistry, genetics, genomics, and biotechnology). Currently www.MolBio.org provides a news service where the web community can post information related to molecular biology (et al.) and bioinformatics. In addition to the news service, www.MolBio.org provides spam free discussion groups.

Do you have information to share such as:

- Conference
- Course
- News Bite
- Research Finding
- Database
- FTP Site
- Mailing List
- Press Release
- Protocol
- Software
- Tip
- Web Site
- Web Based Program/Tool
- Other

Related to the fields of:

- Biochemistry
- Cell Biology
- Genetics
- Molecular Biology
- Biotechnology/Biotech
- Computational Biology
- Genomics
- Other

Then please submit it to www.MolBio.org via the news form at http://www.molbio.org/postnews.cgi. The more info you post, the more useful www.MolBio.org will be. The information you post doesn't need to originate from yourself — it can be anything you come across in searching the web, reading a journal, browsing bionet, etc... If in doubt, post it!

If you have any questions, comments, or requests — feel free to contact me at Alan@MolBio.org. www.MolBio.org is loosely setup as a slashdot (www.slashdot.org) for biology. Follow-ups have been directed to bionet.software.www

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The ISICR newsletter needs additional **associate editors** to help with regular columns, special features, etc. We also welcome volunteers from outside the US to contribute information relevant to interferon and cytokine research in their home countries. Think of the **status** of being an ISICR newsletter editor! Contribute to the ISICR and do something good by joining the editorial team! Contact **Howard Young** via email (**youngh@ncifcrf.gov**) for assignments.

From: Aliquotes v.iv (journal) rogerb@microsoft.com
New Scotland Bovine Labs

COW SYSTEM:
Transgenic protein purification system

Instruction Manual

Introduction to Cow System™:
The Cow cloning system is an advanced protocol for the purification of recombinant proteins from lactating bovine species. The system is more reliable than current sheep cloning methods, requires less starting material, is less expensive and will not cause public controversy when the press get holds of it.

1) Description:
The Cow System ™ is the most powerful system for the cloning and expression of recombinant protein. Target genes are cloned in cow plasmids under control of the bovine serum albumin promotor. The desired product can comprise more than 10% (50kg) of the animal after a few hours of fermentation, in inclusion bodies.

2) Host for cloning:
Suitable cows for cloning include the Cowalbi, which are albino, and allows the black/white screening for the library when plated on the suitable field spread with X-Grass™ (GG) selective medium. Note that the Scottish Highland Cows (SHC) are more sensitive to the heat shock transformation.

3) Preparation of the medium:
You need a very, very big flasks (two million liters), a very, very big shaker and a clothes peg for your nose. The growth medium, "Cow Dip" or
C.D. broth, is made from @m grass, 0.5M hay supplement, 0.2mM ice cream (vanilla flavour), pH7.2. An oxygen carrier, such as myoglobin, can be
added to increase growth and prevent drowning. Alternatively, Farmer Seah(R) provide bovine aqualungs for growth in liquid media. Always,
autoclave the medium in order to kill scrapie prions.

4) Transformation:
You need alt least 12kg of plamid, a vet and a big swimming pool at 37^{C} and a sauna at 42^{C}. It is possible to use the FarmerKit™ from Farmer Seah®. Supercompetent Cowalbi calves are provided with the kit. Recently, a protocol derived from Maniatis has been described by Jersey et al. (1996) using Brute Force™ on mature bovine.

a- Place the cows in a room on ice and mix gently to assure that the cows are in good shape.
b- Add 2kg of plasmid directly in each cow using a clean glove. Rotate gently to mix.
c- Place cows on ice for 30 minutes.
d- Heat shock the cows by placing them in the sauna at 42^{C} for exactly 40 seconds. Do not vortex; the cows will break the mixer.
e- Place the cows in a cold room for 2 minutes.
f- Add two million liters of GG medium.
g- Incubate the cows at 37^{C} with shaking in Earthquake zone for one hour and spread the cows on a green field(*). Note that premade libraries are available from Cowtech (Cambridge).

5) Expression:

a- To start the culture, add two tonnes of transformed cows (0.25 vol. of total bovine prep (TBP)) in the liquid culture (figure 1)

b- Incubate with shaking the culture at 37C until OD_600 of the supernatant reaches 0.8.

c - The cows could be separated by decantation using a shepherd and his dog, by gentle centrifugation (5g) of filtration (filter, 1m).

d- Lyse by osmotic shock in 2M Chocolate Syrup(**) or with three medium shrapnel devices. Atomic weapons are not advised. Note that English cows are very resistant to lysis. It is possible to use a French Press.

e- Purify the product using normal procedures. For enhanced purification, use the Cow-Lyse Kit ™.

6) Cloned gene expression in Cow System™

The plasmid included with this kit is the new pBSE, the Bovine System Expression plasmid. Other Cow-based expression systems can be used but may not over-express to the same extent. When cloning chimaeric gene constructs, remember to use Cowalbi which are missing the gene coding for the restriction enzyme BDNA I. Cowalbi are also immunosuppressed to aid expression of hideously deforming genes.

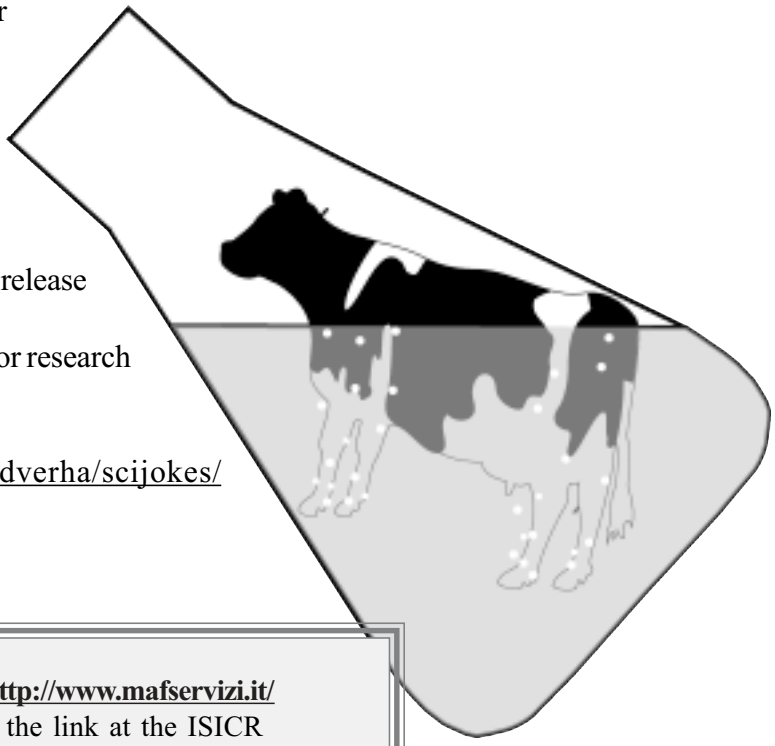
If gene products are poor, try the Rhino Kit(TM). This incorporates a grey/white selection procedure to replace the Blue Whale Kit(TM), which has been discontinued due to poor yields and international pressures.

(*) Single cloned cows could be stored as frozen at -80C or in a field in Greenland.

(**) Note that the use of chocolate syrup osmotic shock can lead to milkshake production in certain bovine species.

(***) pMooscript can be used instead for lower expression levels.

figure 1: Fermentation conditions (Cows floating in a BIG erlenmeyer)



Related products:

New Scotland Bovine Labs Mootagenesis(TM) kit

New Scotland Bovine Labs Cow-Lyse(TM) kit for release of inclusion bodies from bovine and udder sources.

The Cow System is covered by Scottish patent. _For research use only._

Article obtained at: http://www.xs4all.nl/~jcdverha/scijokes/4_4.html#subindex

For the latest **2002 ISICR Meeting** Info, go to **http://www.mafservizi.it/viewcongress.asp?IDC=15&PAGE=-1** or click on the link at the ISICR Homepage (**www.isicr.org**).

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