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

what we reported in (*1*). The phase in which the chains are tilted and have their backbone planes all parallel (*//*) is a multilayer, as we stated in (*1*). This conclusion is based on the intensity profiles of the Bragg rod data from the grazing incidence x-ray diffraction measurements (*1*, figure 1B, top). The full-width at half-maximum (fwhm) of the Bragg rod profiles along the vertical scattering vector q_z of the (11) and (02) reflections [yellow, not red, as stated in (*1*, figure 1B, top)] corresponding to the untilted ($\perp$) phase without additive are each 0.2 $Å^{-1}$, indicating a monolayer. The fwhm's of the three reflections (11, 01, 10) of the tilted phase (*//*) [red, not yellow, as stated in (*1*, figure 1B, top)] without additive indicate a multilayer according to their fwhm of 0.1 $Å^{-1}$. The fwhm's of the (11) and (02) Bragg rods of the untilted phase with additive (*1*, figure 1B, bottom) are almost the same as for the corresponding phase without additive.

This correction in no way contradicts the concluding statement in our abstract that auxiliary molecules designed to completely inhibit development of multilayer polymorphs lead primarily to a single phase monolayer. As stated above, the tilted multilayer phase for arachidamide on 70% formamide is completely inhibited in the presence of these additives. For 100% formamide subphase, the additive inhibits formation of the tilted and untilted multilayer phases, leading to the untilted monolayer phase, as clearly seen in (*1*, figure 2).

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Malaria Vaccine Research

We disagree with the views expressed in the News article "Bumps on the vaccine road" (2 Sept., p. 1371) regarding a perceived lack of leadership in the field of malaria vaccine development.

Despite malaria's global importance, it is a low priority for the private sector. Public sector entities have therefore assumed leadership responsibilities, driving all aspects of research and development. Current funding levels are likely to prove insufficient to allow optimal progress. The required resources and capabilities are beyond those of any single agency, so scarce resources—distributed among different research groups—must be optimally used. Moreover, a coordinated, integrated, and open development process is instrumental to sustained progress.

In 1992, the Department of Defense's (DOD's) U.S. Army Medical Research and Development Command, the U.S. Agency for International Development (USAID), and the National Institute of Allergy and Infectious Diseases (NIAID) jointly put in place mechanisms to expedite the development and evaluation of promising malaria vaccine candidates. These collaborative efforts are being coordinated with the malaria vaccine development sponsored by the Commission of the European Communities (CEC), and the Special Programme for Training and Research in Tropical Diseases of the World Health Organization (WHO/TDR). Last year, the NIAID and USAID sponsored a meeting to acquaint investigators and scientific administrators with candidate vaccines and with the technical, regulatory, and clinical trial issues pertinent to accelerated development.

Today scientists can bring forward their most promising vaccine candidates for accelerated development and evaluation within this public sector framework. Most of the approaches discussed by R. S. Nussenzweig and C. A. Long in their Perspective "Malaria vaccines: Multiple targets" (2 Sept., p. 1381) are in fact being developed under the umbrella of the DOD/USAID/NIAID agreement. Among these are circumsporozoite (CS) protein-based and multiple antigen peptide vaccines, a CS protein-based vaccine to induce cytotoxic T cell responses, a live attenuated vaccinia vector (NYVAC) expressing seven key malaria genes, a recombinant transmission blocking vaccine (Pfs 25), both yeast- and *Escherichia coli*–expressed COOH-terminal regions of MSP-1 (a major malaria bloodstage antigen), alternative formations of the synthetic peptide bloodstage vaccine SPf66, and several nucleic acid vaccination strategies.

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Correction

In our report "Activation of Raf as a result of recruitment to the plasma membrane" (3 June, p. 1463) (*1*), panels E and F of figure