American Association for the Advancement of Science

SCIENCE

5 July 1991 $6.00
Vol. 253 ■ Pages 1–108

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1. Nielson, K. and Mathur, E.J. (1990) Strategies 3:17-19.
2. Nielson, K. and Mathur, E.J. Manuscript in preparation.
3. Nielson, K. and Mathur E.J. (1989) U.S. patents filed.
4. Mullis, K.B., and Faloona, F.A. (1987) Meth. Enzymol. 155:335-350.

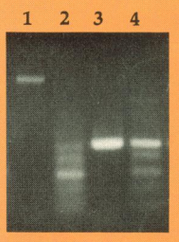

Figure Legend: A photograph of a 1% agarose gel stained with ethidium bromide representing reaction products from PCR amplifications using the GeneAmp™ Kit† from Perkin-Elmer Cetus according to manufacturer's instructions. The reactions were conducted with (lanes 1 and 3) and without (lanes 2 and 4) the inclusion of 1 unit Perfect Match polymerase enhancer. Lanes 1 and 2 represent 100 ng of human genomic DNA amplified with two 26-mer primers separated by 1400 nucleotides. Lanes 3 and 4 represent 100 ng of mouse genomic DNA amplified with two 23-mer primers separated by 550 nucleotides.

Figure 1 shows two examples of *in vitro* amplification reactions that are significantly enhanced by the addition of Perfect Match polymerase enhancer to the polymerase preparation. Note that in lanes 1 and 2, the desired PCR product cannot be detected unless Perfect Match polymerase enhancer is added to the amplification reaction. In lanes 3 and 4, Perfect Match polymerase enhancer not only increases the intensity of the desired amplification products, but dramatically reduces the background artifacts generated by non-specific priming events.

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SCIENCE

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ATTENTION AAAS MEMBERS

Inside AAAS of 28 June 1991 (p. 1861) contained a preliminary list of candidates for the Association's elections for general and section officers. Additional names may be placed in nomination by petition submitted to the executive officer no later than 12 August 1991. Please refer to the 28 June issue for further details.

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■ The American Association for the Advancement of Science was founded in 1848 and incorporated in 1874. Its objectives are to further the work of scientists, to facilitate cooperation among them, to foster scientific freedom and responsibility, to improve the effectiveness of science in the promotion of human welfare, to advance education in science, and to increase public understanding and appreciation of the importance and promise of the methods of science in human progress.

COVER Adélie penguins (*Pygoscelis adeliae*), shown here at a rookery on Torgerson Island near the U.S. Antarctic science base Palmer Station, are a vital link in the Southern Ocean food web. Respiration of carbon dioxide by Antarctic birds and mammals may represent a significant inefficiency in the storage of fixed carbon in the ocean. This phenomenon may affect current models of the global ocean-atmosphere carbon flux. See page 64. [Photograph by David M. Karl]

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Reports

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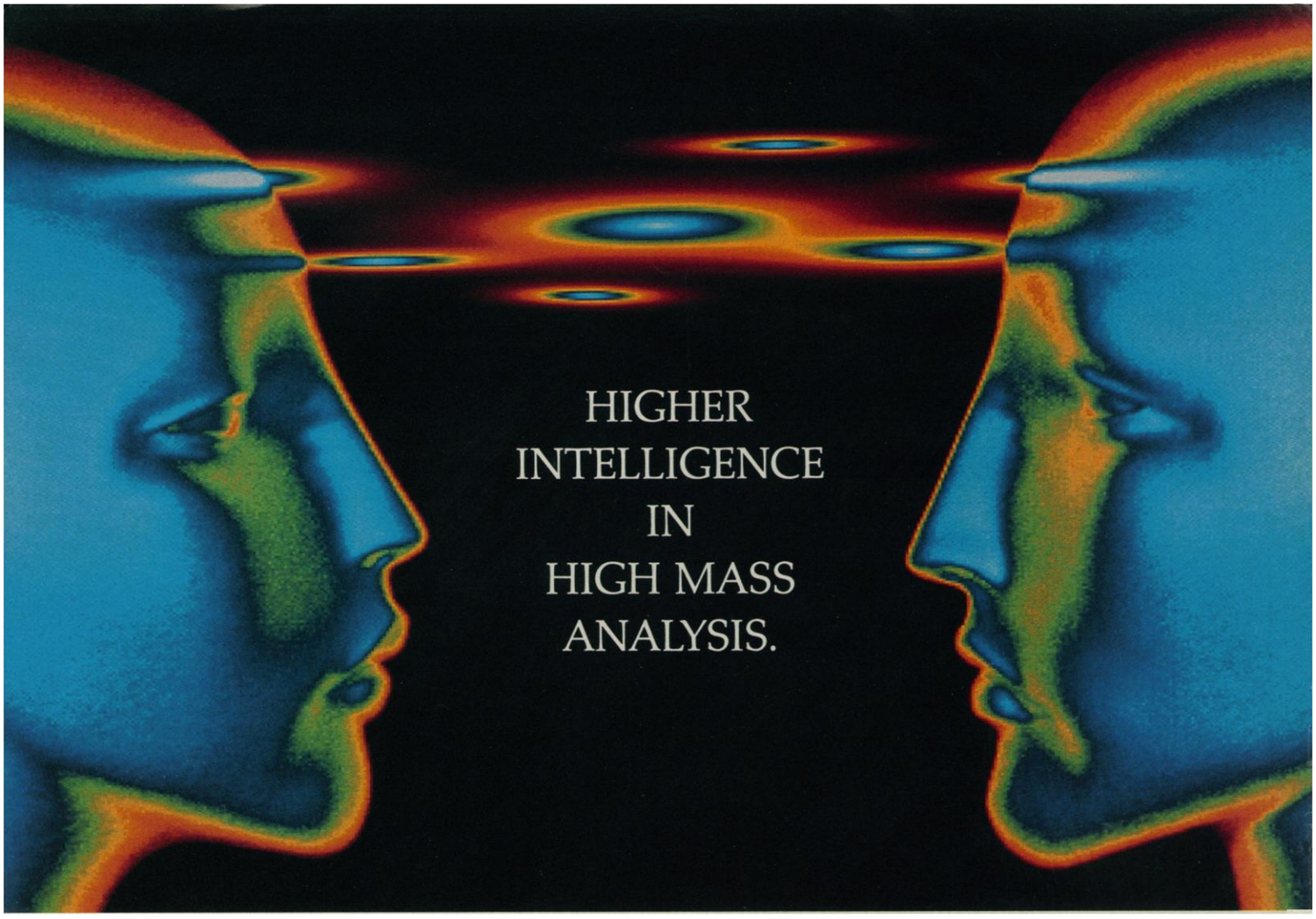
Book Reviews

Products & Materials



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This Week in
SCIENCE

AIDS trends

Estimates of past, present, and future HIV infection rates are hard to calculate and fraught with statistical uncertainty. Brookmeyer (page 37) used the technique of back-calculation to model HIV incidence; the estimates were corroborated with other approaches. The rates of infection were extrapolated to obtain projections of future AIDS incidence and number of individuals with advanced HIV disease. Effective therapies and a decline in underlying infection rates may cause a leveling of AIDS incidence in the next 5 years, but the number of cases of advanced HIV disease needing therapy may increase by 40 percent.

Heavenly atoms

Atoms were once imagined to be tiny solar systems, with electron planets whirling around a central nucleus. The quantum theory that Schrodinger and Heisenberg developed in 1925 dispensed with this intuitively appealing picture. During the last two decades, however, classical methods that were once the domain of astronomers have experienced a renaissance in atomic and molecular physics. Uzer *et al.* (page 42) review developments in semiclassical mechanics, with emphasis on the combination of group theory and nonlinear dynamics to study atoms in electric and magnetic fields.

Anchored receptor

Little is known about ciliary neurotrophic factor (CNTF), which has no structural homology to members of the nerve growth factor (NGF) family. Davis *et al.* (page 59) cloned the receptor for CNTF and found that it is expressed within the nervous system and in skeletal muscle. Sequence analysis revealed that this receptor is unrelated to NGF receptors. However, its extracellular domain is similar to that of a receptor for a cytokine, interleukin-6 (IL-6). The CNTF receptor lacks a cytoplasmic domain, and unlike all other receptors it is held to the cell membrane by a glycosylphosphatidylinositol anchor. The CNTF receptor may require a second signal transducer; one candidate is the one IL-6 uses, gp130.

Defeating dead ends

The sequence of amino acids in a polypeptide chain can suppress the folding of proteins into insoluble aggregates. Mitraki *et al.* (page 54) show that a single amino acid mutation at the center of a polypeptide chain could suppress "dead-end" folding pathways in mutants of the phage P22 tailspike protein that fold normally at lower temperatures but that form aggregates when folding occurs at higher temperatures. The substitution inhibited folding that would have led to aggregation and increased the efficiency of forming the native state.

A leak at the top

One suggestion for dealing with high amounts of atmospheric CO_2 and its attendant greenhouse effect has been to try to put it in the ocean as phytoplankton; Huntley *et al.* (page 64) argue that it may not stay there because of bird and mammal respiration. They analyzed the relatively simple food web in the Southern Ocean, where fixing of CO_2 by phytoplankton at the bottom of the food chain accounts for nearly 15 percent of the world's primary productivity. Birds and mammals at the top of the food chain respire a large fraction of the CO_2, 20 to 25 percent of it, directly back into the atmosphere.

Probable extinction

The elimination and range reduction of two species of eastern Pacific reef-building hydrocorals (*Millepora*) that occurred during the 1982–83 El Niño event has been documented by Glynn and de Weerdt (page 69). Warmer surface waters associated with El Niño caused these species to lose their zooxanthellae (symbiotic dinoflaggelates) and undergo bleaching; despite extensive searches, the two species have not been seen alive off the coast of Panama since 1983. One of these species is unknown outside of Panama, and the authors argue that this event probably was an extinction. Other such widespread disturbances have occurred in tropical marine habitats during the last several decades, but no species extinctions have been noted in coral reefs.

Leukemia homeobox

The proposed TCL3 gene that is the most frequent site of chromosomal rearrangement in T cell acute lymphoblastic leukemia, the t(10;14)(q24;q11) breakpoint, has been cloned by Hatano *et al.* (page 79). The transcript of this gene was expressed in human liver but not normally in thymus or in resting or activated T cells. The gene is a new homeobox, HOX11, and its homeodomain is similar to that of murine *Hlx*. Other translocated genes associated with T cell leukemia also belong to the classic transcription factor families. These genes are intended for other cell lineages but get redirected by translocation into the loci for the T cell receptor.

Ultrasonic hearing

People with hearing impairments can discriminate among acoustic frequencies and recognize words if the sounds are converted into ultrasonic vibrations, according to Lenhardt *et al.* (page 82). Speech signals were translated to high frequencies by amplitude modulation of an ultrasonic carrier and administered directly to the skull. Acutely deaf subjects were able to score above chance level on word recognition tasks. The authors conclude that bone-conducted ultrasonic speech perception could potentially assist in the rehabilitation of hearing disorders.

■ PHILLIP SZUROMI AND DAVID VOSS

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SCIENTIFIC PROGRAM

MONDAY, OCTOBER 21

8:30 am-12:00 pm SESSION I — INFORMATICS

ELBERT BRANSCOMB: Lawrence Livermore National Laboratory – "Managing Genomic Data for the Research Community's Benefit"

EDWARD UBERBACHER: Oak Ridge National Laboratory – "Intelligent Methods for DNA Sequence Feature Recognition and Intepretation"

MINORU KANEHISA: Kyoto University – "Knowledge Information Processing for Genome Analysis"

CHRIS RAWLINGS: Imperial Cancer Research Fund – "Integrating Genome Information: A Knowledge-based Approach"

ROSS OVERBEEK: Argonne National Laboratory – "Setting up an Effective Query Capability: A Radical Proposal"

JULIO CELIS: Aarhus University – "Human 2-D Gel Protein Databases: Linking Protein and DNA Information"

12:00 pm-4:00 pm LUNCH/WORKSHOPS/EXHIBITS/POSTERS

4:00 pm-7:15 pm SESSION II — MODEL ORGANISMS

JOSEPH NADEAU: The Jackson Laboratory – "Encyclopedia of the Mouse Genome and the Database Integration Problem"

ANDRE GOFFEAU: Catholic University of Louvain – "The European Plan to Sequence the Yeast Genome: Progress Report"

KUNIO ISONO: Tohoku University – "Neurogenetics of Taste in *Drosophila*"

FOTIS C. KAFATOS: Harvard University/IMBB, Crete – "Integrated Maps of the *Drosophila* Genome"

EUGENE RINCHIK: Oak Ridge National Laboratory – "Fine-structure Functional and Physical Mapping of Germline Deletions in the Mouse"

TUESDAY, OCTOBER 22

8:30 am-12:00 pm SESSION III — POLITICS

WALTER BODMER: Imperial Cancer Research Fund – "HUGO"

CHARLES R. CANTOR: DOE Human Genome Project – "U.S. Department of Energy"

MARK GUYER: National Institutes of Health – "Index Markers"

KENICHI MATSUBARA: Osaka University – "The Japanese Genome Project as of 1991"

BRONWEN LODER: Commission of the European Communities – "The EC Human Genome Analysis Programme"

12:00 pm-4:00 pm LUNCH/WORKSHOPS/EXHIBITS/POSTERS

4:00 pm-7:15 pm SESSION IV — PHYSICAL MAPS: CAN THEY BE COMPLETED?

GLEN EVANS: Salk Institute – "Physical Maps of Human Chromosomes"

HANS LEHRACH: European Molecular Biology Laboratory – "Of Mice and Men: The Global Analysis of the Mammalian Genome"

ANTHONY CARRANO: Lawrence Livermore National Laboratory – "A Chromosome 19 Physical Map"

ROBERT MOYZIS: Los Alamos National Laboratory – "Physical and Functional Mapping of the Human Genome"

WEDNESDAY, OCTOBER 23

8:30 am-12:00 pm SESSION V — METHOD DEVELOPMENT

RONALD W. DAVIS: Stanford University – "Sequencing the Yeast Genome"

WACLAW SZYBALSKI: McArdle Laboratory, University of Wisconsin – "Sequencing of Eukaryotic Genomes Without Cloning"

PIETER J. DEJONG: Lawrence Livermore National Laboratory – "A New Approach for Completing Contig Maps Using Alu-PCR"

LLOYD M. SMITH: University of Wisconsin – "High-speed DNA Sequencing in Ultrathin Gels"

DAVID WARD: Yale University – "Gene Mapping by Fluorescence In Situ Hybridization"

12:00 pm-4:00 pm LUNCH/WORKSHOPS/EXHIBITS/POSTERS

4:00 pm-7:15 pm SESSION VI — HUMAN LANDMARKS

PETER GOODFELLOW: Imperial Cancer Research Fund – "Chromosome Fragmentation Techniques"

ANTHONY MONACO. Imperial Cancer Research Fund/University of Oxford – "Genome Analysis of the Human X Chromosome"

GRANT R. SUTHERLAND: Adelaide Children's Hospital – "The Fragile X: A Novel Genetic Element"

L. L. CAVALLI-SFORZA: Stanford University – "Diversity and the Origin of Races"

MARY-CLAIRE KING: University of California, Berkeley – "Genetic Analysis of Breast Cancer in Families"

All speakers listed have been confirmed. Others will be added later.

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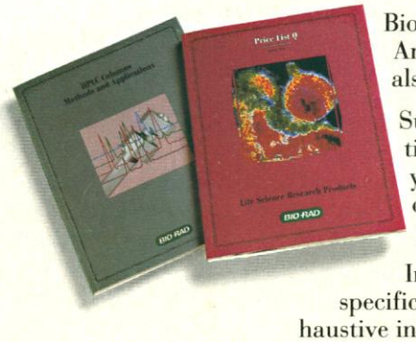

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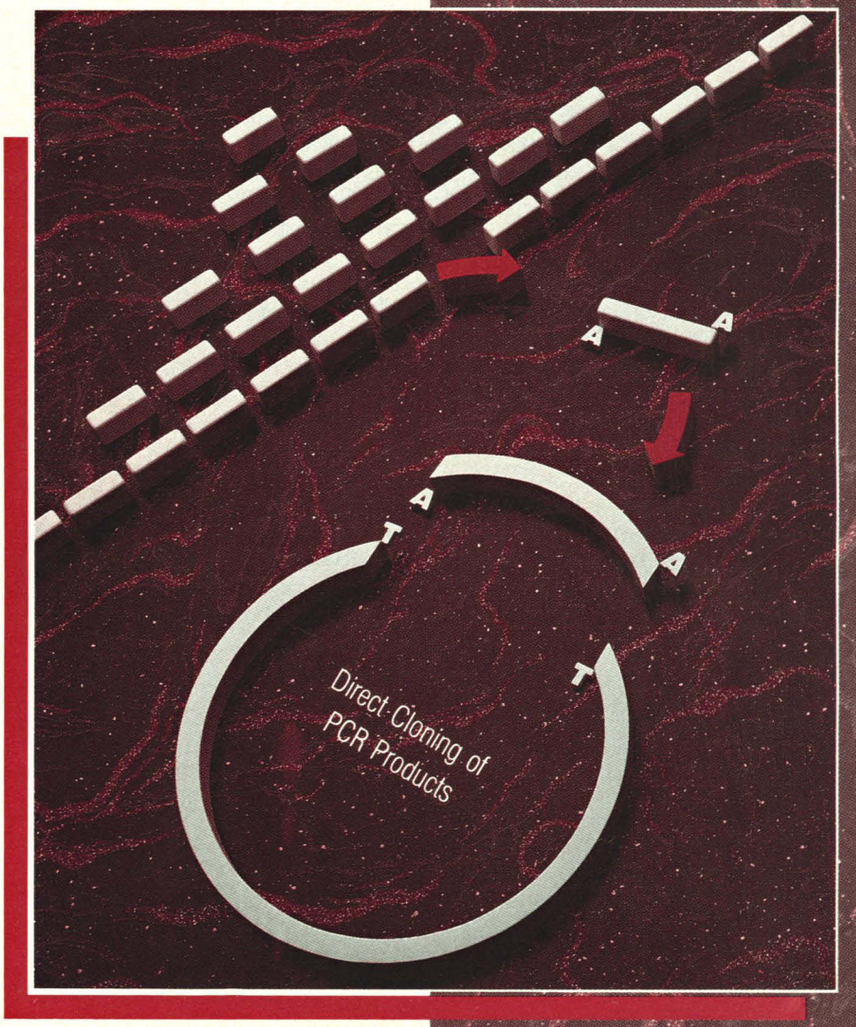

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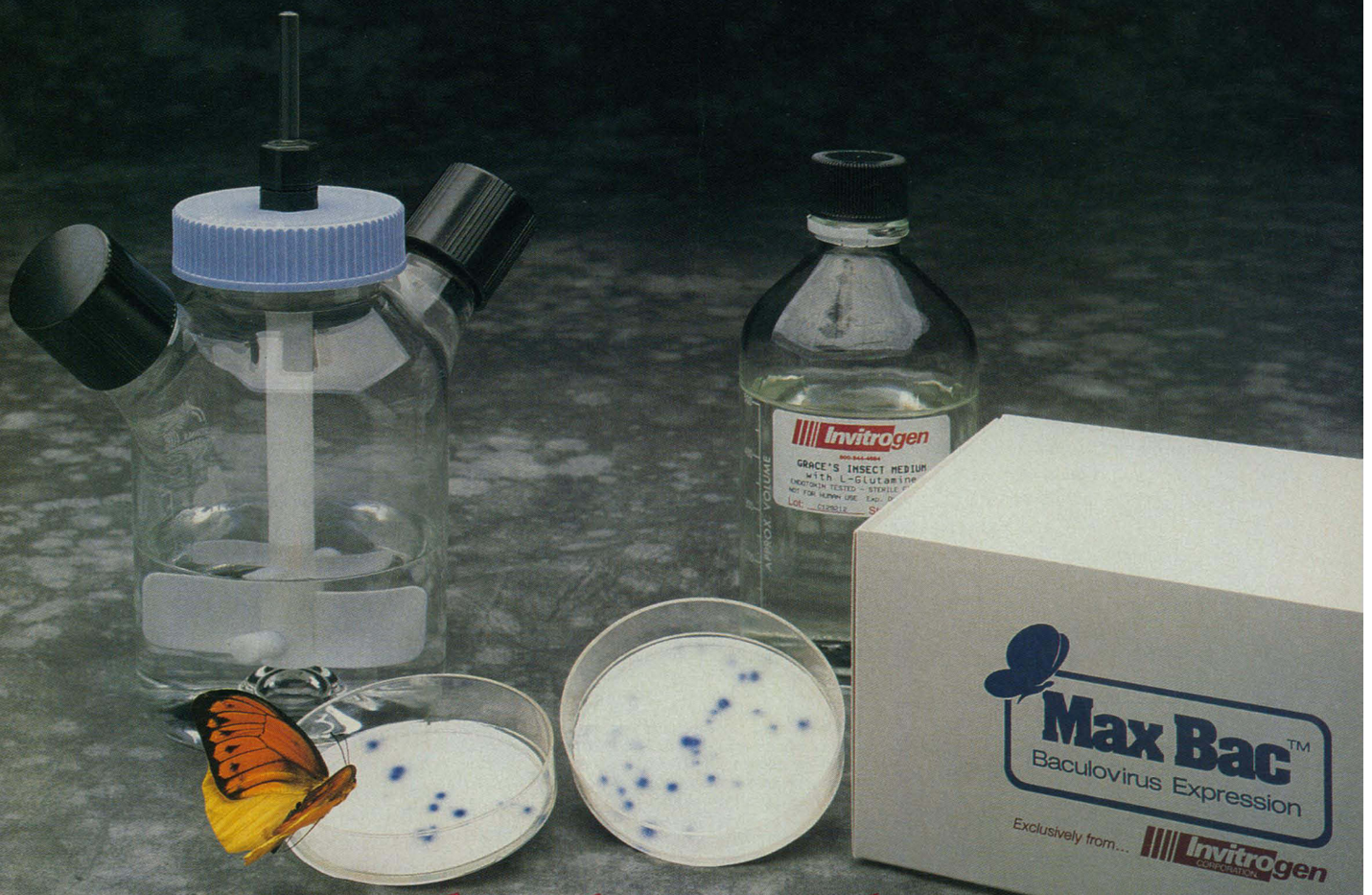

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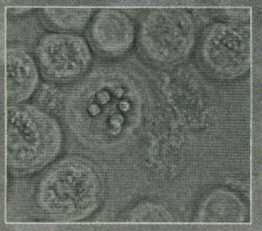

Figure 1. Infected Sf9 insect cells showing viral occlusions.

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