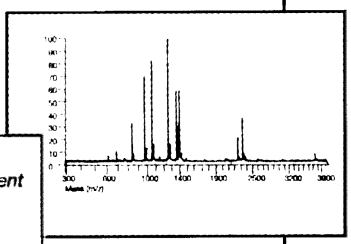
Opinion

Matrix Assisted Laser Desorption Ionization (MALDI) can go a long way in helping to establish the protein map of a specific organism.

The sensitivity of MALDI allows the determination of the molecular mass of proteins/glycoproteins after 2D-gel electrophoresis. This can be achieved either by elution of the protein from a membrane after electroblotting or by direct molecular mass determination on the membrane by MALDI with an infrared laser. The VISION 2000, a MALDI TOF research system, has been designed to have both an Infrared laser as well as the standard UV laser mounted at the same time.



MALDI measurement of a tryptic digest of Human Growth Hormone.

Subsequent enzymatic digest of an individual protein provides a mixture of peptides which can be directly mass analyzed by MALDI without prior separation or cleanup.

Since many of the proteins in question will be known already, database search programs like MASSMAP™ will aid tremendously in identifying these at this stage.

The amino acid sequence of individual peptides can then be determined by Post Source Decay and Precursor Ion Selection directly out of the enzymatic digest revealing the subtle differences in modified proteins.

The VISION 2000 makes all this power of mass and structure analysis available at the low picomole to femtomole range. It should prove an invaluable tool in the biochemistry lab of the future.

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The OPINION column features technical tips & preliminary information relating to instruments designed & built at Finnigan MAT GmbH, Bremen, Germany.

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tive currently under way, to support European infrastructure facilities in three strategically important areas: bioinformatics, macromolecular structure, and stock centers and genetic archives. The need for such support emerged from discussions in expert committees invited to advise Commissioner A. Ruberti on the life sciences in the European Union's (EU's) next Framework Programme. To ensure multilateral action, the Commissioner invited national and international organizations, including EMBL, to develop a coherent plan of facilities on a continental scale, irrespective of location or institutional affiliation. Proposals are to be submitted and evaluated competitively, by the EU's standard procedures. The EMBL resolution supporting this initiative is as follows.

It is widely recognised that modern biological research and biotechnology often depend on unimpeded access to major service infrastructure facilities. Examples include databases of macromolecular sequence and three-dimensional structure, facilities for determination of biological structures at high resolution, and repositories of mutant animals. Technical developments in recent years have greatly increased the complexity and cost of these required facilities. Accordingly, efficiency in resource utilisation and effectiveness in provision of service now require that these facilities operate on an international scale. For maximal added value, these facilities should be coordinated. With the encouragement of the EU, a concrete initiative in this direction is emerging from multilateral discussions, involving national research organisations and EMBL; it envisages applying to the EU for support to establish, develop and maintain infrastructures for the benefit of European life sciences research. The EMBL Council enthusiastically endorses this initiative, with the following understandings:

a. Facilities will be accessible to all EMBL as well as all EU member states.
b. Technical advice will be offered to the coordinating body of the cooperating organisations by international committees of experts, irrespective of nationality, nominated by the organisations and co-chaired as follows:
   - Bioinformatics: P. Zanella, G. Cameron
   - Macromolecular structure: C. I. Brändén, S. Cusack
   - Genetic archives: P. Gruss, P. Rigby
c. The Director-General will participate in the coordinating body of the cooperating organisations.
d. Two core facilities under this action will be the existing EBI [European Bioinformatics Institute] and Grenoble Outstations.
e. As part of the infrastructure initiative, it is expected that the third core facility will be a newly established European EU-funded mouse genetic archive. EMBL notes that a leading candidate for hosting this archive is the Monterotondo [Italy] campus. Subject to being satisfied on the technical, logistic and organisational provisions, with the benefit of advice from the P. Gruss/P. Rigby expert committee, EMBL will be happy to support the candidacy of Monterotondo, considering also the expected positive synergy with research groups to be established on the same campus both by EMBL and by CNR [Consiglio Nazionale delle Ricerche]. While welcoming cooperation, EMBL does not claim control or responsibility for the genetic archive which will be a distinct international institution, and incurs no financial obligation beyond supporting its own four research groups at Monterotondo.
f. Networks of complementary facilities will be associated with the three cores; the nodes will be selected by scientific criteria according to the functions required, without regard to their location, which could be in any EU or EMBL member country.

The second EMBL decision pertains to a separate, bilateral issue—Italy's continuing membership in EMBL. It is in response to the Italian government's request that resources previously committed for "regional groups" in Italy be used to create an international nucleus of research on mouse genetics at the Monterotondo campus near Rome. The EMBL decision is as follows.

In the expectation that an EU-supported mouse genetic archive will be established at Monterotondo near Rome, and that CNR will also move related activities there, EMBL agrees to establish on the same campus four research groups working on mouse genetics, subject to the following conditions:

a. Italy remains an EMBL Member State and contributes its full share of the EMBL Indicative Scheme.
b. These groups are a substitute for the regional groups committed to Italy by [the] Council in December 1993 and will be assigned comparable resources.
c. The group leaders will be recruited internationally, and will be selected by EMBL with the help of a committee of experts appointed by the Director-General.
d. The terms of appointments to these groups will be the same as for other EMBL personnel.
e. Italy undertakes, as necessary, to reach an appropriate host site agreement with EMBL in a timely manner.

These decisions are part of EMBL's continuing efforts toward cooperative development of European molecular biology.

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Expressed Sequence Tags

On behalf of the American Society of Human Genetics, we would like to commend Merck and Company, Inc. for its decision to support an open policy of data and reagent sharing for a comprehensive, publicly available database of human Expressed Sequence Tags (ESTs) and a cor-

responding, freely accessible complementary DNA (cDNA) clone repository. We believe that this initiative will have a great positive impact on human genome research and should significantly accelerate the pace at which genes responsible for human disease are identified by the basic biomedical research community.

The speed and scope of this exciting initiative are particularly noteworthy. Merck has finalized an agreement with the Genome Sequencing Center at Washington University to sequence 400,000 ESTs, each representing approximately 400 base pairs of "single pass" sequence, from the 5′ and 3′ ends of 200,000 human cDNA clones. The clones will be derived from various tissues and developmental stages and thus represent a large fraction of the human gene repertoire. The 3′ end sequences will be highly suitable for generating polymerase chain reaction primer pairs for successfully probing genomic DNA and will therefore facilitate the mapping of specific cDNAs on human chromosomes. The 5′ end sequences will be highly enriched for open reading frames and will therefore facilitate identification of human cDNA–based sequence similarity to proteins of known function in existing databases. New cDNA sequences will be submitted on a daily basis to dbEST (a division of GenBank at the U.S. National Center for Biotechnology Information) and made immediately available to the public through GenBank and its international collaborators, the European Bioinformatics Institute and the DNA database of Japan. Furthermore, the cDNA clones from which the ESTs are derived will be publicly available and distributed freely on request. The nonproprietary aspect of EST data and cDNA clone acquisition and use will maximize the enormous value offered to the biomedical community by this initiative.

The projected magnitude of the throughput for EST sequence generation is impressive and offers great promise for productive applications in the immediate future. Beginning in January 1995, 6000 to 8000 ESTs per week will be generated and deposited in the public databases. Thus, dbEST (which currently contains 32,208 human ESTs) will increase by more than 25,000 ESTs per month over the next 18 months. This rapid growth of data and clone resources, available to individual investigators within the biomedical research community (including industry and academia), will make repeated periodic homology searches for cDNAs of interest an increasingly productive strategy for elucidating basic biological processes and will accelerate progress in research laboratories throughout the world.

Public access to a comprehensive EST database and corresponding cDNA clone repository is virtually guaranteed to make connections between basic biological research and mechanisms responsible for human disease and should do so at an enormous savings in time and resources. We thank Merck and Company, Inc. for providing the support and for adopting an open, nonproprietary policy that assures major advances in the study of human biology.

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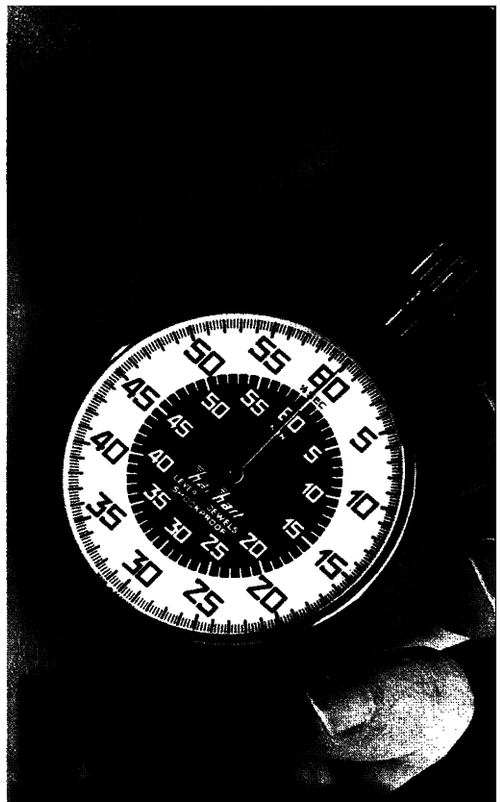
Crystalline Polymorph Construction: Correction

In our report "Control of structure and growth of polymorphic crystalline thin films of amphiphilic molecules on liquid surfaces" (10 June, p. 1566) (*1*), we stated that over both 100% liquid formamide and 70% formamide in water, the amphiphile arachidamide without additive forms two major phases, both of which are multilayers. This is indeed the case over 100% formamide, but further analysis indicates that the phase of arachidamide without additive over 70% formamide in water, in which the molecular chains are aligned with their axes vertical with respect to the liquid surface and the carbon backbone planes of neighboring molecules are orthogonal to one another (⊥), is primarily a monolayer, contrary to



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