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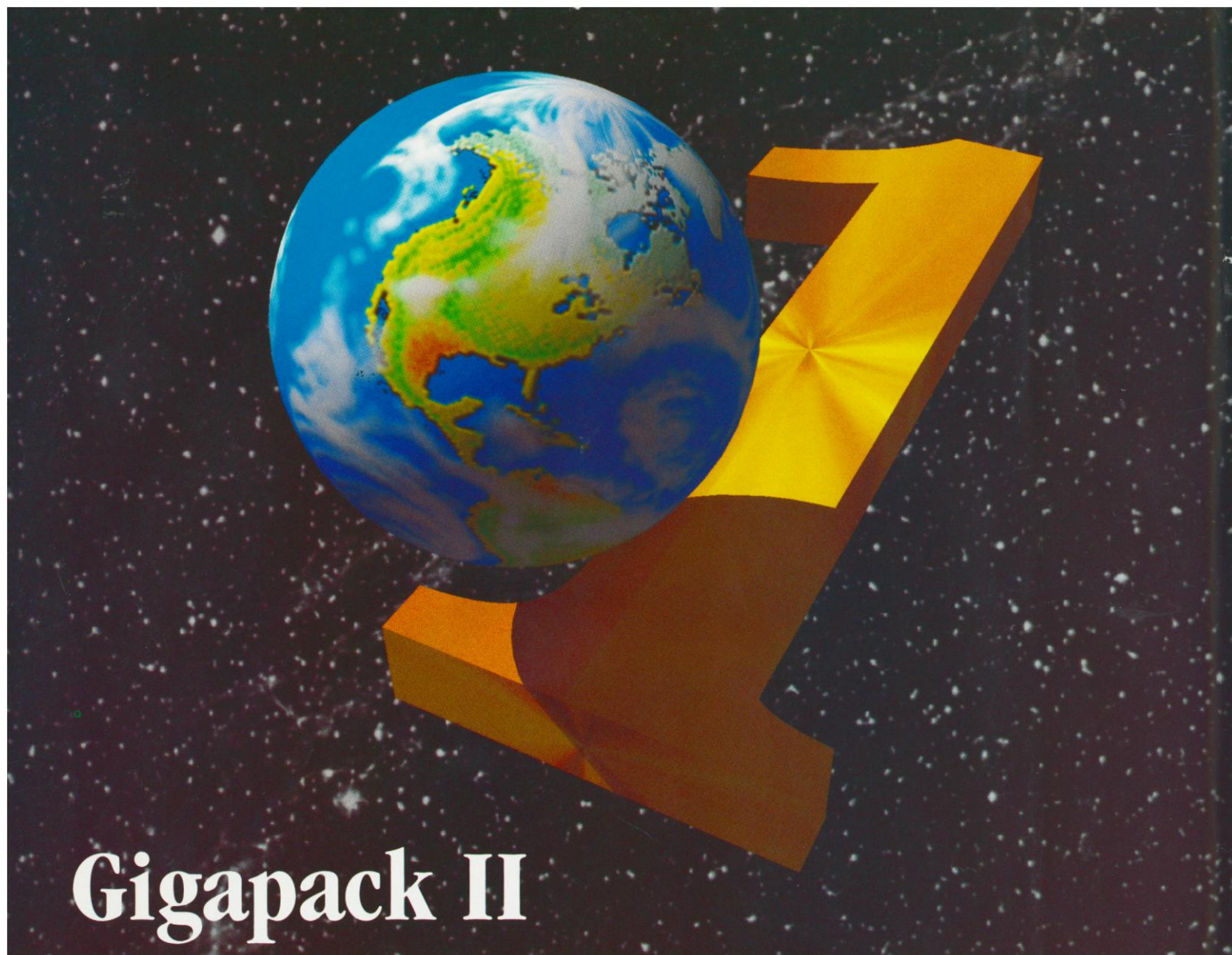
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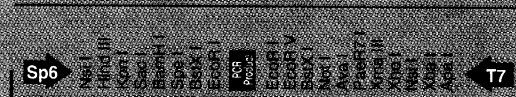
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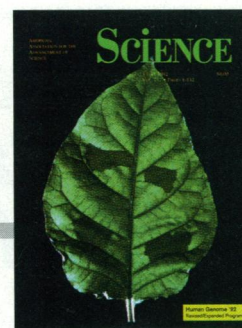
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COVER

Sectors of a tobacco leaf infiltrated with the plant pathogenic bacterium *Erwinia amylovora* or harpin, a protein isolated from it, show collapsed tissue (dark spots); sectors infiltrated with *E. amylovora* mutants that lack harpin have not collapsed. *Erwinia amylovora*

causes fire blight, a severe disease of apple and pear trees; harpin appears to be responsible for the collapse of infiltrated tissue and is required for the development of the disease. See page 85. [Photograph: K. Loeffler]



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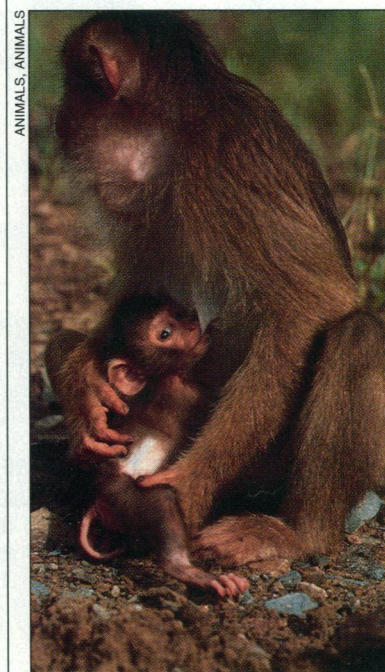
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The pigtail macaque: a new model for HIV infection

Indicates accompanying feature

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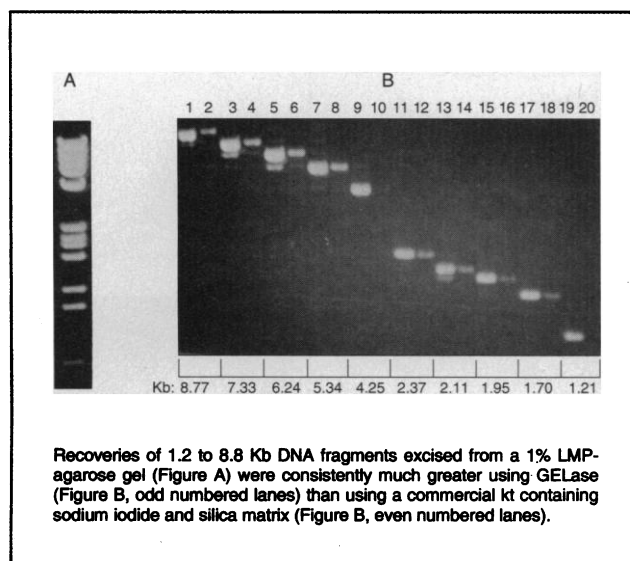
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1. Recovery of DNA is about 100% using GELase.

NaI/glass bead kits give about 50% recovery for 2–15 Kb DNA (see figure) and much less outside of that size range.



2. High molecular weight DNA, even megabase DNA, is not damaged using GELase.

DNA larger than 15 Kb is sheared using NaI/glass bead kits.

3. GELase is easy to use.

Just melt the gel slice with GELase Buffer, add GELase and incubate at 45°C to digest. To concentrate the DNA, add ethanol. The gel digestion products are soluble and won't precipitate with the DNA.

4. GELase is inexpensive.

One unit of GELase digests 600 mg of a 1% LMP-agarose gel in 1 hour in GELase Buffer. With a 10-hour incubation instead of 1 hour, the 200-unit size of GELase is enough to digest more than a KILOGRAM of a 1% gel.

5. DNA purified using GELase is ready to use and biologically active.

Some companies recommend two rounds of purification with a NaI/glass bead kit to obtain DNA for cloning. That's not necessary with GELase. DNA recovered using GELase is ready for use in restriction mapping, cloning, labeling, sequencing or other molecular biological experiments.

6. GELase is active in electrophoresis buffers.

It digests gels in TAE, TBE, MOPS and phosphate buffers. Special NaI/glass bead kits are needed for gels in TBE buffer.

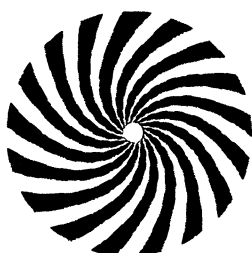
7. Protocols for using GELase are the same for RNA as for DNA.

GELase is RNase-free and active in MOPS or phosphate buffers that are used for RNA gels. In contrast, a special version of NaI/glass bead kit is needed for purification of RNA.

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GELase is a novel enzyme preparation that digests the carbohydrate backbone of agarose into small soluble oligo-saccharides, yielding a clear liquid that will not become viscous or gel even on cooling in an ice bath. It permits simple and quantitative recovery of intact DNA or RNA from low melting point (LMP) agarose gels. GELase contains no contaminating DNase, RNase or phosphatase.

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Neurexins and synapse recognition

A new family of neuron-specific cell-surface receptors, the neurexins, are encoded by at least two genes and appear to be expressed at synaptic junctions. Ushkaryov *et al.* (p. 50), starting with the peptide sequences for the receptor for α -latrotoxin, a component of black widow spider venom, constructed nucleotide probes for screening a complementary DNA library from rat brain. Each of the two genes undergoes alternative splicing at several internal sites, thus producing more than 100 neurexin transcripts. The neurexin sequences are similar to those for molecules such as laminin A that have been implicated in axon guidance and synapse generation. Neurexins may serve as cell-recognition molecules in making synaptic connections.

Solar system chaos

Computer simulations of planetary orbits have indicated that the trajectories are chaotic; the orbits diverge exponentially for arbitrarily small differences in initial conditions. Sussman and Wisdom (p. 56) have carried out a 100-million-year numerical integration of the equations of motion that confirms that the solar system as a whole is chaotic. The calculations were made with the Digital Toolkit, a multiprocessor computer optimized for the solution of systems of differential equations. Separate calculations also show that Jupiter, Saturn, Uranus, and Neptune are independently chaotic (see news story by Kerr, p. 33).

No moving parts

The ultimate in electronic circuit miniaturization would be molecular wires and transistors. Toward that goal, O'Neil *et al.* (p. 63) have designed a molecule that acts as a picosecond electron switch when exposed to short pulses of light. The switching is very fast because it involves no molecular motions but only electron transfer. The molecule, which consists of two porphyrin rings joined by a long dicarboximide bridging group,

changes from being a strong optical absorber at 713 nanometers to strongly absorbing at 549 nanometers.

High-pressure test

Variations of seismic velocities can be related to variations in the density of Earth's mantle and thereby provide important information on its temperature, structure, and dynamics. The traditional relation between compressional wave velocity and density is a linear equation known as Birch's Law. Campbell and Heinz (p. 66) tested Birch's Law by measuring compressional wave velocities of NaCl and KCl in situ at pressures up to 17 gigapascals with Brillouin spectroscopy in a diamond anvil cell. Birch's Law holds over this pressure range except across a structural phase transition in KCl.

Trimming fat

Medium-chain fatty acids (8 to 14 carbon atoms), which are produced and stored by many plants, are important food sources and industrial feedstocks. Voelker *et al.* (p. 72) show that laurate (12 carbon atoms), which is mainly ex-

tracted from the seeds of tropically grown trees, can be synthesized in an annual temperate plant, *Arabidopsis thaliana*. By expressing the gene for a medium-size acyl-carrier protein from the California bay laurel tree in this plant, fatty acid synthesis was redirected from longer chain molecules to laurate. Such approaches could be applied to commercial crops such as rapeseed.

Binding to TAR

Binding of the human immunodeficiency virus-1 (HIV-1) protein Tat to a messenger RNA sequence of HIV-1 called TAR, which has an unusual hairpin structure, is mediated by a single arginine (Arg) residue. Puglisi *et al.* (p. 76), who used nuclear magnetic resonance to study the interaction of TAR, an Arg analog that binds at the Tat site, show that binding modifies the hairpin bulge. The nucleotides that are essential for binding form a base-triple structure that stabilizes Arg hydrogen bonding. Specificity in the binding between Tat and TAR is likely derived largely from the RNA sequence of TAR.

Calcium control

Calcium is released from intracellular stores through channels, one of which is known as the ryanodine receptor because it binds that plant alkaloid. Gianini *et al.* (p. 91) cloned a gene encoding a ryanodine receptor that is expressed in many tissues. Unlike the previously identified ryanodine receptor, this channel was not sensitive to caffeine. The expression of messenger RNA encoding this ryanodine-sensitive calcium channel was increased 30-fold in cells treated with transform-

ing growth factor β . This channel may participate in control of the concentration of free intracellular calcium.

Negative selection

Elimination of developing T cells that could react with ligands of the body (self ligands) is referred to as negative selection; two separate reports deal with the mechanism of this process. Nakayama and Loh (p. 94) show that a protein-tyrosine kinase (p56^{lck}), which is required to stimulate mature T cells, is not required for the antigen-stimulated deletion of immature T cells. Nakayama *et al.* (p. 96) found that maturing T cells that are specific for a self ligand display increased concentrations of intracellular calcium but only when they are inside of a negatively selecting thymus. Although the same antigen receptor of T cells can initiate both positive and negative selection, the signaling pathways may be quite different.

Protecting bone marrow cells

Treatment of tumors with anti-cancer drugs can induce the expression of the human multidrug resistance gene *MDR1*, which encodes an energy-dependent transmembrane protein that pumps drug molecules out of cells. Sorrentino *et al.* (p. 99) transplanted mouse bone marrow cells that contained the *MDR1* gene into mice. Treatment of these mice with the cytotoxic drug taxol caused a substantial enrichment of the transduced cells. Because bone marrow toxicity often limits chemotherapeutic approaches, such an approach could have important clinical applications.

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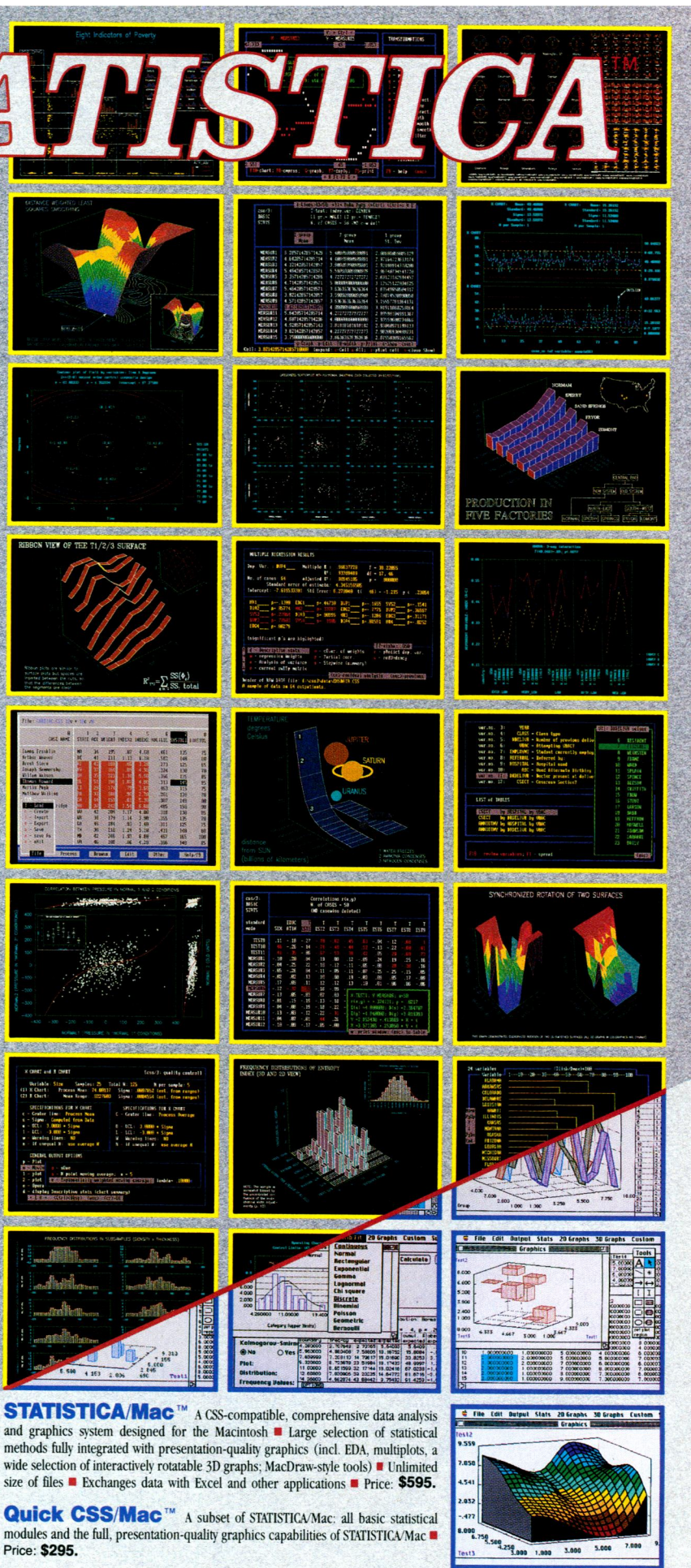
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Revised and expanded program!

HUMAN GENOME '92

The Human Genome Project International Conference

14–17 October 1992 ♦ The Acropolis ♦ Nice, France

Join your colleagues from around the world on the balmy Mediterranean coast as they explore the latest developments in human genome research.

Come to *Human Genome '92*, the 4th annual conference on the Human Genome Project sponsored by the Human Genome Organisation and *Science* magazine. After three years in San Diego, the conference visits Nice, France.

- ♦ Hear leading researchers discuss the latest inroads into the study of the human genome.
- ♦ Present your own research in poster sessions, discussing your work with interested colleagues. The most outstanding submitted abstracts will be selected for oral presentation in a special contributed papers plenary session.
- ♦ Visit the exhibits to investigate the equipment, supplies, and services essential to human genome research.
- ♦ Network with colleagues, to continue the exchange of ideas essential to this international collaborative research effort.
- ♦ In your spare time, explore all that Nice has to offer. Stroll along the beach by the sparkling Mediterranean ... go snorkeling, scuba diving, windsurfing, or even skiing in the nearby Alps ... visit the world-famous Marc Chagall and Matisse museums ... explore the colorful open-air markets and the quaint boutiques of the Old Town ... and savor the delicacies in the city's sidewalk cafes for which the French are so famous.

Travel to Nice is easy and economical; we have great discounts on unrestricted air fares from the United States and a wide selection of hotel accommodations to meet a variety of needs (*see page 14*).

Cutting-edge research ... stimulating exchange with colleagues ... breathtaking surroundings ... economical travel — *Human Genome '92* is all this and more. Use the form on page 16 to register today!

Program co-chairs:

Walter Bodmer, Imperial Cancer Research Fund

Charles R. Cantor, Univ. of California, Berkeley

Jean-Louis Mandel, CNRS/LGME, INSERM

Anton K. Raap, Univ. of Leiden

"New methods for high resolution and multicolor in situ hybridization"

Yoshihide Hayashizaki, Natl. Cardiovascular Rsch. Inst.

"Restriction landmark genomic scanning method and its application"

WEDNESDAY, 14 OCTOBER

Noon–7:00pm Registration
7:00pm–8:30pm Reception in Exhibit Hall

10:00am–4:00pm Exhibits open
2:00pm–4:00pm Poster Session
4:00pm–7:00pm

Human Genetic Diversity

L.L. Cavalli-Sforza, Stanford Univ.

"Genetic diversity and history of the human species"

Alberto Piazza, Univ. of Torino

"Population genetics of Europe"

Kenneth Kidd, Yale Univ. Sch. of Medicine

"Nuclear DNA polymorphisms and evolution of new world populations"

Svante Pääbo, Univ. of Munich

"Ancient and modern DNA sequences as a tool to reconstruct human history"

Julia Bodmer, Imperial Cancer Research Fund

"HLA allele and haplotype frequencies in world populations"

7:00pm–8:00pm HUGO Business Meeting

THURSDAY, 15 OCTOBER

8:30am–Noon

Mapping

Chair: **Bertrand R. Jordan**, INSERM-CNRS

Jean Weissenbach, CNRS, Inst. Pasteur

"The second generation of human linkage maps: The Genethon linkage mapping project"

Daniel Cohen, Ctr. d'Etude du Polymorphisme Humain

"Accelerated physical map of the human genome"

Malcolm Ferguson-Smith, Cambridge Univ.

"Gene order by FISH and FACS"

8:30am–Noon

10:00am–4:00pm

Exhibits open

ApplicationsChair: **Kenichi Matsubara**, *Osaka Univ.***Yusuke Nakamura**, *Japanese Fdn. for Cancer Research*
“The Human Genome Project and cancer genetics”**Ulf Landegren**, *Univ. of Uppsala*
“Ligase-mediated gene detection”**Mathias Uhlen**, *Royal Inst. of Technology*
“Automated DNA sequencing as a clinical tool”**Michel Perricaudet**, *Inst. Gustave Roussy*
“Use of adenovirus vector for gene transfer in vivo”

2:00pm–4:00pm

Poster Session

4:00pm–7:00pm

**Contributed Papers:
Oral Presentations**Chair: **Jean-Louis Mandel**, *CNRS/LGME, INSERM*

(Speakers will be chosen from among those who submit the best abstracts for the poster session presentations.)

Hotel Reservation Form

HUMAN GENOME '92 ♦ Nice, France ♦ 14–17 October 1992

Send confirmation to:

Name _____
(first name) (last name)

Institution/company _____

Address _____

City/state/zip/country _____

Phone _____ Fax _____

Other occupant(s) of room _____

Regular room rates: Daily rates range from 780 FF to 920 FF*. All participating hotels are rated ★★★★★. Please rank the following selection criteria in order of importance, 1–3, (1 being most important):

_____ Lower rate _____ Closer to conference center _____ Higher quality

☐ **Check here for special student rate:** A limited number of rooms are available to student registrants in ★★ hotels at rates ranging from 300 FF to 470 FF*. To apply for one of these rooms, you must attach a copy of your valid student ID card. *If you do not include this proof of student status, your reservation form will be returned unprocessed.***Type of room desired** (check one):☐ Single (1 person, 1 bed) ☐ Double/Double (2 people, 2 beds) ☐ 1-bedroom suite☐ Double (2 people, 1 bed) ☐ Triple (Students only; 3 people, 3 beds)**Arrival date** _____ **Departure date** _____**Deposit required:** Rooms must be guaranteed with a deposit of US \$390 per room (\$125 per room for student registrants) or \$725 per suite, either by VISA, MasterCard, or check.☐ Check enclosed (payable to AAAS on a U.S. bank) ☐ VISA ☐ MasterCard
(No other cards can be accepted.)

Credit card # _____

Exp. date _____ Signature _____

*Exchange rate as of 18 June 1992: 1 FF = US \$0.1878

Reservations: The AAAS Meetings Office will coordinate hotel reservations on a first-come, first-served basis upon receipt of a properly completed *Human Genome '92* housing form. Reservations will be processed in order of receipt, based on choice and availability.**Telephone reservations cannot be accepted;** however, reservation forms using credit cards may be faxed to 202-289-4021.**Use a separate reservation form** for each room requested, *not* for each individual. Send only *one* form if sharing with a colleague.**Please be thorough!** Failure to include all pertinent information will delay processing of your reservation.**Cancellations/changes:** To cancel or change reservations prior to 6 October, contact the AAAS Meetings Office. After that, please contact the hotel directly. For cancellations received between 15 July and 6 October, one-half of room deposit will be refunded. No refunds will be made for cancellations received after 6 October.**Send your completed form and deposit to:***Human Genome '92*
AAAS Meetings Office
1333 H Street, NW
Washington, DC 20005, USAOr fax (credit card deposits only) to:
202-289-4021**Deadline:** Reservation forms must be received at AAAS no later than **18 September 1992**. Housing requests received after 18 September 1992 are conditional on room availability.**It is recommended that you keep a photocopy of this form for your records.**

8:30am–Noon

Model Organisms

Marc van Montagu, *Univ. of Gent*
"The *Arabidopsis* genome"

Piotr Slonimski, *CNRS*
"The esoteric, elusive, but conspicuous genes of *Saccharomyces cerevisiae*"

Eric S. Lander, *Whitehead Inst.*
"Mapping the mouse genome"

Michael Ashburner, *Cambridge Univ.*
"Genome mapping in *Drosophila*"

10:00am–4:00pm Exhibits open

2:00pm–4:00pm Poster Session

4:00pm–7:00pm

cDNA Sequences and Their Uses

Chair: **Lennart Philipson**, *EMBL*

J. Craig Venter, *Natl. Insts. of Health*
"cDNA sequencing as a strategy for new gene discovery"

Kenichi Matsubara, *Osaka Univ.*
"Functional analyses of the human genome"

Charles Auffray, *Inst. d'Embryologie du CNRS*
"The Genexpress cDNA Program: Towards an inventory of the repertoire of transcribed human sequences"

Andrei D. Mirzabekov, *W. Engelhardt Inst. of Molecular Biology*
"cDNA sequencing and sequence comparison by hybridization with oligonucleotide matrix: Advantages and implications"

Rebecca Eisenberg, *Univ. of Michigan*
"Patenting the human genome"

7:30pm–11:00pm Banquet (separate fee required)

Call for Abstracts (Deadline: 3 August)

The poster sessions at **Human Genome'92** provide an informal way for you to discuss your own research with interested colleagues. Also, the best abstracts will be selected for oral presentation in a special plenary session at the meeting. Appropriate topics include original research relating to any of the meeting's plenary sessions.

Requirements for submission: The first author listed on the abstract must be registered for **Human Genome '92** (use form on the following page). A maximum of two abstracts per first author will be selected for oral or poster presentation if they are judged of high quality.

Format of abstracts: Abstracts not conforming to the following format will be returned unprocessed. Type the text of the abstract to fit within a 5" (12.7 cm) square in the center of a sheet of white paper. Use a typewriter or letter-quality (not dot matrix) printer. Use black ink for all hand lettering. Indent, space, underline, and capitalize as in the example on the right. Do not double-space the body of the text. Do not draw a box around the abstract, nor cut out the abstract. Above the 5" (12.7 cm) square, type the name of the plenary session to which the abstract relates. Below and to the left of the square, type the name, address, phone number, and fax number of the presenter. Justify text, if possible.

Mailing instructions: Mail the abstract *flat* (do not fold or bend). Send original plus two photocopies to: Human Genome Contributed Papers, AAAS Meetings Office, 1333 H Street, NW, Washington, DC 20005, USA.

Deadline: Abstracts received after **3 August 1992** will not be accepted.

Acceptance: The organizers will evaluate abstracts and notify of acceptance for poster or oral presentation by mid-September. Poster presenters should design their displays to fit a 1.8 m × .9 m bulletin board. Oral presenters will receive further instructions by mail. Accepted abstracts will be published in the meeting program.

<p>Name of plenary session to which abstract relates</p> <p>(Skip at least 3 lines before beginning abstract.)</p> <div style="border: 1px solid black; width: 80%; margin: 10px auto; text-align: center;"> <p>5"</p> </div> <p style="text-align: center;"><u>Indent 7 Spaces and Type Title in Upper and Lower Case Letters and Underline.</u> PRESENTER'S NAME IN UPPER CASE (Institution Name in Upper and Lower Case Within Parentheses), ADDITIONAL AUTHOR (Institution), etc.</p> <p>Skip one line and type abstract. The full width of the column of typed material should be 5 inches (12.7 cm) and must not extend beyond that. The total length of the material, from top of title to bottom of footnotes, must not exceed 5 inches (12.7 cm). Abstracts that exceed these parameters will be returned. Any special symbols or signs that must be hand lettered should be rendered in black ink as clearly and carefully as possible. The entire submission should be of camera-ready quality so that it can be photographed and printed. Justify, if possible. The printed abstract will be about 2/3 the size of the typed version. Avoid paragraphing, as this wastes space. However, you may use your allotted space to neatly letter equations and diagrams as you deem necessary, as in this example:</p> <div style="text-align: center; margin: 10px 0;"> </div> <p>You may also use your allotted space for footnotes.*</p> <p>*Skip one line and type footnotes, if any.</p>	
<p>Name of Presenter</p> <p>Presenter's Street Address</p> <p>Presenter's City/State/Zip</p> <p>Presenter's Country</p> <p>Presenter's Phone and Fax Numbers</p>	

Advance Registration Form

Deadline: 18 September

(please type or print)

HUMAN GENOME '92

14–17 October 1992 ♦ Nice, France

First name (as you would like it to appear on your badge)			Last name (as you would like it to appear on your badge)		
Institution/company (will appear on badge, subject to abbreviation)					
Mailing address					
City		State		Zip code or postal code	
Country					
Daytime phone number			Fax number		

Check this box ☐ if you need special services due to a disability (we'll contact you before the meeting).

Registration fees¹ (check one)

	Advance	On site	
<input type="checkbox"/> Regular	US \$295	US \$345	\$
<input type="checkbox"/> Graduate student / Post-doc	US \$ 90 ²	US \$115 ²	\$

Additional fee for banquet (optional)

<input type="checkbox"/> Saturday-night banquet	US \$ 50	US \$ 50	\$
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Total \$

Method of payment³: ☐ Check enclosed⁴ ☐ VISA ☐ MasterCard
(no other cards accepted)

Credit card number

Credit card expiration date _____ Signature _____

Send to: Human Genome '92, P.O. Box 630285, Baltimore, MD 21263, USA (Tel: 202-326-6450).

[1] **Deadline for advance registrations** is 18 September 1992. Thereafter, register in person at the Acropolis beginning at noon, 14 October. Registration fee includes all meeting sessions plus two beverage breaks per day, an opening reception, and a meeting program.

[2] **To qualify for student rate**, you must attach a copy of your student ID card or a letter from your advisor or chairman confirming your status as a graduate student or post-doc. Registrations received without appropriate verification will be charged at the Regular rates.

[3] **Registration cancellations** must be received in writing (at the address or FAX number at left) no later than 25 September 1992. *No refunds will be made for cancellations received after this date.* Refunds are subject to a \$50 cancellation charge and will be processed after the meeting.

[4] **Checks** must be in U.S. currency and must be payable on a U.S. bank. Make check payable to AAAS.

Invitation to exhibit

If your organization supplies products or services that are of use to scientists doing human genome research, you should exhibit at **Human Genome '92**.

For information about exhibiting, contact Scott Pierce in the AAAS exhibit sales office at 202-326-6462 (fax: 202-289-4021).

After Human Genome '92...

Consider attending *The First International Conference on Mathematical and Computational Analysis of the Human Genome and Its Mutation Load*, 20–24 October 1992 in Szeged, Hungary.

The meeting is sponsored by Human Genome Research Ltd. and is chaired by Istvan Szentesi, Principal Scientist on the Hungarian Human Genome Project. For more information, call (36) 62-23855 or fax (36) 62-23844.

Discount air fares from the USA

Fly Air France or Delta Air Lines to **Human Genome '92** and you can save with low, discount air fares available for travel departing from and returning to the United States between 8 October 1992 and 31 October 1992.

Air France: Discounted fares are available for round-trip or one-way travel to and from Nice or Paris. There are no minimum stay requirements.

Delta: Discounts apply to coach, business, or first-class travel to and from Nice. Discounts also apply to other European and UK cities, provided one segment is to Nice.

These special fares are available only through the Gil Travel convention reservation desk. Certain restrictions may apply and seats are limited.

For information or reservations, call the toll-free number below and tell the travel specialist that you are attending **Human Genome '92**. Or you can fax your inquiry to the Gil Travel fax number listed below.

Toll-free number: 800-888-5127; **Fax:** 215-742-4050

**1992
AAAS AWARD
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Nominations Invited

- An annual Award for working scientists and engineers from all disciplines who make outstanding contributions to public understanding of science and technology but are *not* members of the media.
- Contributions should have a significant impact on the public; be accurate, timely, and innovative; and convey the meaning, excitement, and significance of scientific activity.
- The Award will be presented during the AAAS Annual Meeting in Boston, Massachusetts, February 11-16, 1993.
- The Award carries a \$5,000 prize.

1991 Award Winner: Stephen H. Schneider
National Center for
Atmospheric Research

For additional information, contact: Patricia S. Curlin,
AAAS Committee on Public Understanding of Science
and Technology, 1333 H Street, NW, Washington, DC
20005, telephone 202/326-6605 or fax 202/371-9849.

Deadline for nominations is 1 August 1992.

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