

ISICR Newsletter 3-3 , September 1996

A Message from the ISICR President

Greetings and welcome to Geneva for the first joint meeting of the ISICR and the ICS. As Humphry Bogart said to Claude Raines at the end of the film Casablanca "... I think this may be the beginning of a beautiful friendship." I certainly hope so.

There are obvious reasons for the two societies to hold joint meetings. Two are: the similarities in the content of the scientific agendas of the members of both; and, the economics of meetings at the end of the 20th century. A meeting with less than 500 in attendance has very little chance of breaking even these days.

Some other areas of where cooperation between the two societies might pay off include publications, standards, and nomenclature. Newsletters, journals, and other publications might be run advantageously as joint ventures. Standards for interferons and cytokines are a major problem at this time. The expertise available in the two groups would be of great help to the WHO and to national agencies seeking to fix scientifically reasonable standards for clinically useful reagents. Indeed, this input might prevent the adoption of standards that do not reflect the complex realities inherent in the biology of cytokines and interferons. Finally, a logical nomenclature is essential in dealing with these substances. This nomenclature should be determined by those active in the field. Both societies, speaking with a joint voice, will be more effective than either alone in deciding which of various standards or terminologies should be adopted.

I hope such cooperation indeed will be forthcoming.

Bob Friedman, President, ISICR

Information from the Membership Committee of the ISICR

Respectfully submitted

Heinz- Kurt Hochkeppel, chair

I would like to first of all take the opportunity to thank Dr. Lois B. Epstein for her nice personnel note published in ISICR Newsletter Vol 3, No. 1, 1996, in which she announced my appointment as the new chair of the ISICR Membership Committee. On behalf of all members of the committee I thank Dr. Epstein for her engaged and devoted work as chairwoman of the ISICR Membership Committee during the previous years.

As of August 6th 1996 ISICR had a total of 866 members which include 755 members who had paid their dues, 10 honorary members, and 101 associate members. In comparison, last year's (1995) total

membership was 793 (paid members: 687). Presently only a fraction of ISICR members uses the possibility to pay their dues in advance. 205 members have paid their dues for 1997, 75 for 1998, 22 for 1999, and 7 for 2000. There are 166 members whose last dues payments were in 1994, and 125 whose last due payments were in 1993; the latter ones are marked for deletion.

Several recommendations voiced by the Membership Committee of ISICR in the previous years in order to attract new members have meanwhile been implemented by the Society, e.g. the ISICR Newsletter, and now, for the first time the joined ISICR/ICS Newsletter, the Young Investigator Award, etc. This is certainly encouraging. However, also in future we will need new, innovative ideas to ensure that ISICR Membership is maintained or increased. I encourage all interested members of ISICR who have suggestions and/or concrete recommendations to contact me or any of the members of the ISICR Membership Committee.

NEW ISICR MEMBERS

The following individuals have joined the ISICR since the last newsletter was published. Contact the ISICR business office for address information.

Helen Atabaidea, Attiki, Greece

Nikolaoe Balatsos, Attikia Hellas, Greece

James Darnell, New York, NY

Sven Erickson, Stockholm, Sweden

Julie Fischer, Nashville, TN

Juergen Harms, Baltimore, MD

Teresa Johnson, Nashville, TN

Thomas Sai- Ying Ko, Boronia, Australia

Georg Kochs, Freiburg, Germany

Yoshihiro Konishi, Kurashiki, Japan

Antonis Koromilas, Montreal, Canada

William Lowther, Baltimore, MD

Paul Massa, Syracuse, NY

Catherine Owczarek, Clayton, Australia

Christopher Park, New York, NY

Brian Pollack, Piscataway, NJ

Steve Ralph, Clayton, Australia

Laura Runkel, Cambridge, MA

Borre Robertsen, Tromsø, Norway

Susan Schafer, Baltimore, MD

Heidi Skrenta, Piscataway, NJ

Milen Vassilev, Sofia, Bulgaria

Kurt Vermeire, Leuven, Belgium

Jon Wiggington, Frederick, MD

News from the ISICR Meetings Committee

The annual meetings of the International Society for Interferon and Cytokine Research (ISICR) cover all aspects of interferon and cytokine research, from the molecular genetics of their induction and action to clinical investigation; current studies on interferons, cytokines and their receptors; signal transduction of cytokines; negative regulation of the cytokine system, physiology and pathology of the cytokine network; and clinical and therapeutic effects of interferons and cytokines. These meetings are attended by an average of 400- 700 members of ISICR and other interested scientists from 38 countries. Eighty-five percent of the participants are from academic/medical institutions and 15% are from pharmaceutical/research laboratories.

Future ISICR Meetings:

1997 - San Diego, California, USA

1998 - Jerusalem, Israel

We have received proposals for Amsterdam, the Netherlands, and Cleveland, Ohio for the years 1999 and 2000 and are reviewing proposals for the years after that. Anyone interested in organizing an annual ISICR meeting, please contact Christine W. Czarniecki for information to assist you in preparing a proposal. Copies of your proposal will be sent to the members of the ISICR Meetings Committee for review. Proposals are then discussed for committee decision at the ISICR Meetings Committee meetings which take place at each Annual ISICR Meeting.

FAMOUS QUOTES

It's what you learn after you know it all that counts Earl Weaver

NEW ISICR BUSINESS OFFICE

The ISICR now has a new business office:

Address all correspondence to :

ISICR Business Office

9650 Rockville Pike

Bethesda, MD 20814- 3998

Tel: 301- 571- 8319

Fax: 301- 530- 7049

Email: isicr@faseb.org

EMPLOYMENT OPPORTUNITIES

Postdoctoral Fellowships

RESEARCH ASSOCIATES IN SPACE BIOLOGY

The current **SPACE SHUTTLE Program** has allowed the development of **SPACE BIOLOGY SCIENCE** that offers exceptional opportunities for research. **NASA** is offering **RESEARCH ASSOCIATE AWARDS** at the postdoctoral level for scientists to conduct Space Biology Research in a university laboratory or non governmental research institute of your choice that can provide the necessary facilities and research environment. Projects should be in the gravitational and space biology discipline. The awards are: \$20,000 for the first year and \$22,000 for the second year. Funding will

begin July 1 to October 1, 1997. US. citizens and permanent resident aliens with Ph.D., M.D., D.V.M., D.M.D. or equivalent degrees are eligible to apply.

PROPOSALS ARE DUE

FEBRUARY 17, 1997.

For information and application booklet contact:

Dr. Gerald Sonnenfeld,

Dept. of General Surgery Research, Carolinas Medical Center,

P.O. Box 32861,

Charlotte, NC 28232.

Tel: (704) 355- 2639

FAX: (704) 355- 7203

MANAGER, REGULATORY AFFAIRS

ICOS Corporation, located in the Pacific Northwest, is a biopharmaceutical company founded to develop medications for the treatment of chronic inflammatory diseases. We are seeking a Manager to join our Regulatory Affairs team. Under the guidance of the Director, the successful candidate will serve as a representative to assigned product development teams; will be responsible for submission preparations; and will participate in the development and implementation of regulatory strategies, evaluating technical changes for regulatory impact. Responsibilities also include managing domestic activities in support of international submissions. A proven ability to problem solve using scientific methodology for regulatory issues is a plus.

Minimum qualifications include: B.S. or M.S. in scientific discipline and 3 years prior experience in regulatory affairs in the pharmaceutical/biotechnology industry. Candidates must possess strong interpersonal skills, good oral and written communications skills, and have a strong desire to work within a team environment.

Please send resume to:

Job Ref: CZA0196

Human Resources

ICOS Corporation

22021 - 20th Avenue SE

Bothell, WA 98021

CGH DNA STANDARDS

The National Institute for General Medical Sciences (NIGMS) Human Genetic Mutant Cell Repository is distributing DNA from cell lines containing from 1 to 5 X chromosomes for use as comparative genomic hybridization standards: 45, X (NA01723A); 46, XX (NA09947A); 47, XXX (NA04626); 48, XXXX (NA01416D); and 49,

XXXXX (NA06061C). DNA from a subject with 49, XYYYYY (NA11419) is also available. All of these are also available as cell cultures. For additional information or a printed catalog, please contact:

NIGMS Human Genetic Mutant Cell Repository

Coriell Cell Repositories

401 Haddon Avenue

Camden, New Jersey 08103

Tel: (800)- 752- 3805, in the United States

(609)- 757- 4849, outside of the United States

Fax: (609)- 757- 9737

European Molecular Biology network newsletter

The latest issue [Vol3 No2] of the European Molecular Biology network

(EMBnet) newsletter 'embnet.news' is now available.

http://www.be.embnet.org/embnet.news/vol3_2/contents.html

http://www.ie.embnet.org/embnet.news/vol3_2/contents.html

http://www.uk.embnet.org/embnet.news/vol3_2/contents.html

The newsletter (and back issues) can also be downloaded in postscript form.

<ftp.be.embnet.org> in the directory `pub/embnet.news/`

<ftp.ie.embnet.org> in the directory `pub/embnet.news/`

<ftp.uk.embnet.org> in the directory `pub/embnet.news/`

Yours,

The embnet.news editorial team

Alan Bleasby

Reinhard Doelz

Robert Herzog

Andrew Lloyd

Rodrigo Lopez

WWW SOURCES

The Antibody Resource Page

The Antibody Resource Page has recently been updated. This website is the only one on the web devoted to collecting links and useful information about antibodies. The webpage contains educational links about antibodies (some with incredible graphics), links to on- line journals that cover antibody-related topics, an essay on the study of antibody molecular recognition, links to on- line antibody sequencing and hybridoma databases, and a miscellaneous section.

I also have a large section designed to help those looking for an antibody: This latter section contains more than 60 links to on- line companies that sell antibodies, many which have searchable catalogues. This section also contains useful tips on how to find antibodies using the internet or otherwise.

I am always looking for new links to add to my page, so if you know of any, please let me know via email. Or just email me to let me know what you think of the page! The URL for the Antibody Resource Page is:

<http://www-chem.ucsd.edu/Faculty/goodman/antibody.html/abpage.htm> 1

Kevin Shreder, Ph.D.

UCSD kshreder@ucsd.edu

BioSCAN (Biological Sequence Comparative Analysis Node)

o The BioSCAN e-mail server databases have been updated. The currently available databases are as follows:

GenBank Release- 93

SWISS- PROT Release- 32

PIR Release- 47

GenPept Release- 93

BioSCAN (Biological Sequence Comparative Analysis Node) is a

computational tool designed for similarity analysis of biological sequences. Its massively parallel computer system performs rapid, rigorous, searches of biosequence databases and is compatible with popular software packages such as BLAST and FASTA.

To receive current set of instructions on using the BioSCAN e-mail server, send an e-mail to the address "bioscan@cs.unc.edu".

Put the word "HELP" or "help" on a line by itself in the body of the message. A tutorial ("tutor.txt") can be retrieved via anonymous FTP to "[ftp.cs.unc.edu](ftp://ftp.cs.unc.edu)" from "/pub/projects/bioscan" directory.

Please send your questions and comments to "bioscan-info@cs.unc.edu".

o Searches: bioscan@cs.unc.edu, <http://genome.cs.unc.edu/>

o User support: bioscan-info@cs.unc.edu

o This research was supported in part by NSF under grant MIP- 9024585. Raj K. Singh singh@cs.unc.edu +1 (919) 962- 1744

DNA ANALYSIS SOFTWARE

This posting announces new versions of 3 separate programs that run on IBM- PC clones. The three programs are fully functional (i.e. not demos) and are freeware. They are:

SorFind, Version 2.8 (download as [sorfin28.exe](#))

SorFind predicts coding exons in vertebrate genomic DNA. An

independent analysis has recently shown the program to have an accuracy similar to GRAIL II. (Burset and Guigo, Genomics, in press).

RepFind, Version 1.7 (download as [repfin17.exe](#))

RepFind identifies common repetitive elements in DNA sequence. The default files are set up to identify primate repeats, such as Alus, L1s, MERs, LTRs etc. The program is user- extendible to identify any repetitive sequence of interest in any organism. The program can also be used to identify and annotate vector contamination. As an option, repeats or vector sequence can be masked with the letter "n" to facilitate database searches.

PromFind, Version 1.1 (download as [profin11.exe](#))

PromFind predicts promoter regions in vertebrate DNA sequence. It

currently is able to identify 60 to 70 percent of promoter regions of 300 bp width to within 200 bp. No prior knowledge of transcription element binding sites is assumed. This program will be published shortly (revised manuscript submitted to CABIOS).

All three programs accept sequence in plain, Fasta, EMBL or GenBank format, and output the sequence, with an added feature table, in EMBL or GenBank format. The programs can be "piped" into one another, allowing the simultaneous identification of promoters, coding exons and repetitive sequence using one command line. A manual is included for each program. The binary executable IBM- PC programs are free of charge. There is also a full GUI under development, but that will be commercial. There are no conditions attached to the use of the DOS programs except that there is no associated warranty.

The three programs have been uploaded to the following servers as of July 9, 1996:

<ftp://iubio.bio.indiana.edu/molbio/ibmpc> (there now)

<ftp://ftp.bchs.uh.edu> (currently inaccessible in /gene- server/incoming

but hopefully will be moved to /gene- server/dos

<ftp://cgat.bch.umontreal.ca> (currently in the /incoming directory)

Comments, bug reports and suggestions for new features are welcome and should be sent by email to hutch@netshop.bc.ca. Inquiries can be addressed to:

Dr. Gordon B. Hutchinson

Department of Medical Genetics

University of British Columbia, Canada

Mailing Address:

c/o RabbitHutch Biotechnology Corp.

P.O. Box 506

108 Mile Ranch, B.C.

V0K 2Z0 Canada

Phone: (604)791- 1937

Fax: (604)791- 1938

E- mail: hutch@netshop.bc.ca

NAOMI

NAOMI - Version Upgrade Announcement

(Please note, NAOMI is provided at zero charge for academic use)

(e- mail contact smb@bioch.ox.ac.uk)

The computer program NAOMI Version 2.4 is available as of now from the NAOMI Web site at:

http://www.ocms.ox.ac.uk/~smb/Software/N_details/naomi.html

or via anonymous ftp

<ftp://nmrz.ocms.ox.ac.uk/pub/smb/naomi>

i.e. at nmrz.ocms.ox.ac.uk

in directory pub/smb/naomi/

Users of versions older than 2.10 will need new license keys to allow the upgrade to work (please contact the author in this case). New features in upgrade:

In main module:

New fully automatic interface to RASMOL

Wild- card selection of residues

Automated identification of interior and exterior residues

new "protwrite" command for outputting protein- level

calculated properties In the NMR module:

New prediction of NOEs from structure command

What is NAOMI?

NAOMI is an easy- to- use, state- of- the- art computer program which is aimed at both specialist and non- specialist researchers who make use of three- dimensional structures of proteins in their work. It has hundreds of users Worldwide. Some facilities offered by the program for working with structure include:

automatic 'key' residue identification

automatic hydrophobic core/packing analysis

automatic hydrogen bonds main- chain and side- chain

identification (including high quality energy calculations)

automatic secondary structure (helix, strand and turn) classification using fuzzy logic

automatic supersecondary structure classification (beta- hairpin loops)

conformational parameters: phi,psi,chi1,chi2,chi3,chi4,chi5 etc

solvent accessibility (both absolute and percentage) calculations

automatic identification of disulphide bonds, salt bridges, chain- breaks

side- chain modelling and manipulation

applying symmetry operators

automatic structure repair (building in missing atoms)

NMR structure refinement module

interfaces to graphics programs (MOLSCRIPT (and thus Raster3D),

RASMOL, INSIGHT and QUANTA to allow automatic preparation of figures and time- efficient visualization of structures.

More details are available on the Web site. NB NAOMI currently works only on Silicon Graphics workstations running IRIX 5.* or IRIX 6.*

Simon M. Brocklehurst,

Oxford Centre for Molecular Sciences, Department of Biochemistry, University of Oxford, Oxford, UK.

E- mail: smb@bioch.ox.ac.uk | WWW: <http://www.ocms.ox.ac.uk/~smb/>

PRANA - NEW PROTEIN STRUCTURE- ACTIVITY ANALYSIS SOFTWARE

PRANA : PC- based program for studying the relationships between structure and activity in protein/ peptide families

by I.Pika, V.Ivanisenko & A.Eroshkin

State Research Center of Virology and Biotechnology "Vector" Koltsovo, Novosibirsk Region, 633159
Russia

E.mail: eroshkin@vector.nsk.su,

Tel: +7 (3832) - 647774,

Fax: +7 (3832) - 328831

The State Research Center of Virology and Biotechnology "VECTOR" is pleased to announce the availability of PRANA v1.0.

PRANA is an easy- to- use, state- of- the- art MSDOS application for studying the relationships between structure and activity in protein/peptide families divided in two groups (by activity, property, evolution, etc.). The program examines the relationships between protein grouping and physico- chemical characteristics (e.g., mean hydrophobicity, Charge, or Volume, alpha- helical or beta- strand moments of Hydrophobicity, etc.) of different regions in their primary structures and delineates the sites and characteristics describing the given grouping. PRANA is based on the program PROANAL (A. Eroshkin, V.Fomin, P.Zhilkin, CABIOS, 1993, 9, 491- 497) and designed to provide analysis of additional data. PROANAL looks for correlations between quantitative data on protein activity and physico- chemical characteristics of the regions in the primary structures. In case of PRANA the analysis is based on aligned amino acid sequences and data on protein grouping (qualitative activity data). The program searches activity- modulating regions in aligned proteins that have different structure characteristics for two groups (biophore or pharmacophore). Student's or Kolmogorov - Smirnov's criteria are used to compare the distributions of the characteristics in two protein groups. The results - found sites and their physico- chemical characteristics as well as all necessary statistical evaluations - are presented in the form of text and histograms that can be saved or printed as required.

PRANA CAN BE USED:

- to find sites and site characteristics that may be responsible for the difference in proteins activity or property;
- to classify newly sequenced proteins/peptides;
- to assist in simulation of protein engineering experiments.

EXAMPLES OF DATA TYPES TO BE ANALYZED

- 15 variants of human alpha- interferons can be divided into two groups of high and low antiviral

activity. The task is to find amino acid residues in IFN- alpha related with this difference in activity;

- influenza A virus M(2) proteins from virus strain resistant or sensitive to amantadine. The task: to find amino acid residues in M(2) involved in amantadine binding and amino acid physico- chemical properties important for this interaction.

- peptides inserted into VP1 protein of poliovirus type 1. Some of mutant viruses were viable, other - not. The task: to find the physico- chemical characteristics of the peptide inserts, that are important for mutant virus viability.

PRANA HAS

* converter from SWISS- PROT, CLUSTAL, GCG, PHYLIP formats to PRANA

input files;

* data files with about 100 amino acid physico- chemical properties;

* examples, manual and help system.

REQUIREMENTS: DOS 3.30 or later, EGA/VGA video card, 400 KB RAM.

PRANA AVAILABILITY

PRANA v1.0 is freely available for academic users through EBI ftp

server <ftp.ebi.ac.uk> (directory /pub/software/dos/prana).

For companies inquire to:

Alexey Eroshkin

SRC VB "Vector"

Koltsovo, Novosibirsk Region

633159 Russia

E.mail: eroshkin@vector.nsk.su

Tel: +7 (3832) - 647774

Fax: +7 (3832) - 328831

PRANA USERS

Don't hesitate to contact us in case of problems, bugs or suggestions. Could you send us your address (Email is preferred) and your feelings about your PRANA experience?

BioMOO, the virtual meeting place for biologists

BioMOO, the virtual meeting place for biologists, is pleased to announce the availability of a new anonymous web access mechanism. The "web ghost" system lets you wander this VR world created by the international biology community. Access to the web ghost system is at: <http://bioinfo.weizmann.ac.il:8000/anon/anonview>

Full presence (live conversation mechanism plus web- based multimedia) is also available via the BioMOO web gateway at:

<http://bioinfo.weizmann.ac.il:8888>

Text- only access may be found at:

<telnet://bioinfo.weizmann.ac.il:8888>

BioMOO is a virtual meeting place for biologists, connected to the Globewide Network Academy. The main physical part of the BioMOO is located at the BioInformatics Unit of the Weizmann Institute of Science, Israel.

BioMOO is a professional community of Biology researchers. It is a place to come meet colleagues in Biology studies and related fields to brainstorm, to hold colloquia and conferences, to explore the serious side of this new medium.

Eric H. Mercer

California Institute of Technology

Division of Biology; 216- 76

Pasadena, CA 91125

TEL # (818) 356- 6822 mercerc@caltech.edu

PROMOTER SCAN version 1.60 for UNIX

PROMOTER SCAN Version 1.60 for UNIX is now available. The program for IBM PCs is NOT YET READY, and will be announced at a later date. Please DO NOT send requests to 'send the PC version when ready'. It will be announced soon. Improvements in UNIX version 1.60 (over version 1.50) are:

- 1) The TATA box prediction has been improved, recognizing approximately 10% more TATA boxes. Also, the TATA box is now used to predict the Transcription Start Site (TSS). In our test set, PROMOTER SCAN reports that 72% of recognized promoters contained TATA boxes; and of those, the TSS is reported to within +/- 10 bases of the actual TSS. PROMOTER SCAN will recognize about 70% of primate promoter sequences, and correctly report the TSS within 10 bases of the actual TSS in 50% of primate promoter sequences, with a false positive promoter prediction rate of about 1 in 17,200 non-promoter bases.
- 2) PROMOTER SCAN now reports the signals that it uses in determining a promoter sequence. The name of the binding factor, its location, strand, and significance weighting are reported (the weighting is used only in discriminating promoter sequences from non-promoter sequences and is NOT related to the overall quality of the signal, or as a measure of it's being an actual binding site or not).

For information on how to obtain the latest copy of PROMOTER SCAN,

send requests to

Dan S. Prestridge, Ph.D.

E-mail: DANP@BIOSCI.CBS.UMN.EDU

Director

Advanced Biosciences Computing Center

University of Minnesota

1479 Gortner Ave.

St. Paul, MN 55108

email: danp@biosci.cbs.umn.edu

Tel: (612) 625- 3744

Fax: (612) 625- 5780

Clinical Trials

POG- 9574 Interleukin- 4 in pediatric patients with refractory acute leukemia Contact : Susan Giovanazzi- Bannon, Chicago, IL TEL: 312- 482- 9944 ext 228.

B95- 0003 Phase I study of interferon- enhanced intraperitoneal radioimmunotherapy for ovarian cancer. Contact: Rudy Meredith, MD- PhD, Univ. of Alabama- Birmingham Birmingham, AL TEL: 205- 934- 2760

T95- 0026 Phase I trial of HUM195 (recombinant humanized anti- CD33) monoclonal antibody and recombinant interleukin- 2 in myelogenous leukemia Contact: Philip Caron, MD- PhD, Memorial Sloan-Kettering Cancer Center, New York, NY TEL: 212- 639- 5508

AECM- 119951142 NCI- T95- 00540 Phase I study of TAX plus DOX/ADR- 529 with and without G-CSF in women with advanced breast cancer. Contact: Joseph A. Sparano Montefiore Medical Center, Bronx. NY TEL: 718- 920- 6706

DUP- 941- 017 NCI- V95- 0785 Phase III randomized study of CI- 941/TAX/G- CSF vs TAX alone in women with stage IV breast cancer. Contact: Donald Nibbelink, Dupont- Merck, Wilmington, DE. TEL: 302- 992- 4638

T94- 0187 A phase II trial of hyperthermic isolated limb perfusion with tumor necrosis factor and melphalan (Alkeran) in patients with unresectable extremity sarcoma and melanoma. Contact: Douglas L. Fraker, MD, Univ. of Pennsylvania, Philadelphia, PA. TEL: 215- 662- 7866

E1694 A phase III study of adjuvant ganglioside vaccination GM2- KLH/QS- 21 therapy versus high dose interferon alpha- 2b for high- risk melanoma (T4 with greater than 4 mm primary or regional lymph node metastasis. Contact: Jean McDonald, Brookline, MA TEL: 617- 632- 3610 or Marj Godfrey, San Antonio, TX TEL: 210- 677- 8808

Reviews of Interest

Bates, P. Chemokine receptors and HIV- 1: An attractive pair? *Cell* 86:1, 1996.

Darnell, J. E. Jr. Reflections on STAT3, STAT5, and STAT6 as fat STATs. *PNAS* 93:6221, 1996.

Degre', M. Interferons and other cytokines in bacterial infections. *J. of Interferon and Cytokine Res.* 16:417, 1996.

Henderson, B, and Wilson, M. Cytokine induction by bacteria: beyond lipopolysaccharide. *Cytokine* 8:269, 1996.

Kennedy, M K. and Park, L.S. Characterization of interleukin- 15 (IL- 15) and the IL- 15 receptor complex. *J. of Clinical Immunology* 16: 134, 1996.

Massague', J. TGF[[Beta]] signaling: Receptors, transducers, and MAD proteins. *CELL* 85:947, 1996.

Shivdasani, R.A. and Orkin, S.H. The transcriptional control of hematopoiesis. *Blood* 87:4025, 1996.

Tagaya, Y., Bamford, R.N., DeFilippis, A.P. and Waldmann, T.A. IL- 15: A pleiotropic cytokine with diverse receptor/signaling pathways whose expression in controlled at multiple levels. *Immunity* 4:329, 1996.

GLOSSARY FOR RESEARCH PAPERS: Strictly Speaking

(author unknown)

THEY WRITE

It has long been known that...

THEY MEAN

I haven't bothered to look up the original reference

THEY WRITE

.of great theoretical and practical importance

THEY MEAN

... interesting to me

THEY WRITE

While it has not been possible to provide definite answers to these questions.

THEY MEAN

The experiments didn't work out, but I figured I could at least get a publication out of it.

THEY WRITE

The W- Pb system was chosen as especially suitable to show the predicted behavior...

THEY MEAN

The fellow in the next lab had some already made up

THEY WRITE

High purity...

Very high purity...

Extremely high purity...

Super- purity...

Spectroscopically pure...

THEY MEAN

Composition unknown except for the exaggerated claims of the supplier

THEY WRITE

A fiducial reference line...

THEY MEAN

A scratch

THEY WRITE

Three of the samples were chosen for detailed study...

THEY MEAN

The results of the others didn't make sense and were ignored..

THEY WRITE

.handled with extreme care during the experiments

THEY MEAN

... not dropped on the floor

THEY WRITE

Typical results are shown...

THEY MEAN

The best results are shown...

THEY WRITE

Although some detail has been lost in reproduction, it is clear from the original micrograph that...

THEY MEAN

It is impossible to tell from the micrograph

THEY WRITE

Presumably at longer times...

THEY MEAN

I didn't take the time to find out

THEY WRITE

The agreement with the predicted curve is excellent

THEY MEAN

fair

THEY WRITE

good

THEY MEAN

poor

THEY WRITE

satisfactory

THEY MEAN

doubtful

THEY WRITE

fair

THEY MEAN

imaginary

THEY WRITE

.as good as could be expected

THEY MEAN

non- existent

THEY WRITE

These results will be reported at a later date

THEY MEAN

I might get around to this sometime

THEY WRITE

The most reliable values are those of Jones

THEY MEAN

He was a student of mine

THEY WRITE

It is suggested that...

It is believed that...

It may be that...

THEY MEAN

I think...

THEY WRITE

It is generally believed that....

THEY MEAN

I have such a good objection to this answer that I shall now raise it.

THEY WRITE

It is clear that much additional work will be required before a complete understanding...

THEY MEAN

I don't understand it

THEY WRITE

Unfortunately, a quantitative theory to account for these effects has not been formulated

THEY MEAN

Neither does anybody else

THEY WRITE

Correct within an order of magnitude

THEY MEAN

Wrong

THEY WRITE

It is to be hoped that this work

will stimulate further work in the field

THEY MEAN

This paper isn't very good but neither are any of the others on this miserable subject

THEY WRITE

Thanks are due to Joe Glotz for assistance with the experiments and to John Doe for valuable discussions.

THEY MEAN

Glotz did the work and Doe explained what it meant.

JURKAT T CELL LINE STABLE TRANSFECTANTS: A CAUTIONARY NOTE

In my lab and a number of nearby labs, we have noticed a problem recovering viable Jurkat T cells that are stably transfected with G418 (Geneticin) resistance (pSV2- neo) if the cells are cultured in G418 at the time of freezing. We have found that removing the G418 for 1 week prior to freezing the transfected lines greatly helps in maintaining cell viability.

Howard Young

HELP US

If you would like to see new features or have comments about the ISICR newsletter contents, please correspond with me. Also I am looking for new associate editors for a two year term beginning Jan. 1997. Many thanks to Drs. Sonnenfeld and Filipic for their help over the last two years.

Send correspondence for the ISICR newsletter to:

Howard Young

Lab. of Experimental Immunology

NCI- FCRDC, 560/31- 23

Frederick, MD 21702- 1201

FAX# 301- 846- 1673

e- mail: young@ncifcrf.gov

RENEW YOUR MEMBERSHIP NOW! DON'T MISS OUT ON FUTURE ISSUES OF THE SOCIETY NEWSLETTER!

MOVING AND FORGOT TO TELL US OR RENEW?

Send the ISICR office your new address

FAX: 301- 530- 7049

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ISICR MEETING

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ABSTRACTS

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