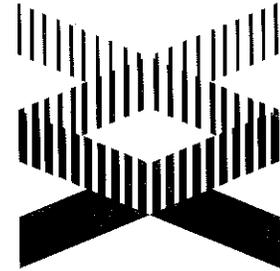


Human Genome news



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Genome Centers Promote Collaboration

NIH, DOE Research Teams Play Key Role in Developing Large-Scale Technologies, Sharing Resources

Human genome research centers, which form an important component of the diverse U.S. Human Genome Project, are made up of several different but interrelated programs. Established by DOE and NIH to foster collaborations by teams of investigators from various disciplines, the centers address major tasks such as genetic and physical mapping, DNA sequencing, informatics related to mapping and sequencing, and technology development. Center projects are also exploring the personal and social impact of new genetic technologies and information.

DOE has designated three genome centers within its national laboratories. Contracts to these centers are funded annually and peer reviewed through site visits every 2 to 3 years. NIH currently supports 11 large-scale mapping and technology development projects (9 of which are funded as centers and 2 as program project grants) in various academic and private-sector institutions. These NIH 5-year grants are reviewed after 3 years, at which time renewal requests are assessed.

The DOE Office of Health and Environmental Research devotes \$28.7 million or 46% of its genome program budget to its three genome centers. The NIH National Center for Human Genome Research spends slightly more than \$26.5 million or 25% of its \$106 million budget on large-scale mapping efforts.

Resource Sharing

Centers play a key role in improving and sharing genome research technology and resources through outside collaborations, public access to laboratory databases, and "visitor laboratories" at which visiting scientists can apply genome center expertise and technology to their own research. In addition, center resources, including biologicals, software and databases, instrumentation, and training opportunities, are available to the entire genome research community. Most centers offer outreach programs to clinicians, educators, journalists, and the general public to foster better understanding of human genetics and research.

Technology Transfer Opportunities

All genome program researchers are encouraged to actively collaborate with the private sector and offer their resources and technologies for commercial development. Some center institutions have technology transfer offices; centers may be contacted for more information. ➡

Centers Described, pp. 2-9

Short descriptions of NIH and DOE genome centers begin on p. 2. Listed are directors, contacts, principal investigators, research goals, some major achievements, and resources available to the entire genome research community (Genome Center Acronym List, p. 10).

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<p style="text-align: center;">GENOME CENTER Directors, Other Key Researchers*</p>	<p style="text-align: center;">MAJOR GOALS</p>
<p>BAYLOR COLLEGE OF MEDICINE (NIH; established 1990) C. THOMAS CASKEY Andrea Ballabio and David L. Nelson, Associate Directors <i>CONTACTS:</i> Sandra McMurtry, Administrator (713/798-6524, Fax: -5386) or David Nelson (-3122; <i>nelson@bcm.tmc.edu</i>); Baylor College of Medicine; Institute for Molecular Genetics; One Baylor Plaza; Houston, TX 77030-3498.</p> <p>OTHER KEY RESEARCHERS Antonio Baldini Charles Lawrence A. Craig Chinault Edward McCabe Richard A. Gibbs</p>	<p>Six core facilities provide support for independently funded physical mapping and positional cloning projects and development of technology, with emphasis on chromosomes 6, 15, 17, and X.</p>
<p>CHILDREN'S HOSPITAL OF PHILADELPHIA (NIH; established 1991) BEVERLY S. EMANUEL <i>CONTACT:</i> Beverly Emanuel (215/590-3856, Fax: -3764; <i>beverly@cit.med.upenn.edu</i>); Children's Hospital of Philadelphia; Division of Human Genetics and Molecular Biology; 34th Street & Civic Center Boulevard; Philadelphia, PA 19104.</p> <p>OTHER KEY RESEARCHERS Jaclyn Biegel Kenneth Buetow (Fox Chase Cancer Center) Eric Rappaport Saul Surrey</p> <p style="text-align: center;">University of Pennsylvania School of Medicine</p> <p>Maja Bucan Chris Overton Marcia Budarf David Searls Kurt Fischbeck Rebecca Taub</p>	<p>Construction of refined genetic and physical maps of chromosome 22, including production of a "sequence-ready" contig of the euchromatic portion of 22.</p>
<p>LAWRENCE BERKELEY LABORATORY (DOE; established 1988) JASPER RINE Sylvia Spengler, Deputy Director <i>CONTACTS:</i> Sylvia Spengler (510/486-4879, Fax: -5717; <i>sylviaj@ux5.lbl.gov</i>) or Jasper Rine (-4047; <i>jdrine@lbl.gov</i>); Lawrence Berkeley Laboratory; Human Genome Center; 459 Donner Laboratory; 1 Cyclotron Road; Berkeley, CA 94720.</p> <p>OTHER KEY RESEARCHERS Jan-Fang Cheng Elaine Ostrander Jeff Gingrich Michael Palazzolo Joseph Jaklevic Stewart Scherer Christopher Martin Ed Theil Victor Markowitz Manfred Zorn John McCarthy</p>	<p>Assembly of physical maps of complete chromosome arms rooted in templates appropriate for sequencing, and development of the capacity to produce genomic sequence of multiple megabases per year. One target is the long arm of chromosome 21. Development of automation and informatics necessary to produce an effective sequencing assembly line and capture, assemble, analyze, and distribute massive amounts of sequence information.</p>

*All located at centers unless otherwise noted.

MAJOR ACCOMPLISHMENTS	AVAILABLE RESOURCES
<p>Identification of several new disease loci, including Fragile X syndrome, DM, CMT disease, Kallman syndrome, and Lowe syndrome.</p> <p>Identification of >1000 YAC clones by PCR screening for target chromosomes.</p> <p>Assembly of contigs in target regions (many contigs >1 Mb from X, 17, 6, and 15).</p> <p>Development of methods for YAC characterization and contig assembly.</p> <p>Development of GDB Lite, a database incorporating GDB chromosome data in a user-friendly format. Also development of a library screening and clone characterization database capable of periodic automatic submission to GDB.</p> <p>Completion of moderate-scale sequencing projects encompassing over 200 kb of human DNA from the X and other chromosomes (including the genes for DMD, XIST, FRAXA, and DM).</p> <p>Establishment of several hundred cell lines from patients with chromosome-linked disorders.</p> <p>Production of detailed physical map of Xpter-Xp21.</p>	<p>Total human YAC libraries (CEPH and Washington Univ.).</p> <p>Chromosome X YAC libraries (Baylor and CHOP).</p> <p>Chromosome 17 and X cosmid libraries (LANL, LLNL).</p> <p>Screening service for chromosome 17p.</p> <p>Numerous patient cell lines and chromosome mapping cell panels for 6, 17, and X (hybrids, deletions, etc.).</p> <p>STs and YACs for many loci on target chromosomes.</p> <p>Database software.</p> <p>NCHGR predoctoral training grant (Chinault).</p>
<p>Construction of maps, including (1) a chromosome 22 framework map based on 15 STRPs; (2) regional assignment of over 200 anchor markers on a regional mapping panel (21 bins); and (3) construction by PFGE of contiguous long-range maps (>15 Mb).</p> <p>Production of clones/markers, including (1) construction of a 1.2X coverage YAC library from a chromosome 22-only somatic cell hybrid; (2) over 200 STs, 25 CA/TG repeat clones, and 70 <i>Not I</i> junction clones; and (3) creation of a normalized human liver cDNA library.</p> <p>Construction (for cytogenetic studies) of a 100-member radiation hybrid panel (characterized by FISH) and 5 somatic cell hybrids from cell lines with deletions or translocations of chromosome 22. Banking of cell lines with chromosome 22 abnormalities.</p> <p>Development of informatics capabilities, including (1) enhancement of existing Sybase to Quintus Prolog interface to support transparent access of all Sybase data types from Prolog; (2) creation of a tool for visualization of DNA sequence features in short sequencing runs; and (3) development of a Postscript tool for generating publication-quality depictions of cytogenetic maps.</p>	<p>Normalized cDNA libraries.</p> <p>STs from human chromosome 22, including TG repeats.</p> <p>Somatic cell hybrid regional mapping panel and radiation hybrid panel.</p> <p>Cell lines from patients with chromosome 22 abnormalities.</p> <p>Center-developed software.</p> <p>YAC screening resource service for chromosome 22 STs.</p>
<p>Completion of an 80-kb P1 clone sequence in 4 months, building on a high-resolution physical-mapping strategy (DOG-tagging) that generates distance, orientation, and gene size resolution (3 kb).</p> <p>Development of novel mapping resources for chromosome 21, including 49 mapped cDNA clones, over 40 dinucleotide repeat-based genetic markers, a YAC contig map, a set of somatic cell radiation hybrids [with David Cox (Stanford Univ.)], a cytogenetic map of the long arm enriched by FISH with 280 YACs and cosmids, and 188 clones forming 21 multiple YAC contigs and 4 single YAC contigs.</p> <p>Development of several instruments supporting automated mapping and sequencing, including a 96-sample thermal cycler for PCR, an imaging station for mapping and sequencing procedures, gel fractionations of PCR products, and an automated colony picker.</p> <p>Development of companion software, including HGCdb, a database variant of ACEDB; a sequence analysis package; database management tools, including ERDRAW, SDT, QST, and OPM Editor; and an automated generator of a user interface that responds to changes in an underlying database.</p>	<p>Automated colony picker and imaging station with supporting hardware for gel casting (Martin Pollard, 510/486-4561).</p> <p>Database management tools: ERDRAW, a graphical editor for entity-relationship schemes; SDT, a translator of relationships; OPM Editor, a graphical editor for object-protocol schemes; and QST for specification of queries (Markowitz, vmarkowitz@lbl.gov).</p> <p>Sequencing-analysis software available for testing; improved interface being developed (stew@genome.lbl.gov).</p> <p>Biological resources: polymorphic genetic marker clones (Ostrander, 510/486-6946); mapped YACs and P1 clones on 21 (Gingrich, -6580); and mapped cDNA clones on 21 (Cheng, -6590).</p>

<p style="text-align: center;">GENOME CENTER Directors, Other Key Researchers*</p>	<p style="text-align: center;">MAJOR GOALS</p>
<p>LAWRENCE LIVERMORE NATIONAL LABORATORY (DOE; established 1990) ANTHONY V. CARRANO CONTACTS: Linda Ashworth, Assistant to Center Director (510/422-5665; ashworth1@llnl.gov) or Anthony Carrano (-5698, carrano1@llnl.gov); Lawrence Livermore National Laboratory; Human Genome Center; Biology and Biotechnology Research Program; 7000 East Avenue, L-452; P.O. Box 808; Livermore, CA 94551.</p> <p>OTHER KEY RESEARCHERS Mark Batzer Richard Langlois Brigitte Brandriff Greg Lennon Elbert Branscomb Harvey Mohrenweiser Pieter de Jong Anne Olsen Emilio Garcia</p>	<p>Development of new cloning, mapping, instrumentation, informatics, and sequencing technologies focused on the assembly, closure, and characterization of a high-resolution ordered clone map of human chromosome 19. The final high-resolution map will consist of cosmid contigs with YACs, BACs, and PACs and an <i>EcoR1</i> restriction map for the minimal spanning set of cosmids; the map will be aligned with genetic maps of chromosome 19.</p> <p>Isolation, mapping, and sequencing of chromosome 19 cDNAs with emphasis on full-length clones.</p> <p>Construction of NLGLP chromosome-specific lambda and cosmid libraries (with LANL) for distribution.</p> <p>Development of new cloning, mapping, and sequencing technologies.</p>
<p>LOS ALAMOS NATIONAL LABORATORY (DOE; established 1988) ROBERT K. MOYZIS Larry L. Deaven, Deputy Director CONTACT: Lynn Clark, Technical Coordinator (505/667-9376, Fax: -2891; moysis@flovax.lanl.gov); Los Alamos National Laboratory; Center for Human Genome Studies; Life Sciences Division, MS M886; Los Alamos, NM 87545.</p> <p>OTHER KEY RESEARCHERS Michael Altherr Dick Keller Tony Beugelsdijk Jon Longmire Michael Cinkosky Mary Kay McCormick Norman Doggett Pat Medvick Jim Fickett Julie Meyne Deborah Grady David Torney Ed Hildebrand Michael Yesley</p>	<p>Assembly of complete high-resolution (0.1 Mb) maps of chromosome 16 and chromosome arm 5p.</p> <p>Determination of the molecular basis of chromosome structure and function and isolation of selected disease genes on chromosomes 5 and 16.</p> <p>Short-term development and support for large-scale physical mapping and sequencing projects and long-term development of tools for the storage, manipulation, and analysis of genome data.</p> <p>Development and application of new methods for physical mapping; use of robotics in handling and storing DNA fragments; construction of DNA libraries from flow-sorted chromosomes; and rapid, inexpensive, large-scale sequencing.</p> <p>Studies of ethical, legal, and social issues arising from the increased availability of genome data.</p>
<p>SALK INSTITUTE (NIH; established 1990) GLEN A. EVANS Harold H. Garner, Associate Director Michael W. Smith, Assistant Director CONTACTS: Glen Evans (619/453-4100, x 279, x376 (lab), Fax: /558-9513 or gevans@salk-sc2.sdsc.edu) or Suzanne Clancy (Center Administrator, x 340 or x151); The Salk Institute; P.O. Box 85800; San Diego, CA 92138. Harold H. Garner (619/455-3464, Fax: -2464; garner@vaxd.gat.com); General Atomics Corporation; Biosciences Division; P.O. Box 85608; San Diego, CA 92186.</p> <p>OTHER KEY RESEARCHERS Stephen Clark John Quackenbush Karin Diggle Tony Romo Jane Hutchinson Licia Selleri Lisa Leonard Ken Snider Ying Lin Yalin Wei David McElligott</p> <p style="text-align: center;">General Atomics Barbara Armstrong Dan Kramarsky Whitney Cunha Mary Petrowski</p>	<p>Assembly of a human chromosome 11 STS-content map with resolution of <500 kb and a low-resolution YAC contig map of nonchimeric YAC clones.</p> <p>Assembly of a high-resolution "sequence-ready" cosmid contig map of human chromosome 11 and other chromosomes, using manual and automated approaches.</p> <p>Construction of high-resolution sequence-sampled maps of several human chromosomes, consisting of 30 to 60% of the DNA sequence in one pass and analysis of the sequence for content.</p> <p>Development of technology, strategies, and instrumentation for large-scale, high-throughput, automated high-resolution physical mapping.</p> <p>Development of an integrated system using an entirely automated approach for sustained high-throughput, one-pass DNA sequencing at a rate of 60 Mb/year and \$0.03/bp.</p> <p>Development of informatics and computational tools using parallel processing computers for analysis of genomic DNA sequence.</p> <p>Production of resources necessary for rapid identification and isolation of disease genes.</p>

*All located at centers unless otherwise noted.

MAJOR ACCOMPLISHMENTS	AVAILABLE RESOURCES
<p>Coverage of an estimated 90% of chromosome 19 with about 800 contigs (assembled from over 12,000 cosmids, using automated fluorescence-based fingerprinting). Rapid closure of gaps with YACs, BACs, and PACs; 232 contigs representing about 50% of the chromosome have been regionally mapped to bands by FISH. Localization of more than 150 genes/polymorphic markers on the contig map. Using FISH, localization of over 500 cosmids to bands, including an ordered set of cosmids spaced an average of 1 Mb over the whole chromosome and 500 kb in selected bands. Organization determined for a number of gene families, including carcinoembryonic, olfactory receptor, zinc finger, cytochrome P450, and D19S11 (with several collaborators). Identification and characterization of the structural defect in DM, the most common form of adult muscular dystrophy (with several collaborators). Development of new vectors for cosmid and P1 cloning systems. Development of novel <i>Alu</i> PCR primers for fingerprinting and forensic analysis. Sequence determination for over 150 kb from chromosome 19 repair gene regions. Development of integrated mapping analysis software with interactive graphical display and linkage to local and national databases. Development of a high-speed flow cytometer and sorter for cell and chromosome purification. Construction of NLGLP chromosome-specific lambda and cosmid libraries from sorted chromosomes 3, 7, 9, 12, 18, 19, 21, 22, X, and Y.</p>	<p>NLGLP large-insert lambda and cosmid chromosome-specific libraries. Cosmid filters, FISH mapping, and cDNA and YAC/BAC/PAC screening for chromosome 19 probes. Assistance in database development, systems management, networking, and in contig assembly by fingerprinting and automated restriction mapping. Graduate and postdoctoral research training through the Institute of Genetics and Genomics at LLNL (Mohrenweiser, 510/423-0534).</p>
<p>Construction of maps, including (1) a high-resolution cosmid/YAC physical map of human chromosome 16 consisting of 500 contigs covering over 95% of the chromosome (map translated into framework STS map of 150 new regionally localized markers) and (2) a framework STS map of human chromosome 5 [with John Wasmuth (UC, Irvine)] consisting of 200 new markers regionally assigned with a resolution of 4 Mb (5q) to 1 Mb (5p). Biological developments, including (1) identification and cloning of the human telomere, the endpoint for genetic and physical maps; (2) determination of unusual 3-D structure of telomeric DNA [with Alex Rich (MIT)]; (3) identification and cloning of highly conserved centromeric repetitive DNA regions, likely human centromere components; and (4) construction of a novel cDNA library from mRNA obtained from a paternally encoded human pregnancy (hydatidiform mole). Development of technology, including (1) NLGLP (with LLNL) chromosome-specific libraries (over 2500 DNA libraries sent to research and production laboratories worldwide, including complete digest libraries for each human chromosome; partial-digest phage and cosmid libraries for human chromosomes 4, 5, 6, 8, 10, 11, 13, 14, 16, 17, 20, X, and Y; and complete digest low-chimeric YAC libraries for human chromosomes 5, 9, 16, and 21); (2) flow-cytometry techniques to detect single DNA molecules, resulting in a CRADA with LTI for codevelopment of a rapid DNA-sequencing technology; and (3) a robot for high-density cosmid/YAC array replication and distribution.</p>	<p>Phage and cosmid libraries developed within NLGLP (see accomplishments). Low-chimeric YAC libraries: total genomic (180 kb, average insert) and chromosome-specific for chromosomes 5, 9, 16, and 21. CEPH Mark II to VII YAC libraries. High-density filter arrays of cosmid and YAC libraries. STS collections for chromosomes 16 (200) and 5 (200). Panel of somatic cell hybrids for sorting each human chromosome. SIGMA, a graphical map editor. cDNA-inform database and software for comparison of sequences. Modified Biomek robot and LANL robot for high-density array construction.</p>
<p>Completion of 300-kb resolution STS map of chromosome 11 based on cosmid end sequencing and containing STS identifiers for all known genes; construction of a low-resolution chromosome 11 physical map with 90% coverage in nonchimeric YAC contigs; 150 cosmids and >200 YACs mapped by FISH. Current chromosome 11 map contains over 2000 loci. DNA sequence determined for 0.3% of chromosome 11. Development of technology for high-throughput automated DNA sequencing (using cosmid templates) and template preparation ("Dr. Prepper" robotics system), high-volume sample handling (GAS robotics), parallel processing sequence analysis (GIST), automated high-throughput PCR, and automated arrayed library analysis. Identification of a leukemia-associated transcription factor gene (HTRX) responsible for >80% of infant leukemias and representing the human homologue of the <i>Drosophila trithorax</i> (<i>trx</i>) gene. Development of high-density plasticware in 384 thin-walled, 384, and 864 well formats and accompanying tools for the Beckman Biomek. Development of Genome Notebook, a portable, network-accessible relational database for genome mapping and sequencing data.</p>	<p>Cosmid libraries: Arrayed chromosome 11-specific cosmid libraries – SRL, 16,000 clones; 11q (11q13-11qter), 1200 clones. Arrayed cosmid libraries for chromosomes 5 and 16. <i>Giardia</i> cosmid libraries (12,000 clones, 2 hosts) and chromosome-specific subsets (Smith). YAC libraries: Total genome – St. Louis; CEPH Mark I; CEPH Mark VI to VII (megabase). Chromosome 11-specific (T. Shows, RPMI, Buffalo, NY). Chromosome 21 minimal tiling set. STSs: Over 390 STSs produced by this lab and >1000 STSs for chromosome 11 (available online via Salk Internet GOPHER server). Cell hybrids: 15 cell hybrid chromosome 11 mapping panels; monochromosomal hybrids for all human chromosomes. Instrumentation: "Dr. Prepper," GAS, GIST, PCR system, Hyb system (Garner). Robotics for Biomek and plasticware (Helix, Inc.). Autopooling system (Evans or Quackenbush). Genome Notebook [Macintosh demo disk (Clark)].</p>

GENOME CENTER Directors, Other Key Researchers*	MAJOR GOALS
<p>STANFORD UNIVERSITY (NIH; established 1990 at UCSF; relocated March 1993) RICHARD M. MYERS David R. Cox, Codirector CONTACTS: Cristina Estébanez (415/812-1915, Fax: -1916; <i>cxe@camis.stanford.edu</i>) or Richard Goold (-1920, Fax: -1916; <i>goold@camis.stanford.edu</i>); Stanford University; Human Genome Mapping Center; Department of Genetics; 855 California Avenue; Stanford, CA 94304.</p> <p>OTHER KEY RESEARCHERS Sidney Cowles Cynthia Keleher Richard Goold Laura Stuvé</p>	<p>Generation of high-resolution human chromosome 4 maps (radiation hybrid and clone) and achievement of complete chromosome coverage in sequence-ready clones. Construction of a radiation hybrid map of the entire human genome with 5000 to 10,000 STSs at an average resolution of 0.5 to 1.0 Mb. Development of technologies for rapid sequencing of selected 2-Mb segments of human chromosome 4.</p>
<p>UNIVERSITY OF CALIFORNIA, BERKELEY, DROSOPHILA GENOME CENTER (NIH; established 1992) GERALD M. RUBIN CONTACT: Gerald M. Rubin (HHMI, UCB, 510/643-9945, Fax: -9947); 539 LSA Bldg.; University of California; Berkeley, CA 94720.</p> <p>OTHER KEY RESEARCHERS Daniel L. Hartl (Harvard University) Christopher H. Martin (LBL) Michael J. Palazzolo (LBL) Allan C. Spradling (Carnegie Institute of Washington, HHMI)</p>	<p>Generation of a physical map of the <i>Drosophila melanogaster</i> genome at about 20-kb resolution by STS-content mapping of a P1 library. Integration into the physical map of sites of high biological interest, including known genes, cDNAs, and lethal P-element insertion sites.</p>
<p>UNIVERSITY OF IOWA COOPERATIVE HUMAN LINKAGE CENTER (NIH; established 1992) JEFFREY C. MURRAY CONTACTS: Nancy Newkirk (319/335-6899, Fax: -6970) or Jeffrey Murray (-6946, Fax: -6970; <i>jmurray@uiowa.edu</i>); Cooperative Human Linkage Center; Department of Pediatrics; University of Iowa; Iowa City, IA 52242.</p> <p>OTHER KEY RESEARCHERS Kenneth Buetow (Fox Chase Cancer Center) Geoffrey M. Duyk (Harvard University) James W. Hanson Val C. Sheffield James L. Weber (Marshfield Medical Research Foundation) Robert F. Weir</p>	<p>Expansion of the linkage map of the entire human genome to an average resolution of 2.5 cM based on high-heterozygosity STRP markers. Evaluation of protection of human subjects and provision of training for social and behavioral scientists on issues of human and molecular genetics.</p>
<p>UNIVERSITY OF MICHIGAN MEDICAL CENTER (NIH; established 1990) FRANCIS S. COLLINS CONTACT: Francis S. Collins (313/747-3416, Fax: /936-9353; <i>francis.s.collins@med.umich.edu</i>); University of Michigan Medical Center; Department of Internal Medicine; Division of Medical Genetics; Ann Arbor, MI 48109-0618.</p> <p>OTHER KEY RESEARCHERS Mike Boehnke Dorene Markel David Burke Miriam Meisler Jeff Chamberlain Paul Meltzer Thomas Gelehrter Walter Panko David Ginsburg Jerry Slightom (Upjohn Company) Thomas Glover Anand Swaroop Jerry Gorski Jeff Trent Paula Gregory</p>	<p>Study of genetic diseases by seven research cores through development and use of novel technologies in positional cloning. Advancement and development of genomic technology, especially development of microsatellite markers, microdissection of metaphase chromosomes, FISH mapping, radiation hybrid mapping, genetic mapping, YAC technology, and DNA sequencing; testing these by application to specific genetic disease problems.</p>

*All located at centers unless otherwise noted.

MAJOR ACCOMPLISHMENTS	AVAILABLE RESOURCES
<p>Completion of over 1100 STSs from human chromosome 4, including 170 SSRs and 50 known genes. Localized (by PCR) 945 of the STSs within 9 bins defined by well-characterized breakpoints from translocation chromosomes.</p> <p>Construction of a radiation hybrid map that includes 672 of the STSs, providing a comprehensive map at a resolution of 0.5 Mb and a framework map at a resolution of 1.0 Mb.</p> <p>Isolation of 775 YACs (average insert size, 400 kb; from CEPH Mark I YAC library) from 404 of the STSs.</p>	<p>Cosmid and plasmid clones for over 1000 chromosome 4 loci.</p> <p>Primer and complete STS sequences (average size of each STS, 300 bp), with PCR conditions of 1100 STSs.</p> <p>Radiation hybrids.</p> <p>YAC clones for 404 chromosome 4 loci.</p> <p>YAC libraries.</p> <p>Educational resources, including tours of the center and lectures on genome science for students and lay groups.</p>
<p>Preparation of robotically arrayed 10,000-member bacteriophage P1 library for automated screening and contig assembly.</p> <p>Construction of a map (by in situ hybridization against polytene chromosomes) for nearly 1500 P1 clones that will be starting points for contig assembly.</p> <p>Construction of a map (by in situ hybridization) for several hundred P-element insertion sites.</p>	<p>Mapped P1 clones.</p> <p><i>Drosophila</i> strains with mapped single P-element insertions will be deposited in the NSF-funded Indiana <i>Drosophila</i> Stock Center for distribution.</p> <p>Adaptation of the <i>C. elegans</i> database, for management and graphical display of <i>Drosophila</i> data.</p>
<p>Development of pilot libraries highly enriched for STRPs.</p> <p>Characterization of single-strand conformation and denaturing gradient gel electrophoresis polymorphisms in candidate genes for craniofacial and ocular disorders.</p> <p>Preliminary incorporation of CEPH genotypes on new STRP microsatellite markers into pre-existing multipoint linkage maps.</p> <p>Construction of multipoint linkage maps using the CEPH database, version 5.0.</p>	<p>Laboratories at Marshfield Medical Research Foundation and University of Iowa available for genotyping to establish disease linkages or mutation detection searches for specific gene or genes, with CEPH maps and STRP resources.</p> <p>Training opportunities with travel and stipend support available for secondary science teachers to develop comprehensive understanding of technology and social and ethical issues related to the Human Genome Project.</p>
<p>Identification of families and individuals with genetic diseases, resulting in collection of 550 blood samples, immortalization of 500 cell lines, and investigation of >200 families with breast cancer.</p> <p>Generation of new microsatellite repeat polymorphisms, including 20 dinucleotide and more than 25 tetranucleotide markers. The latter are from chromosome 17, and many map near the breast cancer locus on 17q.</p> <p>Development of algorithms and software for radiation hybrid mapping, FISH mapping, and estimation of allele frequency based on pedigree data.</p> <p>Construction of radiation hybrid panels and characterization of four somatic cell hybrid lines for the long arm of chromosome 17, and development of large-scale FISH mapping of YAC and cosmid clones.</p> <p>Direct cycled sequencing of PCR products and direct sequence analysis of CA repeats.</p> <p>Screening of 5 to 10 STS markers against 4 YAC libraries each month to complete the chromosome 17 physical map. Production of five different cDNA libraries.</p> <p>Development of methodology in which microdissected material is labeled by PCR and mapped back to metaphase chromosomes.</p>	<p>cDNA libraries from human retinal pigment epithelium, retina, kidney, fetal brain, and whole fetus.</p> <p>Microdissection technology and protocols.</p> <p>Chromosome 17 radiation hybrid panel.</p> <p>Four chromosome 17q somatic cell hybrids.</p> <p>Tetranucleotide and dinucleotide markers from chromosome 17.</p> <p>Chromosome 17q YACs. (The center serves as a community screening resource.)</p> <p>Radiation hybrid mapping software (RHMAP).</p> <p>Educational resources for clinicians, genetic counselors, journalists, and high school teachers.</p>

<p style="text-align: center;">GENOME CENTER Directors, Other Key Researchers*</p>	<p style="text-align: center;">MAJOR GOALS</p>
<p>UNIVERSITY OF TEXAS HEALTH SCIENCE CENTER AT SAN ANTONIO (NIH; established 1992) SUSAN L. NAYLOR <i>CONTACT:</i> Susan L. Naylor (512/567-3842, Fax: -6781); University of Texas Health Science Center; Department of Cellular & Structural Biology; 7703 Floyd Curl Drive; San Antonio, TX 78284-7762.</p> <p>OTHER KEY RESEARCHERS Robin Leach Stephanie Sherman (Emory University) Peter O'Connell Brad Windle</p>	<p>Construction of radiation hybrid, genetic linkage, and contig maps for human chromosome 3. Development of a chromosome 3-specific database (with the University of Utah genome center).</p>
<p>UNIVERSITY OF UTAH (NIH; established 1990) RAYMOND F. GESTELAND and RAY WHITE <i>CONTACT:</i> Raymond Gesteland (801/581-5190, Fax: /585-3910; rayg@genetics.med.utah.edu); University of Utah; Department of Human Genetics; 6160 Eccles Genetics Building; Salt Lake City, UT 84112.</p> <p>OTHER KEY RESEARCHERS Hans Albertson Harold Swerdlow Peter Cartwright Robert Weiss Mark Leppert</p>	<p>Development of resources and technologies for mapping and sequencing, including (1) polymorphic DNA markers for human chromosomes; (2) automated technology for genotyping; (3) organized front-end strategies for large sequencing projects; (4) DNA sequencing technology, including capillary and multiplex approaches; (5) informatics tools to integrate chromosome maps, pedigree data, and large sequence databases; and (6) informatics systems for distributive database searches. Pilot projects for assessment of new sequencing technology.</p>
<p>WASHINGTON UNIVERSITY SCHOOL OF MEDICINE (NIH; established 1990) DAVID SCHLESSINGER <i>CONTACT:</i> David Schlessinger (314/362-1188, Fax: -3208); Washington University School of Medicine; Center for Genetics in Medicine; 4566 Scott Avenue, Box 8232; St. Louis, MO 63110.</p> <p>OTHER KEY RESEARCHERS Buddy Brownstein Phil Green David Chaplin Volker Nowotny Eric Green</p>	<p>Construction of integrated physical and genetic maps of the X chromosome and chromosome 7 and targeted mapping of several megabase regions elsewhere in the human genome.</p>
<p>WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH and MASSACHUSETTS INSTITUTE OF TECHNOLOGY (NIH; established 1990) ERIC S. LANDER David Page and Nat Goodman, Associate Directors <i>CONTACT:</i> Eric Lander (617/258-5192, Fax: -6505; lander@mitwibr.bitnet); Whitehead Institute for Biomedical Research; Nine Cambridge Center; Cambridge, MA 02142.</p> <p>OTHER KEY RESEARCHERS Daniel Cohen (CEPH) Nic Dracopoli (Massachusetts Institute of Technology) Rudolf Jaenisch (Whitehead Institute for Biomedical Research) Joe Nadeau (Jackson Laboratory) Shirley Tilghman (Princeton University, HHMI)</p>	<p>Construction (in 3 years) of a low-resolution physical map of the human genome based on 8500 STSs. Construction of genetic and physical maps of the mouse genome, including a high-resolution genetic map consisting of 6000 SSLPs, integrating 1/4 of these markers with the Copeland/Jenkins cross showing the location of the genes. Production (within 5 years) of a low-resolution physical contig map (average size, 10 to 20 Mb) based on 10,000 STSs.</p>

*All located at centers unless otherwise noted.

MAJOR ACCOMPLISHMENTS	AVAILABLE RESOURCES
<p>Production of framework hybrids that divide chromosome 3 into 21 regions. Construction of 2 genetic linkage maps, one with 52 markers and another with 26 dinucleotide repeats, and a radiation hybrid map with 92 loci. Isolation and assembly of 137 simple repeat polymorphisms for chromosome 3. Design and assembly of PCR primers for 81 genes and 9 RFLPs. Development of a semiautomated system for PCR reactions and an automated gel loader using robotics for both CEPH screening and analysis of radiation hybrids.</p>	<p>Framework hybrids for chromosome 3. PCR primers for polymorphic dinucleotide repeats and genes mapping to chromosome 3. Scheme for automating CEPH typing. Chromosome 3-specific database (in development with the University of Utah). Pre- and postdoctoral training in human genome research. CEPH YAC library (inserts, >1 Mb).</p>
<p>Generation of >1200 STSs (mapped 1052, of which 650 are SSRs). Construction of a chromosome 17 map with 72 markers spaced an average of 4.2 cM apart. Development of (1) a transposon system for breaking up large DNA fragments into ordered sets for large-scale sequencing projects; (2) capillary gel electrophoresis method for sequencing DNA; and (3) instrumentation for efficient, automated implementation of multiplex technology for large-scale sequencing. Sequenced 100 kb of the neurofibromatosis gene as a pilot test of the transposon front-end system. Developments for informatics, including (1) pedigree editor; (2) system for implementation of transposon mapping system; (3) a new algorithm for automated calling of DNA sequence from autoradiograms; and (4) dedicated parallel architecture chips for very fast DNA sequence comparisons. Establishment of an ELSI program for community outreach.</p>	<p>Reagents and sequences for mapping. Genome technology workshop scheduled for June 1993. Visitor laboratory available to give visiting scientists access to biological and technological laboratory resources.</p>
<p>Completion (with collaborators) of the YAC coverage of a number of loci, including 2 Mb in the Huntington's region and 4 Mb in the major histocompatibility complex. Assembly of chromosome 7 materials that include >700 STSs [of which 100 are highly polymorphic linkage probes obtained originally from Jean Weissenbach (Institut Pasteur) and Ray White (University of Utah)] and a set of over 2500 chromosome 7-specific YACs that are low in cocloning. Assembly of over 40% of the X chromosome in contigs ranging up to 9 Mb in length, with rationalized maps available for Xq26-qter. Large contigs are now being aligned in Xp, Xq13, and Xq24-q26, and 60 highly polymorphic or gene-specific markers placed along the chromosome with cognate YACs. Wide distribution of Washington Univ. human YAC library. Assembly of robot-assisted workstation to screen YAC libraries, including the capacity for up to 1800 PCR reactions per day. Formulation and initial testing of STS-content mapping. Development of algorithms and software for analysis of STS-content and radiation hybrid mapping data, and for choosing PCR primers. Design and construction of a database for STS-content mapping data.</p>	<p>High-throughput PCR machine. Information on PCR conditions and end-cloning protocols. Software to run a Zymark side-loader arm in conjunction with a Biomek robot for robot-assisted screening. SEGMAP (YAC contig assembly software). Reliable procedures to recover YAC insert ends and sequence them automatically. Software for STS development and data storage.</p>
<p>Construction of a map having >1000 SSLPs. Construction of a mouse genome YAC library with 700-kb average inserts. Implementation of an efficient approach for screening entire YAC libraries. Implementation of a center-pioneered object-oriented database for genomic data. Introduction of YACs into mouse ES cell lines and into the mouse germline. Development of new technologies to increase automation ("waffle iron" thermocycler, which can handle 16 microtitre dishes at once), STS screening robot.</p>	<p>Mouse genome YAC library. Primers for mouse SSLPs (available from Research Genetics, Inc., Huntsville, AL). Software for choosing primers and genetic mapping. "Waffle iron" thermocycler prototype (Automated Systems, Cambridge, MA). CEPH Mark II to VII (inserts, 400 kb to >1 Mb) YAC library.</p>

Genome News

Gene Alterations Believed Responsible for Congenital Deafness, Soft-Tissue Tumor

Researchers Discover Gene Involved in Two Diseases

Researchers led by Beverly Emanuel at Children's Hospital of Philadelphia (CHOP) have shown for the first time that different alterations in a single human gene can cause two unrelated types of human disease. Alterations in PAX3, a gene found on chromosome 2, are responsible for the congenital deafness known as Waardenburg syndrome and for alveolar rhabdomyosarcoma, a relatively rare and often lethal soft-tissue tumor that most frequently affects teenagers. The study was published in the February issue of *Nature Genetics*.

CHOP investigators found that a new hybrid gene is produced when portions of PAX3 and another gene on chromosome 13 are exchanged. This hybrid gene is believed to produce the protein responsible for causing alveolar rhabdomyosarcoma. In Waardenburg syndrome, a mutation probably prevents PAX3 from producing its normal protein.

Understanding the genetic cause of alveolar rhabdomyosarcoma has three important implications, said Frederick Barr (CHOP):

- Scientists will be able to study how the abnormal fusion gene causes cancer.
- The distinctive fused gene provides an unmistakable fingerprint that doctors can use to diagnose the cancer and

determine the extent of metastasis and the effectiveness of therapy.

- The protein produced by the fused gene is unique to the cancer cells, a difference that may lead to new cancer treatments.

Alveolar rhabdomyosarcoma is a particularly invasive cancer that affects the trunk and limbs; 1 in 100,000 preteens and teenagers are diagnosed each year. According to Richard Womer (CHOP), the cancer invades surrounding tissue and often spreads to distant parts of the body before the first symptom—a lump—appears. An aggressive combination of five chemotherapeutic drugs, white cell growth factors, radiation, and surgery is used to fight the cancer. Womer stated that translating this molecular advance into diagnostic probes will greatly facilitate the diagnosis, staging, and treatment of affected children.

Emanuel said, "This research finding is yet another example of the importance of the Human Genome Project. It was information derived from the maps of human and mouse chromosomes that made this discovery possible." Other researchers who worked on this study include Jaclyn Biegel and John Holick of CHOP and Naomi Galili and Giovanni Rovera of the Wistar Institute.◊

Genome Center Acronym List

ACEDB *Caenorhabditis elegans* Database

BAC bacterial artificial chromosome

cDNA complementary DNA

CEPH Centre d'Etude du Polymorphisme Humain

CHOP Children's Hospital of Philadelphia

CMT Charcot-Marie-Tooth

CRADA Cooperative Research and Development Agreement

DM myotonic dystrophy

DMD Duchenne muscular dystrophy

ELSI ethical, legal, and social issues

ES embryonic stem

FISH fluorescence in situ hybridization

FRAXA fragile X locus

GAS Genome Automation System

GDB Genome Data Base

GIST Genome Informatics System on Transputers

HHMI Howard Hughes Medical Institute

LANL Los Alamos National Laboratory

LBL Lawrence Berkeley Laboratory

LLNL Lawrence Livermore National Laboratory

LTI Life Technologies, Inc.

MIT Massachusetts Institute of Technology

NCHGR National Center for Human Genome Research

NLGLP National Laboratory Gene Library Project

NSF National Science Foundation

PAC P1 artificial chromosome

PCR polymerase chain reaction

PFGE pulsed-field gel electrophoresis

RFLP restriction fragment length polymorphism

RPMI Roswell Park Memorial Institute

SSLP single-sequence-length polymorphism

SSR simple sequence repeat

STRP short tandem repeat polymorphism

STS sequence tagged site

UC University of California

UCB University of California, Berkeley

UCSF University of California, San Francisco

XIST candidate gene for X-inactivation center

YAC yeast artificial chromosome

Chromosome Coordinating Meeting 1992

The Chromosome Coordinating Meeting (CCM), held in Baltimore November 15–17, 1992, represented an important stage in international coordination of human genome mapping and sequencing. CCM 92, attended by nearly 150 people, was an experimental transition between Human Gene Mapping (HGM) 0.5 meetings, at which data entry and editing were prime activities, and future workshops, which will be conducted in a setting of continual database updating. Cochaired by Peter Pearson [Genome Data Base (GDB) at Johns Hopkins University] and Kay Davies (John Radcliffe Hospital, U.K.), CCM 92 focused primarily on genome program policy issues. Future meetings will concentrate more on scientific and technical issues.

Most CCM 92 participants represented individual chromosome communities as organizers of recent or pending single-chromosome workshops (SCWs) or as GDB editors charged with data entry, validation, and maintenance. Other attendees included Human Genome Organization (HUGO) staff, funding agency observers, and present and past members of the HUGO Human Genome Mapping Committee (HGMC).

Topics discussed at the meeting included the role of SCWs and the need to avoid workshop overlapping and to report meeting data quickly through GDB.

Problems in linking information from sequence databases (e.g., GenBank[®]) with map data in GDB were discussed. Attendees agreed that the correct naming of sequenced genes could be ensured by using GDB as a conduit between sequence databases and the nomenclature committee.

Attendees agreed to try to increase the number of journals that insist on using officially designated gene symbols. Tom Shows (Roswell Park Memorial Institute) presented information about NOMEN, a new computer program that automatically generates gene symbols and names from basic descriptive information provided by the investigator. NOMEN observes naming conventions already in place.

The changing role of GDB editors and the creation of curatorial positions were discussed at length. Participants agreed that editors should be nominated at SCWs when possible and appointed by HGMC after

consideration of candidates' scientific and computing expertise and access to essential network connections and databases. The activities and productivity of individual editors should be reviewed on a yearly basis and inefficient editors rotated off as necessary. The assistance of curators supported by GDB will allow editors to concentrate more on editorial decisions rather than on data entry and correction.

Attendees expressed a strong desire to return to large meetings in which more investigators can participate. SCWs could be held every 1 to 2 years, depending on the amount of data gathered between meetings. Scientific needs might be adequately served by periodic CCMs without the overhead associated with editorial database access and by occasional SCWs alternating with larger HGM-style conferences.

CCM 93 is planned for November 10–12 in Tsukuba, although sources of financing, particularly for transportation to Japan, have not yet been defined. The exact meeting format and agenda are still under discussion—a major topic is likely to be consensus map construction.◊

A summary of the CCM 92 meeting is contained in the introduction to various committee reports in the first volume of the *Genome Priority Reports* series. This 1993 *Cytogenetics and Cell Genetics* publication is available for \$397 from bookstores or S. Karger Publishers; 26 W. Avon; P.O. Box 529; Farmington, CT 06085 (800/828-5479 or 203/675-7834, Fax: -7302).

CCM 93 organizer:

- Nobuyoshi Shimizu (Keio University School of Medicine, Tokyo)

University of Michigan Human Genome Center Holds Workshops

The University of Michigan Human Genome Center in Ann Arbor will offer workshops for genetic counselors and high school science teachers this summer. Purposes of the workshops are to provide instruction in molecular genetics and encourage attendees to incorporate the study of genome technology and its implications into their everyday counseling or classes. Application information is given below.

- **Genetic Counselors.** An NIH-supported short course on molecular genetics will be held August 1–7 for U.S. genetic counselors. Registration fee and other expenses will be the responsibility of attendees. [Contact: Diane Baker (313/763-2933, Fax: -3784)].
- **High School Science Teachers.** Two DOE- and NIH-supported hands-on workshops for secondary science teachers from the Great Lakes region will be offered July 12–16 and August 16–20. Assistance is provided for travel, lodging, and subsistence. Enrollment is limited to eight teachers each from Ohio, Michigan, Indiana, Illinois, Wisconsin, and Minnesota. [Contact: Paula Gregory; University of Michigan Human Genome Center; 2570 MSRB II; Ann Arbor, MI 48109-0674 (313/747-2738, Fax: /763-4692)].◊

Genome News

**Human
Genome**
news



This newsletter is intended to facilitate communication among genome researchers and to inform persons interested in genome research. Suggestions are invited.

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National Center
for Human
Genome Research



HUGO Invites Applications

The Human Genome Organization (HUGO) will hold its annual election of new members this summer. Now composed of 538 members from 35 countries, HUGO invites applications from anyone actively interested in human genome research. Application forms are available from HUGO members and the offices of HUGO Americas and HUGO Europe (note new address for HUGO Europe).

HUGO Americas

Diane Hinton
7986-D Old
Georgetown Road
Bethesda, MD 20814
301/654-1477,
Fax: /652-3368

HUGO Europe

One Park Square
West
London NW1 4LJ
United Kingdom
(Int.) 44/71/935-8085,
Fax: -8341

For consideration this year, completed forms should be mailed (not faxed) to arrive at HUGO Americas by June 15. Applications must be supported by two HUGO members (not five, as was previously the case) and accompanied by a one-page curriculum vitae and a list of up to five key publications.◊

✓ Informatics Resource

Version 3.0 of the Listing of Molecular Biology Databases (LiMB), a tool for locating and accessing data sets and designing and linking pertinent databases, has been released. LiMB contains (1) a brief database list, (2) a data dictionary describing the meanings of fields in a LiMB entry, (3) a full database list, and (4) a cross index of databases and data types. LiMB data are gathered from questionnaires, journals, and the BIOSCI electronic bulletin board.

This preliminary release, to be confirmed by a full questionnaire cycle, offers over 100 databases (25 more entries than release 2.0). To acquire LiMB, send the message text (*limb-data*) to (*bioserve@life.lanl.gov*). For information only, send the message text (*limb-info*) to the same address.

Additional copies of LiMB in hardcopy or floppy disk are available on request. [Contact: Christian Burks; LiMB; Theoretical Biology and Biophysics Group, T-10, K710; Los Alamos National Laboratory; Los Alamos, NM 87545 (505/667-7510; Internet: *limb@life.lanl.gov*).]◊

HUGO, UNESCO Sponsor Course on Data Banks, Computer Support in Moscow

An international lecture course on Data Banks and Computer Support of the Human Genome Project is planned for September 13-17 in Moscow to disseminate information on data banks in molecular biology and genome studies. Attendees will discuss data bank structure; applied program packages; and the retrieval and use of databases of biological sequences, human genes, physical mapping, medical genetics, and proteins. Special attention will be given to integrating scientists from Eastern Europe and developing countries into international information networks. Hardware and software conforming to world standards will be provided, along with detailed information on databases and software available in Russia. The course is hosted by Andrei Mirzabekov of the Engelhardt Institute of Molecular Biology.

Sponsored by HUGO and the United Nations Educational, Scientific, and Cultural Organization (UNESCO), the classes are open to qualified scientists from all countries. The \$500 registration fee includes accommodations and meals, but attendees must cover their own travel expenses. Applications should be submitted as soon as possible to Valentina Tsitovich; Engelhardt Institute of Molecular Biology; Vavilov St. 32; Moscow 117984, Russia [Int. Fax: 7(095) 135-14-05; E-mail: *tsitov@imb.msk.su.internet* or *makarv%imb.mb.free@suearn2.bitnet*].◊

DOE, AlliedSignal To Host Technology Transfer Conference

DOE and the Kansas City Division of Allied-Signal Inc. will host IndustryTech '93, a technology transfer conference for U.S. industry, on May 5-7 in Kansas City, Missouri. IndustryTech '93 is designed to help small- and medium-sized businesses leverage federal funds and make use of advanced technologies that have been researched and developed in the U.S. defense industry. Opportunities will be offered for one-to-one discussions with project engineers about product and manufacturing problems. The meeting will feature exhibits by DOE national laboratories and their major contractors. [Contact: Ron Fippinger; Show Management Office; 900 Jorie Boulevard, Suite 220; Oak Brook, IL 60521 (708/990-2070, Fax: -2077).]◊

Foreign Subscribers Asked To Confirm Addresses

To update the HGN mailing list and conserve resources, HGMIS requests that foreign subscribers confirm their addresses by faxing or mailing a copy of their newsletter label to the HGMIS address on p. 12. Corrections should be made as needed. Names not confirmed by September 1 will be removed from the mailing list. ◊

¶ Genome-Related Publications

Gene Mapping: Using Law and Ethics as Guides, edited by George Annas (Boston University) and Sherman Elias (University of Tennessee, Memphis), brings together essays by some of the nation's leading experts in genetics, medicine, health law, history and philosophy of science, and medical ethics. These essays assess the state of modern human genetics and the Human Genome Project and explore legal and ethical guidelines for preventing misuse of genetic information. The book was developed from a January 1991 workshop supported by the NIH National Center for Human Genome Research in Bethesda, Maryland. 1992, \$39.95. [Oxford University Press, Inc.; 2001 Evans Rd., Cary, NC 27513 (800/451-7556 or 919/677-0977, Fax: -1303).] ◊

geneWATCH is a bimonthly newsletter published by the Council for Responsible Genetics (CRG), a nonprofit organization whose purpose is to create a forum for discussing, evaluating, and distributing information about the social impact of genetic engineering. **geneWATCH** covers social issues in genetics and biotechnology and includes a bibliography of recently published resources as well as reviews of pertinent books and reports. Individual subscriptions, \$24 for 6 issues. [Contact: CRG, 19 Garden Street; Cambridge, MA 02138 (617/868-0870).] ◊

The Alliance of Genetic Support Groups has released the following two publications:

- **Health Insurance Resource Guide** provides a basic understanding of the U.S. health insurance system and serves as a guide to finding information, particularly for people with genetic disorders. \$10. [March of Dimes, Supply Department; 1275 Mamaroneck Avenue; White Plains, NY 10605.]
- **Directory of National Genetic Voluntary Organizations and Related Resources** links service providers and consumers with appropriate support organizations and agencies. \$10. [Alliance of Genetic Support Groups; 35 Wisconsin Circle, #440; Chevy Chase, MD 20815-7015.] ◊

GDB USER SUPPORT, REGISTRATION

To become a registered user of GDB and OMIM, contact one of the User Support offices listed at right (a user may register to access both Baltimore and a remote node). Questions, problems, or user-registration requests may be sent by telephone, fax, or e-mail. User-registration requests should include name, institutional affiliation, and title (if applicable), street address (no P.O. box numbers), telephone and fax numbers, and e-mail address.

GDB and OMIM Training Schedule

Comprehensive hands-on training courses on the use of GDB and OMIM will have at least one computer workstation for two participants. Registrants will receive at least 3 weeks notice if insufficient registration causes class cancellation.

- The general course for scientific users provides a basic understanding of the databases and relationships among different types of data.
- The course for users with editing privileges includes instructions on adding, modifying, and deleting GDB data.

Class frequency and location will be determined by demand (schedule below). Courses are free, but attendees must pay their own travel and lodging expenses. Hotel information and directions will be mailed with registration materials.

As interest in GDB continues to grow, organizations around the world will offer training that requires access to GDB in Baltimore. Notifying GDB User Support about planned training activities will enable the staff to ensure database availability by scheduling maintenance and repairs at other times.

COURSE REGISTRATION INFORMATION

Contact U.S. GDB User Support Office (at right).

PLANNED EXHIBITIONS (acronym list, p. 16)

- AAP/AFCR/ASCI, Washington, D.C., Apr. 30–May 3

Course	Dates
BALTIMORE	
General User	April 26–27
General User	June 21–22
Editing	May 10–11

Cytogenetics and Cell Genetics 61, 243–62 (December 1992) contains a complete report of the **First International Human Chromosome 12 Workshop** [HGN 4(5), 12 (January 1993)] held September 18–20, 1992, at Oxford University. ◊

USER SUPPORT OFFICES

United States

GDB User Support
Applied Research Laboratory
William H. Welch Med. Library
Johns Hopkins University
2024 E. Monument Street
Baltimore, MD 21205-2100
410/955-7058
Fax: 410/614-0434
Internet: help@welch.jhu.edu

The Help Line is staffed from 9 a.m. to 5 p.m. EST for information on accounts and training courses, technical support, and data questions. Calls received after hours will be forwarded to the appropriate voice mail and returned as soon as possible. To obtain a user's local Sprint-Net (Telenet) number for locations within the United States: 800/736-1130.

United Kingdom

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Calendar of Genome Events* (acronyms, p. 16)

April

18-20. 2nd Int. Chromosome 9 Workshop; Cape Cod, MA [D. Kwiatkowski, 617/278-0384, Fax: /734-2248]

18-21. *3rd Int. Workshop on Human Chromosome 5; Laguna Beach, CA [J. Wasmuth, 714/856-7067, Fax: /725-2688]

21-23. 1st Central/Eastern European Conf. on Biotechnology and Business; Prague [SCE, 212/998-7171, Fax: /995-3139]

23-24. 4th Int. Human Chromosome 21 Workshop; Paris [J. Delabar, (Int.) 33/1-42-730-960, Fax: -659]

26-27. 11th Ann. ATCC Biotechnology Patent Conf.; Washington, DC [ATCC, 301/231-5566]

May

2-4. 1st Int. Workshop on Chromosome 8; Vancouver, Canada [S. Wood, 604/822-6830, Fax: -5348]

5-7. IndustryTech '93: Technology Transfer Conf.; Kansas City, MO [R. Fippinger, 708/990-2070, Fax: -2077]

6-9. ESGH 25th Ann. Meeting; Barcelona, Spain [Secretary, (Int.) 34/3453-9289, Fax: -2494]

9-12. AMIA 1993 Spring Congress; St. Louis [AMIA, 301/657-1291, Fax: -1296]

9-12. *4th Ann. X Chromosome Workshop; St. Louis [M. Thomas, 314/362-7259, Fax: -1232]

12-16. Genome Mapping & Sequencing; Cold Spring Harbor, NY [CSHL, 516/367-8346, Fax: -8845]

14-15. 4th Int. Workshop on Chromosome 3; Groningen, Netherlands [C. Buys, (Int.) 31/50-632-925, Fax: -947]

16. Chromosome 3 & Cancer; Groningen, Netherlands [see contact: May 14-15]

16-17. *National Advisory Council for Human Genome Research; Bethesda, MD [J. Ades, 301/402-2205, Fax: -2218]

19-22. 84th Annual Meeting of AACR; Orlando, FL [AACR, 215/440-9300, Fax: -9313]

20. †Nancy Wexler: Long Day's Journey into Night—Search for the Huntington's Disease Gene; Bethesda, MD [NCHGR Lecture Series, C. Dahl, 301/402-0838]

20-22. 1st Int. Workshop on Chromosome 7; Marburg, Germany [K.-H. Grzeschik (Int.) 49/6421-28-4080, Fax: -5630]

24-25. 3rd Workshop on Int. Cooperation for the Human Genome Project: Legal Aspects; Bilbao, Spain [J. Sanchez-Asian, (Int.) 34/6-36-98500, Fax: -01453]

June

2-4. ICES-ELPHO '93; Sandefjord, Norway (Preliminary Congress Workshops: June 1) [N. Solum, (Int.) 47/2-868-226, Fax: -303]

2-9. Symposium: DNA & Chromosomes; CSHL [see contact: May 12-16]

10-12. 1st Int. Chromosome 14 Workshop; Toronto [D. Cox, 416/813-6384, Fax: -4931]

17. †Jasper Rine: Dog Genome Initiative—Towards the Genetics of Morphology and Breed Traits; Bethesda, MD [see contact: May 20]

21-23. 2nd Int. Workshop on Chromosome 6; Berlin [A. Ziegler, (Int.) 49/30-3035-2617, Fax: -3778]

26-29. Human Gene Therapy; Washington, DC [NYAS, 212/838-0230, Fax: -5640]

July

7-9. 1st Int. Conf. on Intelligent Systems for Molecular Biology; Bethesda, MD [J. Shavlik, 608/262-7784, Internet: *ismb@nlm.nih.gov*]

10-11. Chromosome 4 Workshop; Stanford, CA [R. Myers, 415/476-8138, Fax: -8217]

12-26. *Open Problems in Computational Molecular Biology: 3rd Int. Workshop; Telluride, CO [A. Konopka, 301/846-5396]

19-20. 2nd Int. Workshop on Chromosome 18; Nijmegen, Netherlands [A. Geurts van Kessel, (Int.) 31/80-614105, Fax: -542151]

31-Aug. 4. DNA Damage: Effects on DNA Structure and Protein Recognition; NYAS, Burlington, VT (poster abstracts by May 1) [see contact: June 26-29]

August

3-6. 6th Int. Workshop on the Fragile X and X-Linked Mental Retardation; Cairns, Australia [G. Sutherland, (Int.) 61/8-204-7284, Fax: -7342]

6-10. Sci. Innovation 1993: New Techniques in Biomolecular Research; Boston [AAAS, 202/326-6450, Fax: /289-4021]

9-13. STM '93: Int. Conf. on STM; Beijing, China [C. Bai, (Int.) 86/1-256-8158, Fax: -9564]

15-21. 17th Int. Congress of Genetics; Birmingham, UK [D. Smith, (Int.) 44/21-414-5888, Fax: -3850]

17-22. MacroMolecules, Genes, and Computers: Chapt. Three; Waterville Valley, NH [D. Macden, 415/570-6667, x8803, Fax: /572-2743]

24-29. Molecular Genetics of Bacteria & Phages; CSHL [see contact: May 12-16]

29-Sept. 3. *Artificial Intelligence and the Genome at IJCAI '93; Chambéry, France [J.-G. Ganascia, (Int.) 33/1-4427-4723, Internet: *ganascia@laforia.ibp.fr*]

September

8-12. Eukaryotic DNA Replication; CSHL [see contact: May 12-16]

9-13. *E. Coli* Genome Meeting; Madison, WI [M. Ellingson, 608/262-2755, Fax: -3453]

October

5-9. ASHG 43rd Annual Meeting; New Orleans (abstract deadline: June 1) [M. Ryan, 301/571-1825, Fax: /530-7079]

13-16. DNA: The Double Helix. Forty Years: Perspective and Prospective; NYAS, Chicago (poster deadline: July 2) [see contact: June 26-29]

23-27. Genome Sequencing and Analysis V; Hilton Head, SC [S. Wallace, 301/216-9567, Fax: /977-7233]

November

14-17. HGM 93 Workshop; Kobe, Japan [HGM Secretariat, (Int.) 81/6-454-4811, Fax: -4711] ◊

Training Calendar**

May

3-8. cDNA Library Techniques; LTI, Germantown, MD [L. Kerwin, 800/952-9166, Fax: 301/258-8212]

5. Intro. to PCR; Philadelphia [BTP, 800/821-4861, Fax: 515/232-8306]

6-7. Basic Cloning and Hybridization Techniques; BTP, Philadelphia [see contact: May 5]

10-11. GDB/OMIM Training Courses [see schedule, p. 13]

10-14. Recombinant DNA Methodology; Columbia MD [Exon-Intron, Inc., 410/730-3984, Fax: -3983]

10-14. Recombinant DNA Methodology; Washington, DC [CATCMB/CUA, 202/319-6161, Fax: -4467]

17-18. Clinical Applications of PCR; BTP, Durham, NC [see contact: May 5]

17-21. *Introductory Linkage Course; New York [K. Montague, 212/960-2507, Fax: /568-2750]

17-21. Advanced Topics in Recombinant DNA; Exon-Intron, Inc., Columbia, MD [see contact: May 10-14]

17-21. PCR Techniques; LTI, Germantown, MD [see contact: May 3-8]

20-21. Quantitative RNA-PCR; BTP, Durham, NC [see contact: May 5]

22-24. PCR Techniques; CATCMB/CUA, Washington, DC [see contact: May 10-14]

23-28. Genome Research into Cancer and Genetic Disease; Leiden, Netherlands [P. Osseweijer, (Int.) 31/15-785140, Fax: -782355]

24-25. DNA Sequencing without Radioactivity; BTP, Durham, NC [see contact: May 5]

25-28. DNA Sequencing; CATCMB/CUA, Washington, DC [see contact: May 10-14] ■

*Attendance at meetings listed with asterisk is either limited or restricted. Dates may change; check with contact person.

**Dates and course status may change, and courses may also be offered at other times and places; check with contact person.

†NCHGR-funded event.

For Your Information

June

6-12. Kennedy Institute of Ethics 19th Annual Intensive Bioethics Course; Washington, DC [D. Michutka, 202/687-6771]

6-19. In Vitro Mutagenesis; Chapel Hill, NC [W. Litaker, 919/966-1730, Fax: -6821]

7-8. Basic IVD Approval Process; San Francisco, [BioConferences Int., Inc., 301/652-3072]

7-11. Expression of Recombinant DNA in Mammalian Cells; CATCMB/CUA, Washington, DC [see contact: May 10-14]

7-11. Recombinant DNA: Techniques & Applications; Rockville, MD [ATCC, 301/231-5566, Fax: /770-1805]

8-9. Quantitative RNA-PCR; BTP, Lincoln, NE [see contact: May 5]

9-11. Recombinant DNA for Chemists; Washington, DC [ACS, 800/227-5558 or 202/872-4508, Fax: -6336]

13-26. Human Gene Mapping and Sequencing; Salt Lake City, UT [Genome Tech. Workshop, 801/585-5606, Fax: /581-7796]

14-18. Recombinant DNA Techniques I; LTI, Germantown, MD [see contact: May 3-8]

14-25. Workshops for Secondary School Biology Teachers: Project Genetics; Winter Park, FL [J. Hendrix, 800-537-9604]

15-18. PCR/Cycle DNA Sequencing; ATCC, Rockville, MD [see contact: June 7-11]

21-25. Recombinant DNA and PCR Methods for Diagnosis of Microbial and Neoplastic Disease; CATCMB/CUA, Washington, DC [see contact: May 10-14]

21-26. Recombinant DNA Techniques II; LTI, Germantown, MD [see contact: May 3-8]

21-26. Natl. HGP Workshop for Secondary Science Teachers; Kansas City [D. Collins, Fax: 913/588-3995]

27-July 2. Chromatin and Transcription; Copper Mountain, CO (application deadline: April 16) [FASEB, 301/530-7093, Fax: -7014]

28-July 2. In Situ Hybridization; CATCMB/CUA, Washington, DC [see contact: May 10-14]

July

3-8. Restriction Endonucleases and Modification Methyltransferases: Structures and Mechanisms; FASEB, Saxtons River, VT [see contact: June 27-July 2]

5-25. *Arabidopsis* Molecular Genetics; Cold Spring Harbor, NY [CSHL, 516/367-8346, Fax: -8845]

6-10. DNA-Binding Proteins/Transcriptional Regulators; CATCMB/CUA, Washington, DC [see contact: May 10-14]

12-16. *Genome Technology and its Implications: A Hands-On Workshop for Educators; Ann Arbor, MI (also offered Aug. 16-20) [P. Gregory, 313/747-2738, Fax: /763-4692]

12-16. Protein & Nucleic Acid Separation Techniques; CATCMB/CUA, Washington, DC [see contact: May 10-14]

18-31. Transcription; Chapel Hill, NC [see contact: June 6-19] ♦

U.S. Genome Research Funding Guidelines

Note: Investigators wishing to apply for NIH and DOE funding are urged to discuss their projects with agency staff before submitting proposals.

NIH National Center for Human Genome Research (NCHGR)

Application receipt dates:

- R01, P01, R21, R29, P30, P50, K01,* and R13 grants – February 1, June 1, and October 1.
- Individual postdoctoral fellowships and institutional training grants – January 10, May 10, and September 10.
- Small Business Innovation Research Grants (SBIR: firms with 500 or fewer employees) – April 15, August 15, and December 15.
- Research supplements for under-represented minorities – applications are accepted on a continuing basis.
- Requests for Applications (RFAs) – receipt dates are independent of the above dates. Notices will appear in *HGN* and other publications.

*Expedited review possible. Check with NCHGR during application development phases.

Program announcements are listed in the weekly *NIH Guide for Grants and Contracts*,* which is available through

- Hard-copy subscription: call 301/496-7441.
- Electronic version (E-Guide): Access through one of the following methods.
 1. Institutional Hubs. A designee receives automatic updates and distributes them locally to researchers. To use this NIH-preferred method, send a message naming the responsible person to Rebecca Duvall (BITNET: q2c@nihcu, Internet: q2c@cu.nih.gov).
 2. NIH Grant Line (also known as DRGLINE). User reads electronic bulletin board for weekly updates. Connection is through a modem, and a new feature allows files to be transmitted rapidly via BITNET or Internet. For more information, contact John James (301/496-7554 or BITNET: zns@nihcu).

*Full text of RFAs listed in the NIH grants guide may be obtained from either of the two electronic sources or from NIH NCHGR in Bethesda, Maryland (301/496-0844).

DOE Human Genome Program – Proposals Due July 15

Solicitations for proposals were announced in the *Federal Register* 58(30), 8746-48 and in *Science* and other publications. Preproposals are due in April; proposals are due July 15.

For funding information or general inquiries, contact the program office via

- 301/903-6488, Fax: -8521, or Internet: #genome%er@mailgw.er.doe.gov or genome@oerv01.er.doe.gov

SBIR Grants

DOE also invites small business firms to submit grant applications addressing the human genome topic of SBIR programs, which are designed to strengthen innovative firms in research and development and to contribute to the growth and strength of the nation's economy. Applications are invited in the following three subtopics only: (1) Development of Improved DNA Sequencing Technologies; (2) Improvements in Genetic Data Storage, Processing, and Analysis; and (3) Development of Innovative Materials or Dissemination Techniques to inform students and the lay public about benefits, opportunities, and challenges arising from the Human Genome Project. For more information, contact

- Samuel Barish; SBIR Program Manager, ER-16; DOE; Washington, DC 20585 (301/903-5707).

Human Genome Distinguished Postdoctoral Fellowships

Most recent deadline: February 1. For further information, contact

- Linda Holmes, Oak Ridge Institute for Science and Education (615/576-4805).♦

¶ Genome-Related Publication

Gnome News, published quarterly by the U.K. Human Genome Mapping Project (HGMP), reports news from the HGMP Resource Center; information on genome research and relevant databases and software; descriptions of computing courses, services, and facilities; and listings of resources related to humans and model organisms. Announcements of workshops and meetings of interest to the genome community are included, along with reference library news and Genome Data Base updates. [Subscriptions available without charge from Christine Bates; HGMP Resource Center; Clinical Research Center; Watford Road, Harrow, HA13UJ (Int. 44-81/869-3446, Fax: -3807).]♦

